

GenCore version 5.1.4-p5.4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:28:24 ; Search time 29.3732 Seconds

(without alignments)
1816.682 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_198

Perfect score: 1038
Sequence: 1 QGGTSPRCDCAGDFHKKIG.....CPTSTLGCSPRCACAVCGMR 174

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O/cgn2.1/USPTO.spool/US0999334/runat.27032003_115457_15378/app_query.fasta.1.2346
-DB=Issued_Patents_NA -QPM=firstap -SUFRTX=ini -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdl
-LIST=45 -DOCALLIGN=200 -THR.SCORE=pcr -THR.MAX=100 -THR.MIN=0 -ALIGN=15
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-NO.XLPXY -NO.MAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:*
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5: /cgn2.6/prodata/1/ina/PCPUS.COMB.seq:*
6: /cgn2.6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1038	100.0	1254	3	US-08-915-469-3 Sequence 3, Appl1
2	1038	100.0	1634	4	US-08-928-069-11 Sequence 11, Appl1
3	1038	100.0	1634	4	US-08-928-069-11 Sequence 9, Appl1
4	1038	100.0	1783	3	US-08-815-469-1 Sequence 1, Appl1
5	950	91.5	1438	4	US-08-928-069-5 Sequence 5, Appl1
6	950	91.5	1438	4	US-08-928-069-5 Sequence 5, Appl1
7	666	64.2	433	4	US-08-828-683A-2 Sequence 2, Appl1
8	666	64.2	433	4	US-08-828-683A-2 Sequence 2, Appl1
9	212.5	20.5	1049	4	US-08-804-166-1 Sequence 1, Appl1
10	212.5	20.5	1049	4	US-08-804-166-1 Sequence 1, Appl1
11	211	20.3	1956	2	US-08-910-991-1 Sequence 10, Appl1
12	205.5	19.8	1301	4	US-08-804-166-7 Sequence 7, Appl1

13	205.5	19.8	1301	4	US-08-910-991-7 Sequence 7, Appl1
14	205	19.7	600	2	US-08-050-319B-47 Sequence 47, Appl1
15	205	19.7	600	2	US-08-465-982-47 Sequence 47, Appl1
16	203.5	19.6	1202	4	US-08-804-166-3 Sequence 3, Appl1
17	203.5	19.6	1202	4	US-08-910-991-3 Sequence 3, Appl1
18	203	19.6	2062	1	US-08-050-319B-24 Sequence 24, Appl1
19	203	19.6	2062	2	US-08-465-982-47 Sequence 24, Appl1
20	203	19.6	2161	4	US-09-106-038A-1 Sequence 1, Appl1
21	203	19.6	2175	1	US-09-505-250-3 Sequence 3, Appl1
22	203	19.6	2175	1	US-08-321-668-1 Sequence 1, Appl1
23	203	19.6	2175	1	US-08-837-941-1 Sequence 1, Appl1
24	203	19.6	2175	1	US-08-126-016-1 Sequence 1, Appl1
25	203	19.6	2175	4	US-08-054-970-1 Sequence 1, Appl1
26	203	19.6	6889	5	US-08-286-740-2 Sequence 2, Appl1
27	203	19.6	6889	5	PCT-US95-09576-2 Sequence 2, Appl1
28	203	19.6	6886	2	US-08-627-151A-6 Sequence 6, Appl1
29	201	19.4	1147	4	US-08-804-166-5 Sequence 5, Appl1
30	201	19.4	1147	4	US-08-910-991-5 Sequence 5, Appl1
31	200.5	19.3	483	4	US-09-326-394-1 Sequence 1, Appl1
32	200.5	19.3	1478	4	US-09-149-922-6 Sequence 6, Appl1
33	191	18.4	543	4	US-09-513-007-3 Sequence 3, Appl1
34	191	18.4	2440	4	US-09-513-007-1 Sequence 1, Appl1
35	190	18.3	1724	5	PCT-US96-12374-1 Sequence 1, Appl1
36	189	18.2	1724	4	US-08-509-024-1 Sequence 1, Appl1
37	189	18.2	1724	4	US-09-333-279-1 Sequence 1, Appl1
38	182	17.5	579	4	US-09-146-950-3 Sequence 3, Appl1
39	182	17.5	591	4	US-09-146-950-19 Sequence 19, Appl1
40	182	17.5	1596	4	US-09-146-950-17 Sequence 17, Appl1
41	182	17.5	1929	4	US-08-146-950-1 Sequence 1, Appl1
42	182	17.5	4622	4	US-08-509-024-6 Sequence 6, Appl1
43	182	17.5	4622	4	US-09-333-279-6 Sequence 6, Appl1
44	170.5	16.4	477	1	US-08-050-319B-53 Sequence 53, Appl1
45	170.5	16.4	477	2	US-08-465-982-53 Sequence 53, Appl1

ALIGNMENTS

RESULT 1
US-08-915-469-3
Sequence 3, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREMITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO. 6153402 yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285

FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-08-815-469-3

Alignment Scores:
Pred. No.: 3, 22e-86 Length: 1254
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-08-815-469-3 (1-1254)

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OY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 73 CAGGGGGGCGCTGTAAGCCCCAGAGGTGAGTGTGCGGGTACTTCCACAGAAGATTGGT 132
OY 21 LeuPheCysArgGlyCysProAlaGlyHisLysLeuLysAlaProCysThrGluPro 40
Db 133 CTGTTTGTTCAGAGGCTGCCAGGGGGCACTACTGAGGCCCTTGCACGGAGGCC 192
OY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 193 TGGGGAACCTCCACCTGCTGTGTGTCGCCAAGACACCTTCTGGCGTGGAGAACCC 252
OY 61 HisAsnSerGluCysAlaValArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 253 CATAATTTCGAATGTCCTCCGCTGCGCTGTGATGACAGGCGCTCCAGGTGGCGTG 312
OY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 313 GAGAACTGTTCAAGAGTGGCCGACACCCGCTGTGGCTGTAAAGCAGGCTGGTTTGGAG 372
OY 101 CysGlnValSerGlnCysValSerSerSerProPheThrCysGlnProCysLeuAspCys 120
Db 373 TCCAGAGTACGCAATGTCTGACAGCTTACCTTCTACTGTGCAACCATGCTAGACTGC 432
OY 121 GlyAlaLeuHisArgHisLysThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 433 GGGGCGCTTCACCGCACACACAGCGCTTCTCCCGAAGATACACTGTGGAGCC 492
OY 141 CysLeuProGlyPheThrGlnHisLysGlyCysValSerCysProThrSerThrLeu 160
Db 493 TCCCTGCTCCGCTTATGATGACATGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 552
OY 161 GlySerCysProGluArgCysAlaValAlaValCysGlyTrpArg 174
Db 553 GGGAGCTGTCCAGAGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 594
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RESULT 2
US-08-928-069-11

Sequence 11, Application US/089928069

Patent No. 6462176

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-3 POLYPEPTIDE

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

US-08-928-069-11

Alignment Scores:
Pred. No.: 4, 57e-86 Length: 1634
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-08-928-069-11 (1-1634)

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OY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 161 CAGGGGGGCGCTGTAAGCCCCAGAGGTGAGTGTGCGGGTACTTCCACAGAAGATTGGT 220
OY 21 LeuPheCysArgGlyCysProAlaGlyHisLysLeuLysAlaProCysThrGluPro 40
Db 221 CTGTTTGTTCAGAGGCTGCCAGCGGGGCACTACCGAAGGCCCTTGCACGGAGGCC 280
OY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 261 TCGGCAACTCTCACCTGCTGTGTGTGTCGCCAAGACACTTCTTGGCTGGGAGAACAC 340
OY 61 HisAsnSerGluCysAlaValArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 341 CATAATTTCGAATGTCCTCCGCTGCGCTGTGATGACAGGCGCTCCAGGTGGCGCTG 400
OY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 401 GAGAACTGTTACAGAGTGGCCGACACCGCGTGTGGCTGTAAAGCAGGCTGGTTTGGAG 460
OY 101 CysGlnValSerGlnCysValSerSerSerProPheThrCysGlnProCysLeuAspCys 120
Db 461 TCCAGAGTCAACCAATGTGTAGACAGTTACCTTCTACTGCTCAACCATGCTAGACTGC 520
OY 121 GlyAlaLeuHisArgHisLysThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 521 GGGGCGCTGTCCAGCGCACACAGGCTACTCTGTTCCTCCGCAAGATACACTGTGGAGCC 580
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QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 581 TGCTGCTGCTCTATGAAACATGGCGATGGCTGCTGCTGCCACGACGACCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTTParg 174
DB 641 GGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGCTGGAGG 682

RESULT 3
US-08-828-683A-9
: Sequence 9, Application US/08828683A
: Patent No. 6469144
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Minipatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/828,683A
: FILING DATE: 31-Mar-1997
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/625328
: FILING DATE: 1-Apr-1996
: APPLICATION NUMBER: 08/710802
: FILING DATE: 23-Sep-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Marschang, Diane L.
: REGISTRATION NUMBER: 35,600
: REFERENCE/DOCKET NUMBER: P1007P1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5416
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1634 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-828-683A-9

Alignment Scores:
Pred. No.: 4.57e-86 Length: 1634
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-08-828-683A-9 (1-1634)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysValGlyAspPheHisGlyTTParg 20
DB 161 CAGGGCGGCACTCGTAGGCCAGGCTGTACTGTGCCGTGACTTCCACAAAGAGTTTGT 220
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 221 CTGTTTGTTCAGAGGCTGCCAGCGGGGAGACTACCTGAAGGCCCTTGCACGGAGGCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTTPGluAsnHis 60

DB 281 TGGCGCAATCCACCTGCTTGTGTGTGCCCAAGACACCTTCTTGCGGAGAACAC 340
QY HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 341 CATATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGACAGAGCTCCACAGTGGCGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTTPPheValGlu 100
DB 401 GAGAACTGTCCAGAGTGGCGGACACCGCTGTGCTGTAAGCCAGAGCTGGTTGTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 461 TGCCAGGTCACCAATGTGTACAGCAGTTCACCTTCTACTGCAACATGCTTACAGCTGC 520
QY 121 GlnAlaLeuHisArgHisThrArgLeuLeuCysSerArgAspThrAspCysGlyThr 140
DB 521 GGGGCCCTGCACCGCCACACAGGCTACTGTCTCCCGAGATGACTGAGTGGAGCC 580
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 581 TGCTGCTGCTCTATGAAACATGGCGATGGCTGCTGCTGCCACGACGACCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTTParg 174
DB 641 GGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGCTGGAGG 682

RESULT 4
US-08-815-469-1
: Sequence 1, Application US/08815469
: Patent No. 6153402
: GENERAL INFORMATION:
: APPLICANT: Yu, Guo-Liang
: APPLICANT: Ni, Jian
: APPLICANT: Dixit, Vishva
: APPLICANT: Gentz, Reiner L.
: APPLICANT: Dillon, Patrick J.
: TITLE OF INVENTION: Death Domain Containing Receptors
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
: STREET: 1100 New York Ave., NW, Suite 600
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/815,469
: FILING DATE: HEREWITHE
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: No. 6153402 Yet Assigned
: FILING DATE: 06-FEB-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/028,711
: FILING DATE: 17-OCT-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/013,285
: FILING DATE: 12-MAR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Steffe, Eric K.
: REGISTRATION NUMBER: 36,688
: REFERENCE/DOCKET NUMBER: 1488, 0310003/EKS/KRM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1783 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 198..1481
US-08-815-469-1

Alignment Scores:
Pred. No.: 5,13e-86 Length: 1783
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-08-815-469-1 (1-1783)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 303 CAGGGCGGCACTCTGACCCCGAGGTGTGACTGTGCGGTGACTTCCACAGAGATTGGT 362
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 363 CTGTTTGTTCAGAGAGCTGCGCCAGCGGGGACTACTGAAAGGCCCTTGCACGAGGCC 422
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 423 TGGCGCAACACCACTGCTGTGTGTGCCAAGACACTTCTGGCTGGGAGAACAC 482
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 483 CATTAATCTGAATGTGCGCTGCGCAGGCTGTGATGAGAGGCGCTCCAGGTGCGCTG 542
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 543 GAGAACTGTCAGAGTGGCGGACACCGCGCTGTGCTGAAGCCAGCTGTGTGGAG 602
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 603 TGGCAGGTCCAGCAATGTGCACAGTTCACCTTCACTGCAACACATGCTAGACTGC 662
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 663 GGGGCCCTGACCGCCACACAGCGCTACTGTGTCCGAGAGATGACTGTGGAGCC 722
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 723 TGCCTGCTGGCTTCTATGAACATGGGAGATGGCTGTGCTGCCGCCACGAGACCTTG 782
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
DB 783 GGGAGCTGTCCAGAGCGCTGTCGCCGTGCTGCGCTGGAGG 824

RESULT 5

US-08-928-069-5

Sequence 5, Application US/08928069
Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928, 069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschanz, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

US-08-928-069-5

Alignment Scores:
Pred. No.: 4.3e-78 Length: 1438
Score: 950.00 Matches: 163
Percent Similarity: 93.68% Conservative: 0
Best Local Similarity: 93.68% Mismatches: 3
Query Match: 91.52% Indels: 8
DB: 4 Gaps: 1

US-09-993-234-6_COPY_25_198 (1-174) x US-08-928-069-5 (1-1438)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 449 CAGGGCGGCACTCTGACCCCGAGGTGTGACTGTGCGGTGACTTCCACAGAGATTGGT 508
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 509 CTGTTTGTTCAGAGAGCTGCGCCAGCGGGGACTACTGAAAGGCCCTTGCACGAGGCC 568
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 569 TGGCGCAACCACTGCTGTGTGTGCCAAGACACTTCTGGCTGGGAGAACAC 628
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 629 CATTAATCTGAATGTGCGCTGCGCAGGCTGTGATGAGAGGCGCTCCAGGTGCGCTG 688
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 689 GAGAACTGTCAGAGTGGCGGACACCGCGCTGTGCTGAAGCCAGCTGTGTGGAG 748
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 749 TGCAGGTCCAGCAATGTGTGACAGTTCACCTTCTAATGCAACATGCTTACACTGC 808
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 809 GGGGCCCTGACCGCCACACAGCGCTACTGTGTCCGAGAGATGACTGTGGAGCC 868
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 869 TGCCTGCTGGCTTCTATGAACATGGGAGATGGCTGTGCTGCCGCCACGAGATTCCTA 928
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
DB 929 -----GCTGTCGTGGAGTGGAGG 946

RESULT 6

US-08-828-683A-5
Sequence 5, Application US/08828683A

Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION NUMBER: US/08/828,683A
APPLICATION NUMBER: <Unknown>
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-828-683A-5
Alignment Scores:
Pred. No.: 4.3e-78 Length: 1438
Score: 950.00 Matches: 163
Percent Similarity: 93.68% Conservative: 0
Best Local Similarity: 93.68% Mismatches: 3
Query Match: 91.52% Indels: 8
DB: 4 Gaps: 1
US-09-993-234-6_COPY_25_198 (1-174) x US-08-828-683A-5 (1-1438)
QY 1 GlnGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 449 CAGGGCGGCGACTGTAAGCCAGGAGTGACTGTGCGGCTGACTCCACAAGAAGTTGGT 508
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 509 CTGTTTGTTCAGAGGCTGCCAGCGGGGACATACCTGAAGGCCCTTCGACGAGAGGCC 568
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 569 TGCAGCACTCCACCTGCTGTGTGCCCAAGACACCTTCTGGCTGGAGAACAC 628
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 629 CATATTTCTGAATGTGCGGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGAGTGGCGCTG 688
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
DB 689 GAGAACTGTTCAGAGTGGCGGACACCGCTGTGGCTTAAGCCAGGCTGTTTGTGTAG 748
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120

DB 749 TGCCAGGTACGCAATGTGTGAGCAGTTCACCTTCTACTGCCAACCATGCTTAGACTGC 808
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 809 GGGGCGCTGACACCGCCACACAGGCTACTGTGTCCGAGAGATATGACTGTGGACC 868
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 869 TGCCCTGCGCTTCTATGAACATGGCATGGCTGCTGCTGCCCCACGTAATTCCTA 928
QY 161 GlySerCysProGlnArgCysAlaValCysGlyTyrParg 174
DB 929 -----GCTGTGCGGATGAGAG 946
RESULT 7
US-08-928-069-2
Sequence 2, Application US/08928069
Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-928-069-2
Alignment Scores:
Pred. No.: 8.2e-53 Length: 433
Score: 666.00 Matches: 127
Percent Similarity: 93.48% Conservative: 2
Best Local Similarity: 92.03% Mismatches: 5
Query Match: 64.16% Indels: 5
DB: 4 Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x US-08-928-069-2 (1-433)
QY 2 GlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGlyLeu 21
DB 22 GCGGCGACTGTAAGCCAGGAGTGACTGTGCGGCTGACTCCACAAGAAGTTGGTGTG 81
QY 22 PheCysCysArgGlyCysProAla-GlyHisTyrLeuLysAlaProCysThrGluProCys 41

DB 82 TTTTGTGCAAGGCTGCCCCAGCGGGCACTTACCTGAGGCCCCCTTGACAGGACCCCTG 141
QY 41 sglYasnSerThrcysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHisI 61
DB 142 CGC-AACTCCACCTGCTTGTGTGTCGCCCAAGACACCTTCTTGCGCTGGAGAACCA 200
QY 61 sasnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeuG 81
DB 201 TAAATTCGAATGTGCCCCCTGCGAGGCTGTGATGAGCAGCGCTCCAGTGGCGCTGGA 260
QY 81 uasnCysSerAlaValAlaAspThrArgCysGlyCysIysProGlyTrpPheValGluC 101
DB 261 GAAGTGTTCACAGCTGGCGGACACCGCTGTGCTGTAGCAGGCGGTGTGTGGAGTG 320
QY 101 sglN-ValSerGlnCysValSerSer-SerProPheTyrcysGlnProCysLeuAspCys 120
DB 321 CCAGGCTCAGCAATGTGCTCAGCAGTTTCAACCTTCTAATGCCAACATGCTGACTGC 380
QY 121 gLYAlaLeuHisArgHisThrArgLeuLeuCys-SerArgArgasp 135
DB 381 GGGGCCCTGCACGACACACGCGCTAATNTGTTTCCCGCAGAGAT 426

RESULT 8

US-08-828-683A-2
; Sequence 2, Application US/08828683A
; Patent No. 6468144

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPalin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-828-683A-2

Alignment Scores:

Pred. No.: 8,2e-53 Length: 433
Score: 666.00 Matches: 127
Percent Similarity: 93.48% Conservative: 2
Best Local Similarity: 92.03% Mismatches: 5
Query Match: 64.16% Indels: 5

DB: 4 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-08-828-683A-2 (1-433)
QY 2 gLYAlaLeuHisArgHisThrArgLeuLeuCys-SerArgArgasp 135
DB 22 GCGGCACTGTAGCCCCCAGAGGTGTGACTGTGCGGTACTTCCAGAAAGATGTGCTG 81
QY 22 PheCysArgGlyCysProAla-GlyHisTyrcysAlaProCysThrGluProC 41
DB 82 TTTTGTGCAAGGCTGCCCCAGCGGGCACTTACCTGAAAGCCCCCTTGCACGAGCCCTG 141
QY 41 sglYasnSerThrcysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHisI 61
DB 142 CGC-AACTCCACCTGCTTGTGTGTCGCCCAAGACACCTTCTTGCGCTGGAGAACCA 200
QY 61 sasnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeuG 81
DB 201 TAAATTCGAATGTGCCCCCTGCGAGGCTGTGATGAGCAGGCGCTCCAGTGGCGCTGGA 260
QY 81 uasnCysSerAlaValAlaAspThrArgCysGlyCysIysProGlyTrpPheValGluC 101
DB 261 GAAGTGTTCACAGCTGGCGGACACCGCTGTGCTGTAGCAGGCGGTGTGTGGAGTG 320
QY 101 sglN-ValSerGlnCysValSerSer-SerProPheTyrcysGlnProCysLeuAspCys 120
DB 321 CCAGGCTCAGCAATGTGCTCAGCAGTTTCAACCTTCTAATGCCAACATGCTGACTGC 380
QY 121 gLYAlaLeuHisArgHisThrArgLeuLeuCys-SerArgArgasp 135
DB 381 GGGGCCCTGCACGACACACGCGCTAATNTGTTTCCCGCAGAGAT 426

RESULT 9

US-08-804-166-1
; Sequence 1, Application US/08804166
; Patent No. 6193972

GENERAL INFORMATION:

APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
TITLE OF INVENTION: Hybrid Proteins
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 22207

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,166
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996

ATTORNEY/AGENT INFORMATION:

NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: CAMPBELL-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 737-3528
TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1049 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 278..1047
US-08-804-166-1

Alignment Scores:
Pred. No.: 7.74e-11 Length: 1049
Score: 212.50 Matches: 52
Percent Similarity: 42.26% Conservative: 19
Best Local Similarity: 30.95% Mismatches: 82
Query Match: 20.47% Indels: 15
Gaps: 6

US-09-993-234-6_COPY_25_198 (1-174) x US-08-804-166-1 (1-1049)

OY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 329 CAAGAGGCGAGTGGCGATGCTGTGTCCCAAGGAAATATATATCCACCCTCAAAATAT 388
OY 21 LeuPheCysCysArgGlyCysProAlaGlyHisLysIleLysAlaProCysThrLysPro 40
DB 389 TCCATTTCCTGTACCAAGTCCCAAGAACCTACTGTACATGACTGTCAGGCCG 448
OY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 449 GGGCAGATGAGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 508
OY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 509 CTCAGA---CACTGCTCAGTGGCTCCCAATGCGAAGAAATGCGTGCAGTGAGATC 565
OY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
DB 566 TCTTCTTGCACAGTGGACCGGACCGGACCGTGTGCTGCACAGAGAACCCAGTCCGAT 625
OY 101 Cys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnProCys 117
DB 626 TATTGAGTGAACCTTTTCCAGTGC-----TTCAATTGCGAGCTCTGC 670
OY 118 LeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 137
DB 671 CTCAT---GGGACCGTGCAC-----CTCTCTGCCAGAGAAACAGAACACC 715
OY 138 CysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThr 157
DB 716 GTGTGACCTGCCATGACGAGTTCTTCTTAAGAGAAACGAGTGTCTCTGTCGCGGT 775
OY 158 SerThrLeuGlySerCysProGlu 165
DB 776 GCTGCCCAGGT---TGCCAGAA 796

RESULT 10
US-08-910-991-1
Sequence 1, Application US/08910991
Patent No. 6194177
GENERAL INFORMATION:
APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,991
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/804,166
FILING DATE: 20 February 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CAMPBELL-2B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1049 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 278..1047
US-08-910-991-1

Alignment Scores:

Pred. No.: 7.74e-11 Length: 1049
Score: 212.50 Matches: 52
Percent Similarity: 42.26% Conservative: 19
Best Local Similarity: 30.95% Mismatches: 82
Query Match: 20.47% Indels: 15
DB: 4 Gaps: 6

US-09-993-234-6_COPY_25_198 (1-174) x US-08-910-991-1 (1-1049)

OY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 329 CAAGAGGCGAGTGGCGATGCTGTGTCCCAAGGAAATATATATCCACCCTCAAAATAT 388
OY 21 LeuPheCysCysArgGlyCysProAlaGlyHisLysIleLysAlaProCysThrLysPro 40
DB 389 TCCATTTCCTGTACCAAGTCCCAAGAACCTACTGTACATGACTGTCAGGCCG 448
OY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 449 GGGCAGATGAGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 508
OY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 509 CTCAGA---CACTGCTCAGTGGCTCCCAATGCGAAGAAATGCGTGCAGTGAGATC 565
OY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
DB 566 TCTTCTTGCACAGTGGACCGGACCGGACCGTGTGCTGCACAGAGAACCCAGTCCGAT 625
OY 101 Cys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnProCys 117
DB 626 TATTGAGTGAACCTTTTCCAGTGC-----TTCAATTGCGAGCTCTGC 670
OY 118 LeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 137
DB 671 CTCAT---GGGACCGTGCAC-----CTCTCTGCCAGAGAAACAGAACACC 715
OY 138 CysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThr 157
DB 716 GTGTGACCTGCCATGACGAGTTCTTCTTAAGAGAAACGAGTGTCTCTGTCGCGGT 775

OY 158 SerThrLeuGlySerCysProGlu 165
DB 776 GGTGCCCCAGGT---TGCCAGAA 796

RESULT 11
US-08-762-308-10
; Sequence 10, Application US/08762308
; Patent No. 5925548
; GENERAL INFORMATION:
; APPLICANT: Beutler, Bruce A.
; APPLICANT: Bazzoni, Flavia M.
; TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY
; NUMBER OF SEQUENCES: SIGNAL
; CORRESPONDENCE ADDRESS: 11
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,308
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/224,593
; FILING DATE: 05-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSD:335--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 418-3000
; TELEFAX: 474-7577
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1956 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-762-308-10

Alignment Scores:
Pred. No.: 2,42e-10 Length: 1956
Score: 211.00 Matches: 52
Percent Similarity: 40.23% Conservative: 18
Best Local Similarity: 29.89% Mismatches: 86
Query Match: 20.33% Indels: 18
DB: 2 Gaps: 6

US-09-993-234-6_COPY_25_198 (1-174) x US-08-762-308-10 (1-1956)

OY 3 GlyThrArgSerProArg-----CysAspCysAlaGlyAspPheHisLysLysLeu 19
DB 198 GGTACCGGAGAAAGGATAGCTTGTCGCCAAGAAAGTATGTCATTCTAAGAAC 257

OY 20 GlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGlu 39
DB 258 AATTCGATCTGCTGCGCAACCAAGTGCACAAAGAACCTTCTGAGAGAGACTGTCGAGAT 317

OY 40 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGlnAsn 59
DB 318 CTAGGCGCGGATACAGTCTGACAGGAGTGAAGGAGGACCTTTACGCGTTCCAGAGAT 377

OY 60 HisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAla 79
DB 796 GGTGCCCCAGGT---TGCCAGAA 796

DB 378 TACCTCAGG---CAGTGTCTCAGTTCAGACATGTCGGAAAGAAATGTCGCCAGGTGGAG 434
OY 80 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal 99
DB 435 ATCTCTCTCTGCGCAACGTCAGACAGACACGCTGTGCGCTTGAAG-----479

OY 100 GluCysGlnValSerGlnValSerSerSerProPheTyrCysGlnProCysLeuAsp 119
DB 480 GAGAACAGATTCCACAGCTACCTGAGTGAAGACACACTCCAGTCCGTCGACCTCACCCCC 539

OY 120 CysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGly 139
DB 540 TGC-----TTCAAGCGCACCGTGCACATCCCTGTAGAGAGACTGAGAACACCGTGTGT 593

OY 140 ThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThr 159
DB 594 AACTGCCATCAGAGCTTCTTGTGAGAGAAAGAGAGTGGCTCCCTTGC-----641

OY 160 LeuGlySerCysPro-----GluArgCysAlaAlaValCys 171
DB 642 ---AGCCACTGCAAGAAAGATGAGAGTGTATGAGTGTGTC 680

RESULT 12
US-08-804-166-7
; Sequence 7, Application US/08804166
; Patent No. 6193972
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,166
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,936
; FILING DATE: 20 February 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: CAMPBELL-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1301 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 279..1287
US-08-804-166-7

Alignment Scores:
Pred. No.: 4.49e-10 Length: 1301

Score: 205.50 Matches: 51
Percent Similarity: 40.91% Conservative: 21
Best Local Similarity: 28.98% Mismatches: 83
Query Match: 19.80% Indels: 21
DB: 4 Gaps: 7

US-09-993-234-6_COPY_25_198 (1-174) x US-08-804-166-7 (1-1301)

QY 1 GlnGlyLThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 330 CAAGAGGCGAGTGGCGATAGTGTGTGCCCAAGAAATATATCCACCCCAAAATAT 389
QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 390 TCGATTGCTGTACCAAGTGCACAAAGAACCTTACTGTGCAATGATGATCCAGGCCG 449
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGlnAsnHis 60
DB 450 GGGCAGATACGAGTCCAGGAGGTGTGAGAGCGGCTCTCCACCGCTTCAGAAACCCAC 509
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 80
DB 510 CTCAGA---CACTGCTCAGCTGTGCTCCAAATGCCGAAAGAAATGGGTGAGATC 566
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 567 TCTTCTTGACACAGTGCACCGGACACCGTGTGTGCTGCAGAGAAACAGTACCGGAT 626
QY 101 Cys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnProCys 117
DB 627 TATTGAGTGAACCTTTTCCAGTGC-----TTCAATTTGAGCGCTCTGC 671
QY 118 LeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 137
DB 672 CTCAT---GGACCGGTGCAC-----CTCTCTCCAGAGAAACAGAACACAC 716
QY 138 CysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThr 157
DB 717 GTGTGCACCTGCATGCGATTTCTTCTTAAGAGAAACGATGTGTCTCTGT----- 770
QY 158 SerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys 171
DB 771 -----ACTAAGTGAAGAAAGCCTGAGTGCAGAGATTGTGC 809

RESULT 13

US-08-910-991-7

Sequence 7, Application US/08910991

Patent No. 6194177

GENERAL INFORMATION:

APPLICANT: Campbell, Robert K.

APPLICANT: Jameson, Bradford A.

APPLICANT: Chappel, Scott C.

TITLE OF INVENTION: HYBRID PROTEINS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street N.W., Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 22207

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/910,991

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/804,166

FILING DATE: 20 February 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CAMPBELL-2B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1301 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 279..1287

US-08-910-991-7

Alignment Scores:

Pred. No.: 4.49e-10

Score: 205.50

Percent Similarity: 40.91%

Best Local Similarity: 28.98%

Query Match: 19.80%

DB: 4 Matches: 1301
Conservative: 21
Mismatches: 83
Indels: 21
Gaps: 7

US-09-993-234-6_COPY_25_198 (1-174) x US-08-910-991-7 (1-1301)

QY 1 GlnGlyLThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 330 CAAGAGGCGAGTGGCGATAGTGTGTGCCCAAGAAATATATCCACCCCAAAATAT 389
QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 390 TCGATTGCTGTACCAAGTGCACAAAGAACCTTACTGTGCAATGATGATCCAGGCCG 449
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGlnAsnHis 60
DB 450 GGGCAGATACGAGTCCAGGAGGTGTGAGAGCGGCTCTCCACCGCTTCAGAAACCCAC 509
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 80
DB 510 CTCAGA---CACTGCTCAGCTGTGCTCCAAATGCCGAAAGAAATGGGTGAGATC 566
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QY 101 Cys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnProCys 117
DB 627 TATTGAGTGAACCTTTTCCAGTGC-----TTCAATTTGAGCGCTCTGC 671
QY 118 LeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 137
DB 672 CTCAT---GGACCGGTGCAC-----CTCTCTCCAGAGAAACAGAACACAC 716
QY 138 CysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThr 157
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QY 158 SerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys 171
DB 771 -----ACTAAGTGAAGAAAGCCTGAGTGCAGAGATTGTGC 809

RESULT 14

US-08-050-319B-47

Sequence 47, Application US/08050319B

Patent No. 5633145

GENERAL INFORMATION:

APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbings
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robbings, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..597
US-08-050-319B-47
US-08-050-319B-47
Alignment Scores:
Pred. No.: 1,79e-10 Length: 600
Score: 205.00 Matches: 52
Percent Similarity: 40.688 Conservative: 20
Best Local Similarity: 29.388 Mismatches: 81
Query Match: 19.758 Indels: 24
Gaps: 8
US-09-993-234-6_COPY_25_198 (1-174) x US-08-050-319B-47 (1-600)
QY 3 GlyThrArgSerProArg-----CysAspCysAlaGlyAspPheHisLysIle 19
Db 103 GGGGACAGGAGAGAGATAGTGTGTCCACAGGAAATATATACACCCCTCAAAAT 162
QY 20 GlyLeuPheCysArgGlyCysProAlaGlyHisLysIleValAlaProCysThrGlu 39
Db 163 AATTCGATTTCCTTACCAAGTGCACAAAGAACCTACTGTCAATGATGTCACGGC 222
QY 40 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsn 59
Db 223 CCGGGGCGAGATAGGACTGCAGGAGAGTGTAGAGCGGCTCTCACCCTTCAGAAAC 282
QY 60 HisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAla 79
Db 283 CACCTCACA---CACTGCTCAGCTGCTCCAAATGCCGAAAGGAAATGGCTCAGGTGAG 339
QY 80 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal 99
Db 340 ATCTCTTTCGACAGTGCAGCAGCCGCTGTGTGCTGCAGGAGAAACACAGTACCGG 399
QY 100 GluCys-----GlnValSerGlnCysValSerSerProPheTyCysGlnPro 116
Db 400 CATATTGAGAGTGAACCTTTTCCAGTGC-----TTCAATGTCAGCCTC 444

QY 117 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgAspThr 136
Db 445 TGCCTCAAT---GGGACCGTGCAC-----CTCTCTGCGCAGGAGAAACAGAAC 489
QY 137 AspCysGlyThrCysLeuProGlyPheTyGlnHisGlyAspGlyCysValSerCysPro 156
Db 490 ACCGTGTGACCTGCATGCGAGGTTCCTTCTAAGGAAACGAGTGTCTCTCTCT 546
QY 157 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaValAlaCys 171
Db 547 -----AGTAACTGTAGAAAGCCTGAGTGCACGAACTGTGC 585
RESULT 15
US-08-465-982-47
Sequence 47, Application US/08465982
Patent No. 5863786
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbings
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,982
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319
FILING DATE: 10-May-1993
ATTORNEY/AGENT INFORMATION:
NAME: Robbings, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..597
US-08-465-982-47
US-08-465-982-47
Alignment Scores:
Pred. No.: 1,79e-10 Length: 600
Score: 205.00 Matches: 52
Percent Similarity: 40.688 Conservative: 20
Best Local Similarity: 29.388 Mismatches: 81
Query Match: 19.758 Indels: 24
Gaps: 8
US-09-993-234-6_COPY_25_198 (1-174) x US-08-465-982-47 (1-600)
QY 3 GlyThrArgSerProArg-----CysAspCysAlaGlyAspPheHisLysIle 19
Db 103 GGGGACAGGAGAGAGATAGTGTGTCCACAGGAAATATATACACCCCTCAAAAT 162


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Db 103 GGGGACAGGAGAGAGATAGTGTGTGCCACAGGAAATATATCCACCCTCAAAAT 162
QY 20 GlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGlu 39
Db 163 AATTCGATTGCTGTACCAAGTCCACAAAGAACCTTACTGTACAAATGACTGTCCAGGC 222
QY 40 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsn 59
Db 223 CCGGGGACGAGTACGAGCTGAGGAGAGTGTAGAGCGGCTCTCCACCGCTTCAGAAAAAC 282
QY 60 HisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAla 79
Db 283 CACCTCAGA---CACTGCTCAGCTGCTCCAAATGCGAAAGAAATGGTCAGGTGGAG 339
QY 80 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal 99
Db 340 ATCTCTTCTTGACAGTGGACCGGACACCGTGTGTGCTGCAGAGAAACCAAGACCGG 399
QY 100 GluCys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnPro 116
Db 400 CATTAATTGAGTGAAGAAACCTTTTCCAGTGC-----TTCAATTGCAGCCCTC 444
QY 117 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 136
Db 445 TGCTCTCAAT---GGGACCGTGCAC-----CTCTCTGCACAGAGAAACAGAAC 489
QY 137 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 156
Db 490 ACCGTGTGACCTGCATGCAGTTCCTTTCTAAGAGAAAGAGTGTGTCTCCGT--- 546
QY 157 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys 171
Db 547 -----AGTAACGTGTAGAGAAAGCCTGAGAGTGCACGAAATTGTGTC 585
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Search completed: April 6, 2003, 23:29:46
Job time : 35.3732 secs

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GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:35:34 ; Search time 4846.17 Seconds

(without alignments)
2504.221 Million cell updates/sec

Title: US-09-993-234-6

Perfect score: 2323
Sequence: 1 MEORPRGCCAAVAAALLLVLL.....ERMIGDCVEDLRSLQRGP 417

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlh
-O=/cgn2.1/USPTO/US0993234/runat_27032003_115455_15349/app.query.fasta.1.2346
-DB=GenDb1 -QFMT=fastcap -SUFFIX=trge -MINMATCH=0.1 -LOOPEXT=0 -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=biom62 -TRANS=human4.0.cdi -ALIGN=15 -MODE=LOCAL
-DOCCALIGN=200 -THR.SCORE=PCT -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=tbl -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0993234.cgn.1.1.8534.runat.27032003.115455.15349 -NCPU=6 -ICPU=3
-NO_XIPXY -NO_MMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-NARN.TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenDb1:***
1: gb_da:***
2: gb_htg:***
3: gb_in:***
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10: gb_ro:***
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12: gb_sy:***
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18: em_in:***
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20: em_om:***
21: em_or:***
22: em_ov:***
23: em_pat:***
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25: em_pl:***
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27: em_sts:***
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29: em_vl:***
30: em_htg_hum:***
31: em_htg_inv:***
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33: em_htg_mus:***
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36: em_htg_mam:***
37: em_htg_vrt:***
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40: em_htgo_mus:***
41: em_htgo_other:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2323	100.0	1254	6 AR119657	AR119657 Sequence
2	2323	100.0	1254	9 HS072763	U72763 Human death
3	2323	100.0	1254	9 HS078029	U78029 Human aopto
4	2323	100.0	1254	9 HS094501	U94501 Human lymph
5	2323	100.0	1634	9 HS074611	U74611 Human Apo-3
6	2323	100.0	1662	6 AX055442	AX055442 Sequence
7	2323	100.0	1662	6 AX201344	AX201344 Sequence
8	2312.5	99.5	1257	9 HS094502	U94502 Human lymph
9	2281	98.2	1557	9 HS083597	U83597 Human death
10	2281	98.2	1557	9 HS075380	U75380 Human aopto
11	2271.5	97.8	1355	9 HS094503	U94503 Human lymph
12	2267	97.6	1783	6 AR119656	AR119656 Sequence
13	2254.5	97.1	1743	6 AX331947	AX331947 Sequence
14	2254.5	97.1	1743	9 HSWSL1	Y09392 H.sapiens m
15	2242	96.5	1669	9 AF026070	AF026070 Homo sapi
16	2242	95.9	1250	6 AX150176	AX150176 Sequence
17	2218.5	95.5	1763	9 AF026071	AF026071 Homo sapi
18	2176.5	93.7	1198	9 HS094504	U94504 Human lymph
19	2085.5	89.8	1143	9 HS094510	U94510 Human lymph
20	2016.5	86.8	1119	9 HS094509	U94509 Human lymph
21	1951	84.0	1087	9 HS094505	U94505 Human lymph
22	1644.5	70.8	952	9 HS094506	U94506 Human lymph
23	1575.5	67.8	4811	9 AB051851	AB051851 Homo sapi
24	1556.5	67.0	4825	9 AB051850	AB051850 Homo sapi
25	1556.5	67.0	53962	9 AL158217	AL158217 Human DNA
26	1404.5	60.5	838	9 HS094507	U94507 Human lymph
27	1397	60.1	1665	10 AF329969	AF329969 Mus muscu
28	1255	54.0	1619	10 BC017526	BC017526 Mus muscu
29	1221	52.6	1581	9 AK094463	AK094463 Homo sapi
30	1221	52.6	2053	9 AK094468	AK094468 Homo sapi
31	1150.5	49.5	705	9 HS094508	U94508 Human lymph
32	1051	45.2	809	9 HS094512	U94512 Human lymph
33	1039.5	44.7	816	6 AX335086	AX335086 Sequence
34	1039.5	44.7	816	9 HS083598	U83598 Human death
35	1034	44.5	808	9 HS075381	U75381 Human aopto
36	973	41.9	196368	2 AL772240	AL772240 Mus muscu
37	673	28.0	97483	2 AC118359	AC118359 Rattus no
38	667	28.7	651	9 HS083599	U83599 Human alter
39	636	27.4	18015	10 AF134858	AF134858 Mus muscu
40	415	17.9	2004	4 SSU19994	U19994 Sus scrofa
41	404.5	17.4	1956	10 M50377	M50377 Murine tumo
42	404.5	17.4	2068	10 M60468	M60468 Mouse tumor
43	404.5	17.4	2063	10 X59238	X59238 Murine mRNA
44	404.5	17.4	2086	10 BC004599	BC004599 Mus muscu
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RESULT 1

ALIGNMENTS

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Oy	241	MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr	260
Db	721	ATGAGAGCGTGACCCCAACGACGCCAACCATTGTCCACCTTGACGACAGGCCAACACC	780
Oy	261	LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer	280
Db	781	CTTTACACCTCTGTGCACGACGAGAAGATCTGCACCGCTCCAGCTTGCGTAGAACAC	840
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Oy	301	AspGlnLeuProSerSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer	320
Db	901	GACCAGTGTGCCAGCACAGCTCTGGCCCGCTGCTCGGCCACACTCTGCCAGAGTCC	960
Oy	321	ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuThrAspValMetasp	340
Db	961	CCAGCCGGCTCGCCACGCCATGATGCTGCACCCGGGCCCGAGTCATACGACGATGGAGC	1020
Oy	341	AlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu	360
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Db	1081	ATCGAAGCCGTGGAGGTGGATCGGCGCCCTCCCGACACAGATACAGATGCTCAAG	1140
Oy	381	ArgTrpArgGlnGlnGlnLeuProAlaGlyLeuGlyAlaValTyrlAlaLeuGluThrGmet	400
Db	1141	CGGTGGCGCCACAGACGACGCCGGGGCGTCGGAGCCGCTTACCGCGCCCTGCAGCCCATG	1200
Oy	401	GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro	417
Db	1201	GGGCTGGACGGCTGCTGGAGACATTTGCCACCGCTGCACGCGGCGCCG	1251
RESULT 2			
LOCUS	HSU72763	1254 bp	mRNA linear PRI 15-NOV-1996
DEFINITION	Human death receptor 3 (DR3) mRNA, complete cds.		
ACCESSION	U72763		
VERSION	U72763.1		
KEYWORDS	GI:1669511		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1 (bases 1 to 1254)		
AUTHORS	Chinnaiyan,A.M., O'Rourke,K., Yu,G.-L., Lyons,R.H., Garg,M.,		
	Duan,R., Xing,L., Gentz,R., Ni,J. and Dixlt,V.M.		
TITLE	Signal transduction by DR3, a death domain-containing receptor		
JOURNAL	related to TNFR-1 and CD95		
MEDLINE	97081063		
PUBMED	8875942		
REFERENCE	2 (bases 1 to 1254)		
AUTHORS	Chinnaiyan,A.M., O'Rourke,K., Yu,G.-L., Lyons,R.H., Garg,M.,		
	Duan,R., Xing,L., Gentz,R., Ni,J. and Dixlt,V.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (29-SEP-1996) Pathology, University of Michigan Medical		
FEATURES	School, 1301 Catherine St., Box 0602, Ann Arbor, MI 48109, USA		
Source	Location/Qualifiers		
	1..1254	/organism="Homo sapiens"	
gene	1..1254	/db_xref="taxon:9606"	
CDS	1..1254	/gene="DR3"	
		/gene="DR3"	

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 VGNSTWPTGPETPEALCPQVYTWSDQPSRALGPAAATLSESPAGSPAMMLOPQPO
 LYDVAIDAVPARRMKEFVRLTGLREAEIEAVEIGRFRDOQYEMLKRRWROOQPAIGLA
 VYAALEIRMGLDQCEVDELRSRLORGP*
 BASE COUNT 201 a 420 c 407 g 226 t
 ORIGIN

Alignment Scores:

Pred. No.: 2,646-114 Length: 1254
 Score: 2323.00 Matches: 417
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-09-993-234-6 (1-417) x HS094501 (1-1254)

QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaAlaLeuLeuValLeu 20
 1 ATGGAGACACGGCGCGGGGCTGGCGGGGCGGGCGCGCGCTCTCTGGTGTCTG 60
 QY 21 GYAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
 61 GGGGGCCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
 QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
 121 AAGAGATGTGTCTGTTGTTGTCAGAGAGCTGCCAGCGGGGCGACTACGAAAGCCCTT 180
 QY 61 CysThrGlnProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
 181 TGCAGGAGACCTTGGCGGCACTCCACCTCTGTGTGTGTCACCAACACCTTCTTGCC 240
 QY 81 TPGluAsnHisAsnSerGlyCysAlaArgCysGlnAlaCysAspGlnAlaSer 100
 241 TGGGAGAACACCATATTCATATGTGCCCCCTGCCAGGCTGTATATAGCAGGCTTC 300
 QY 101 GlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
 301 CAGGTGGCGCTGGAGAACTGTCAGAGTGGCGGACACCGGCTGTGCTAAAGCCAGCG 360
 QY 121 TrpPheValGlyCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
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 QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgTrpAspThr 160
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 481 GACTGTGGGACCTGCTGCTGCTCTATGAACATGAGGAGGCTGCGTGCCTGCCCC 540
 QY 181 ThrSerThrLeuGlySerCysProGlyAspGlyCysAlaAlaValCysGlyTrrArgGlnMet 200
 541 ACGAGAGACCTTGGGAGGCTGTCACAGGCGCTGTGCGCTGTGTGTGGAGGCGAGTGG 600
 QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeu 220
 601 TCTGTGGTCCAGTGTCTCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
 QY 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGlnAlaGly 240
 661 ACCTACACATACCCGACACGCTGGGCTCACAAAGCCCTGTATTACTGCATGAGAGCTGGG 720
 QY 241 MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
 721 ATGGAGGCTCTACCCACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
 QY 261 LeuLeuAlaProProAspSerSerGlyLysIleCysThrValGlnLeuValGlyAsnSer 280
 781 CTTTACGACCTCTGACAGCAGTGTGACAGATCTGCACCGCTCAGTGTGTGTGTGTGTGTGT 840

QY 281 TrpThrProGlyTyrProGlyThrGlnGlnAlaLeuCysProGlnValThrTrpSerTrp 300
 841 TGGACCCCTGGCTACCCCGAGAGCCGAGAGGCGCTGTGCCCGCAGGTGACATGTCTCTGG 900
 QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGlyUser 320
 901 GACCACTGGCCGACAGAGCTTGGCCCCCGCTGCTGCGCCACACTCTGCGCAGAGTCC 960
 QY 321 ProAlaGlySerProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
 961 CCAGCGGCTCGGCGACCATGATGTGTGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020
 QY 341 AlaValProAlaArgArgTrpLysGlyPheValArgThrLeuGlyLeuArgGlnAlaGly 360
 1021 GCGGTCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
 QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
 1081 ATCGAAGCCGTGGAGGTGGAGATCGGCGGCTTCCGAGACGACGATGATGCTCAAG 1140
 QY 381 ArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
 1141 CGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1200
 QY 401 GlyLeuAspGlyCysValGlnAspLeuArgSerArgLeuGlnArgGlyPro 417
 1201 GGGCTGAGCGGCTGCGTGGAAAGACTTGGCGAGCGGCTGCGAGCGGCGGCGGCGGCGG 1251

RESULT 5
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 LOCUS HS074611 1634 bp mRNA linear PRI 02-JAN-1997
 DEFINITION Human Apo-3 mRNA, complete cds.
 ACCESSION U74611
 VERSION U74611.1 GI:1763292
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens.

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 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
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 DOGCTLPYERHGDCGVCSPETLSCSPRCANCGMOMFVQVLLHRTGLYVPLILGA
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BASE COUNT 300 a 528 c 519 g 287 t
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Alignment Scores:
 Pred. No.: 3,51e-114 Length: 1634
 Score: 2323.00 Matches: 417
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-993-234-6 (1-417) x HS074611 (1-1634)

QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
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QY 21 GlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
 DB 149 GGGGCCCCGGCCAGGCGCGGCGTACGCGCCAGGTGTGCTGTGCGGTACTTCCAC 208

QY 41 LysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
 DB 209 AAGAAGATTGGTCTGTGTGTGTGAGAGGCTGCCAGCGGGGCGTACTGAAAGCCCT 268

QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
 DB 269 TGCACGGAGCCCTCGCGGCACTCCACTGCTGTGTGTGCGCCAGACACCTTTTGGCC 328

QY 81 TrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSer 100
 DB 329 TGGGGAACACCAATTAATTCGATGATGCGCCGCTCCAGGCGCTGGAAGACAGCCCTCC 388

QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
 DB 389 CAGGTGGGCGTGGAGACGTTTACAGAGGCGGACACCGGTGTGTGTGTGTGTGTGTGTGT 448

QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerSerProPheThrCysGlnPro 140
 DB 449 TGGTTTGTGGAGTCCAGAGTCCAGCCAAAGTGTCCAGCAGTTCACCTTCTACTGCCAACCA 508

QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgAlaAspThr 160
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QY 161 AspCysGlyThrCysLeuProGlyPheThrGlnHisGlyAspGlyCysValSerCysPro 180
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QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrTrpArgGlnMet 200
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QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValAlaProLeuLeuGlyAlaThrLeu 220
 DB 689 TTTCTGGGCTCAGGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 748

QY 221 ThrTyrThrTyrArgHisCysTyrProHisLysProLeuValThrAlaAspGlnAlaGly 240
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 DB 809 ATGGAGAGCTGTGAGACCCACACCGCGCCACCACTGTGTGTGTGTGTGTGTGTGTGTGTGT 868

QY 261 LeuLeuAlaProProAspSerSerGlyLysIleCysThrValGlnLeuValGlyAsnSer 280
 DB 869 CTCTACACACTCTGTGACACAGTGAAGATGTGCACCGTCCAGTGTGTGTGTGTGTGTGTGTGT 928

QY 281 TrpThrProGlyTyrProGluThrGlnGlnAlaLeuCysProGlnValThrTyrSerTrp 300
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QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGlnSer 320
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QY 321 ProAlaGlySerProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
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QY 341 AlaValProAlaArgArgTrpLysGlnPheValArgThrLeuGlyLeuArgGlnAlaGly 360
 DB 1109 GCGGTGCCAGCGCGCGCGGTGGAGAGATTCGCGCAGCGCTGGGCGGCGGCGGCGGCGG 1168

QY 361 IleGluAlaValAlaGluValGluThrArgPheArgAspGlnGlnTyrGluMetLeuLys 380
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QY 381 ArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlnArgMet 400
 DB 1229 CGCTGGCGCCAGACAGACCGCGCGGCGCTCGGAGCGCTTACGGCGCGCTGTGAGCGCATG 1288

QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
 DB 1289 GGGCTGGAGCGCTGCTGTGAAGACTTGGCGAGCGCGCTGTGAGCGGCGCGG 1339

RESULT 6
 AX055442 1662 bp DNA linear PAT 13-JAN-2001
 LOCUS AX055442
 DEFINITION Sequence 72 from Patent WO0073452.
 ACCESSION AX055442
 VERSION AX055442.1 GI:12228713
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1662)
 Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J.,
 Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L.,
 Tumas, D., Watanabe, C.K. and Wood, W.I.
 Compositions and methods for the treatment of immune related
 diseases
 Patent: WO 0073452-A 72 07-DEC-2000;
 location/Qualifiers
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 source 1..1662
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 302 a 540 c 531 g 289 t
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Alignment Scores:
 Pred. No.: 3,57e-114 Length: 1662
 Score: 2323.00 Matches: 417
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

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QY 21 GlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
 DB 163 GGGGCCCCGGCCAGGCGCGGCGTACGCGCCAGGTGTGCTGTGCGGTACTTCCAC 222

QY 41 LysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
 DB 223 AAGAAGATTGGTGTGTGTGTGTGCGAGAGCTGCCAGCGGGGCGACTTGAAGGCCCT 282

OY	61	CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeu	80
Db	283	TGCACGAGCCCTCCGGCACTCCACTGCTGTGTGTCCCAACACACTTCTTGGCC	342
OY	81	TrpClnuShiHisAsnSerGluCysAlaIatGysGlnAlaCysAspClnuAlaSer	100
Db	343	TGGGAGAACCCCAATATTTCTGAAATGTGCCCGCTGCCAGCGCTGTGATGACGACGGCTTC	402
OY	101	GlnValAlaLeuGlnuAsnCysSerAlaValAlaAspThrArgCysGlyCysIysProGly	120
Db	403	CAGTGGCGCTGGAGAACCTGTTCACCACTGTGCCGACACCCGCTGTGGCTGTAAAGCAGGC	462
OY	121	TrpPheValGluCysGlnValSerGlnCysValSerSerSerProPheThrCysGlnPro	140
Db	463	TGGTTTGTGGAGTCCACAGTCCAGCAATGTTGTACAGAGTTCAACCCCTTACTATGCCAACCA	522
OY	141	CysLeuAspCysGlyAlaLeuShiAsnHisThrArgLeuLeuCysSerArgArgAspThr	160
Db	523	TGCCATGACTCGGGGGGCGCTGCACCGCCACACAGGGCTACTGTCTCCGCGAGAACTACT	582
OY	161	AspCysGlyThrCysLeuProGlyPheThrGlnHisGlyAspGlyCysValSerCysPro	180
Db	583	GACTGTGGAGACTCCCTGCTGGCTTCTATGAACATAGGGGATGTGCTGCTGTCTGGCC	642
OY	181	ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyThrArgGlnMet	200
Db	643	ACGAGCACCCCTGGGGAGCTCTCCACAGACGCTGTGCCGTCTGTGGCTGACGACAGATG	702
OY	201	PheThrValGlnValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeu	220
Db	703	TTCGTGGCTCAGGTGCTCTGGCTGTGGCTGTGTGTGCTCCCTCTGCTTGGGGCCACCTGTG	762
OY	221	ThrThrThrTrpArgHisCysTrpProHisIlysProLeuValThrAlaAspGluAlaGly	240
Db	763	ACCTACACATACCGCCGACCTGTGGCTTCACAAACCCCTGGTTACTGACAGATCAACTGTGG	822
OY	241	MetClnuAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr	260
Db	823	ATGGAGGCTCTGACCCACCCACCGCCGCCCACTCTCACTTGGACAGCCCCACACCC	882
OY	261	LeuLeuAlaProProAspSerSerGluIlysIleCysThrValGlnLeuValGlyAsnSer	280
Db	883	CTTTACACACTCTCTGACACACATGAAAGATGTGCACCGTCACTGGTGGGTAAACGC	942
OY	281	TrpThrProGlyTrpProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrp	300
Db	943	TGGACCCCTGTGATACCCCGAGACCCAGAGAGCGCTCTGCCACAGTGCATAGCTCTGG	1002
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OY	321	ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuThrAspValMetAsp	340
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OY	341	AlaValProAlaArgArgTrpIysGluPheValArgThrLeuGlyLeuArgGlnAlaGlu	360
Db	1123	GGGTGTCCACCGCGCGCTGGAAGAGATTCGTCCGACCTCGGGCTGTGCCAGGACAG	1182
OY	361	IleGluAlaValGlnValGluIleGlyArgPheArgAspGlnGlnThrGluMetLeuIys	380
Db	1183	ATCGAACCGCTGAGGTGGAGATCGGCGCTTCCGAGACCAACAGTACGACTGTCTCAAG	1242
OY	381	ArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluIuArgMet	400
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OY	401	GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417	
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LOCUS	AX201344	1662 bp	DNA	linear	PAT 30-AUG-2001
DEFINITION	Sequence 23 from Patent WO0153486.				
ACCESSION	AX201344				
VERSION	AX201344.1	GI:15391165			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 1662) Ashkenazi, A.J., to Goddard, A., Godowski, P.J., Gurey, A.L., Hillan, K.J., Masters, S.A., Pan, J., Pitt, R.M., Roy, M.A., Smith, V., Stone, D.M., Watanabe, C.K. and Wood, W.I.				
TITLE	Compositions and methods for the treatment of tumour				
JOURNAL	Patent: WO 0153486-A 23 26-JUL-2001;				
FEATURES	GeneTech, Inc. (US)				
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BASE COUNT	1..1662				
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Score:	2323.00	Matches:	417		
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Best Local Similarity:	100.00%	Mismatches:	0		
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Db	153 GGGGGCCGGGGCCAGCGGGCGACCTGTAACCCAGAGTGTGACCTGTCGGCTACCTCCAC	222			
OY	41 LysLys111eGlyLeuPheCysArngLyCysProAlaG1YH1StyLeuLysAlaPro	60			
Db	223 AAGAAGATTGGCTCTTTTGTTCAGAGGCTCCGACGGGGGACTACTGTAAGGCCCT	282			
OY	61 CysTThg1uProCysG1YASnSerThCysLeuValCysProGlnAspThrPheLeuAla	80			
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OY	81 TTPG1uASnH1SH1ASnSerG1uCysAlaATgCysGlnAlaCysAPG1uGlnAlaSer	100			
Db	343 TGGGAGAACACCAATATCTGAATGTGCCCGCTGCACAGCCTGTGATGAGCAGGCTCC	402			
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Db	403 CAGTGGCGCTGGAACCTGTCACAGAGGCCGACACCCCGTGGCTGTAAAGCAGGC	462			
OY	121 TTPheValG1uCyG1NValSerG1ncYsValSerSerProPheThyCysGlnPro	140			
Db	463 TGGTTTGGAGATGCGCAGTCAAGCCAAATGTGCACAGATTCACCTTCTACTGCCAACCA	522			
OY	141 CysLeuAspCysG1YAlaLeuH1SArH1StHrATgLeuLeuCysSerATgArH1SPThr	160			
Db	523 TGCCTAGACTCGGGGGCCCTGCACCGCCACACACGGCTACTGTGTCCCGCAGAAATACT	582			
OY	161 ASPCysG1YThCysLeuProG1YheThyArg1uH1SG1YAAG1YcysValSerCysPro	180			
Db	583 GACTGTGGACCTGCTGCTGTCTTCTATGAACATGGGAGATGGGTGGCTGCTCGCCCC	642			
OY	181 ThrSerThrLeuG1YSerCysProG1uATgCysAlaAlaValCysG1YTPArGlnMet	200			
Db	643 ACGACACCTCGGGGAGGTGTCCAGAGGCTGTGCCGCTGTGTGGCTGGAGGCAATG	702			

Db 603 CTGGCTGGCTTGTGTGCTCCCTTCCTTGGGGCCACCTTGACCTTACATACACCGCCAC 662

Qy 227 CysTTPProHIsLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrPro 246

Db 663 TGTGTGGCTCACAAGCCCTCGGTACTGCGAGATGAGACTGGATGGGGCTCTGACCCCA 722

Qy 247 ProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAsp 266

Db 723 CCACCGCCACCATCTGTACACCTTGACAGCGCCACACCTCTAGACACTCCCTGAC 782

Qy 267 SerSerGluLysIleCysThrValGlnLeuValGlyAsnSerThrPhrProGlyTyrPro 286

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Qy 287 GluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerArg 306

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Qy 307 AlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySerProAla 326

Db 903 GCTCTGGCCCTGCTGCGCCACACTCTGCGCAGAGTCCACAGCCGCGCTGCCAGCC 962

Qy 327 MetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAlaArgArg 346

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Qy 367 GluIleGlyArgPhaArgAspGlnGlnIleGlnMetLeuLysArgTrpArgGlnGln 386

Db 1083 GAGATGCGCGCTTCCGAGACAGCAGTACGAGTCTCAACCGCTGGCGCCAGCAGCAA 1142

Qy 387 ProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysVal 406

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Db 1203 GAAGACTTGGCAGCGCTGCGAGCGCGCGCG 1235

RESULT 10

LOCUS HSU75380 1557 bp mRNA linear PRI 05-APR-1997

DEFINITION Human apoptosis-mediating receptor TRAMP mRNA, partial cds.

ACCESSION U75380.1 GI:1695924

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1557)

AUTHORS Bodmer, J. L., Burns, K., Schneider, P., Hofmann, K., Steiner, V., Thome, M., Bormand, T., Hahne, M., Schrotter, M., Becker, K., Wilson, A., French, L. E., Browning, J. L., Macdonald, R. and Tschopp, J.

TITLE TRAMP, a novel apoptosis-mediating receptor with sequence homology to tumor necrosis factor receptor 1 and Fas (Apo-1/CD95)

JOURNAL Immunology 6 (1), 79-88 (1997)

MEDLINE 9052839

PUBMED 9052839

REFERENCE 2 (bases 1 to 1557)

AUTHORS Bodmer, J. L., Burns, K., Schneider, P., Hofmann, K., Steiner, V., Thome, M., Bormand, T., Hahne, M., Schrotter, M., Wilson, A., French, L. E., Browning, J. L., Macdonald, R. and Tschopp, J.

TITLE Direct Submission

JOURNAL Submitted (18-OCT-1996) Institute of Biochemistry, University of Lausanne, 155 Chemin des Boveresses, Epalinges, CH 1066, Switzerland

FEATURES

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location/Qualifiers

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/note="contains a death domain; similar to TNF receptor"

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BASE COUNT 286 a 508 c 477 g 286 t

ORIGIN

Alignment Scores:

Pred. No.: 5.45e-112 Length: 1557

Score: 2281.00 Matches: 410

Percent Similarity: 99.76% Conservative: 0

Best Local Similarity: 99.76% Mismatches: 1

Query Match: 98.19% Indels: 0

Gaps: 0

US-09-993-234-6 (1-417) x HSU75380 (1-1557)

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Qy 27 GlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGlyLeuPhe 46

Db 70 GGCACCTGTACCCACAGGTGTGACTGTCCGCTGATCTCCACAAAGATTTGCTGTTT 129

Qy 47 CysCysArgGlyCysProAlaGlyHisLysLysAlaProCysTrpGluProCysGly 66

Db 130 TGTTCACAGAGCTGCCCGCGCGGACACTCAAGAGCGCCCTTGACAGAGCCCTGGGGC 189

Qy 67 AsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHisHisn 86

Db 190 AACTCACCTGCTGTGTGTGCTCCCAAGACACTTCTTGGCTGGGAGAACCAACATAT 249

Qy 87 SerGluCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeuGluAsn 106

Db 250 TCTGAATGTGCCCGCTGCGAGCGCTGTGATGAGAGAGCTCCAGGTGGCGCTGGAGAC 309

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Qy 147 LeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThrCysLeu 166

Db 430 CTGCACCGCCACACAGCGTACTGTCTGTCCGAGAGATGACTAGCTGTGGAGACTGCTG 489

Qy 167 ProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeuGlySer 186

Db 490 CTGGCTCTATGAACATGGCGATGGCTGCTGCGCCACGAGACACCTGGGGAGC 549

Qy 187 CysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheThrPValGlnValLeu 206

Db 550 TGTCCAGAGCGCTGTCCGCTGTGTGGCTGGAGGCAATGTTCTGGGTCCAGGTCTC 609

QY 207 LeuAlaGlyLeuValValProLeuLeuLeuGlyAlaLeuThrLeuThrTyrrThrArgHis 226
Db 610 CTGGCTGGCCCTTGTGGTCCCTCTGCTGGGGCCACCCCTGACATACATACCCGAC 669
QY 227 CysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrPro 246
Db 670 TGCTGGCTCACAAGACCCCTGGTACTGCAATGAACTGGATGGAGGCTCTGACCCCA 729
QY 247 ProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAsp 266
Db 730 CCACGGCCACCATCTGTACACCTTGAGACAGGCCACACCTTCTACACCTCTGAC 789
QY 267 SerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrrPro 286
Db 790 AGCAGAGAGAAGATCTGCACCGCTCACTGGGTAAACAGCTGAGACCCCTGGCTACCCC 849
QY 287 GluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerArg 306
Db 850 GAGACCCAGAGAGCCCTCTCTCCCGACAGTACATGCTCTGGAGACAGTTGCCACAGAGA 909
QY 307 AlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySerProAla 326
Db 910 GCCTTGGCCCGCTGTGGCCACACTCTGCCAGAGTCCCGACGGGCTGGCCAGCC 969
QY 327 MetMetLeuGlnProGlyProGlnLeuTyrrAspValMetAspAlaValProAlaArgArg 346
Db 970 ATATGCTGACGCGCGGCGCCGACGCTCTACAGCTGATGACGCGGCTCCACAGCGCGCGC 1029
QY 347 TrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValGluVal 366
Db 1030 TGGAGAGAGTTCCTGCGACGCTGGGGCTGGGAGGACAGATCGAAGCGCTGGAGGTG 1089
QY 367 GluIleGlyArgPheArgAspGlnGlnTyrrGluMetLeuLysArgTrpArgGlnGlnGln 386
Db 1090 GAGATGCGCGCTTCCGACAGCAGAGTACAGATGCTCAAGCGCTGGCCGACGACAG 1149
QY 387 ProAlaGlyLeuGlnValAlaValTyrrAlaAlaLeuGlnArgMetGlyLeuAspGlyCysVal 406
Db 1150 CCGCGCGGCTCGGAGCGGCTTACGCGGCGCTGGAGCGCATGGGGCTGGAGCGGCTGGCTG 1209
QY 407 GluAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 1210 GAAGACTTGGCGCAGCGGCTGACGACGAGCCCG 1242

RESULT 11
HSU94503 1355 bp mRNA linear PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 2 mRNA, alternatively
DEFINITION spliced, complete cds.
ACCESSION U94503
VERSION 094503.1 GI:2071952
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1355)
AUTHORS Scraton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1355)
AUTHORS Scraton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source 1..1355
/organism="Homo sapiens"

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/cell_line="HeLa"
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599..700
/note="Insertion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable retained intron leading
to premature transcriptional termination"
BASE COUNT 223 a 441 c 451 g 240 t
ORIGIN
misc_feature
Alignment Scores:
Pred. No.: 1,49e-111 Length: 1355
Score: 2271.50 Matches: 416
Percent Similarity: 92.24% Conservative: 0
Best Local Similarity: 92.24% Mismatches: 1
Query Match: 97.78% Indels: 35
Dbs: 9 gaps: 1
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QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeuLeu 20
Db 1 ATGGAGCAGCGCGCGCGGCTGGCGCGGCTGGCGCGGCTGGCGCGGCTGGCGCGGCTGG 60
QY 21 GluAlaArgAlaGlnGlyIleThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 61 GGGCGCGGCGCGCGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGG 120
QY 41 LysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrrLeuLysAlaPro 60
Db 121 AAGAAGATGGTGTCTTTTGTTCAGAGCGCTGCCACGCGGCGCATCTGAAAGCGCCCT 180
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValLysProGlnAspThrPheLeuAla 80
Db 181 TGCAGGAGCGCTGGCGCAACTCCACTGCTGTGTGTCGCCAAGACACCTTCTGGCC 240
QY 81 TrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
Db 241 TGGGAGAACACCATATTCTGAAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCC 300
QY 101 GlnValAlaLeuGlnAsnGlyCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
Db 301 CAGGTGGCGCTGGAGAACTGTTCAGACAGTGGCGCACACCGCTGTGGCTGAACCCAGGC 360
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrrCysGlnPro 140
Db 361 TGGTTTGTGAGTGCCAGGTCAGCAATGTGTGCGAGTTCACTTCTACTGCAACCA 420
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 421 TGGCTAGACGCGGGGGCGCGACCGCGCACACAGCGCTACTCTGTCCCGCAGAGAACT 480
QY 161 AspCysGlyThrCysLeuProGlyPheTyrrGluHisGlyAspGlyCysValSerCysPro 180
Db 481 GACTGTGGGACCTGCCCTGGCTTCTATGACATGGCATGGCTCGTCTCGTCCGCC 540
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrrArg 198
Db 541 ACAGACACCTGGGAGCTGTCCAGAGCGCTGTGCGCTGTGTGTGGTGAGGACAGAT 600

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QY 198 ----- 198
Db 601 AGGTGTGTCTGGGATGCGATGGAGAGACTGTGAGACCGAGGAGGGGGGTGAG 660
QY 199 ----- Glnmethetripvalignvalleu 206
Db 661 GAGGGGGGACACCAACACCAACCAACCAAGCTGTTTCAGTG-TTTCGGGGTCGAGGTC 719
QY 207 LeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrrTrpArgHis 226
Db 720 CTGGCTGGCTTGTGGTCCCTCTGCTGTGGGGCCACCTGACATACATACATCCGCCAC 779
QY 227 CysTrpProHisIleCysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrPro 246
Db 780 TGTGGGCTTCACAAAGCCCTGCTGTACTGCAATGAGATGGAGGTGAGGCTGTGACCCCA 839
QY 247 ProProAlaThrHisIleuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAsp 266
Db 840 CCACGGCCACCACTGTCTACCTTGGACAGCGCCACACCTTCTAGCACCTCTCTGAC 899
QY 267 SerSerGluIleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrrPro 286
Db 900 AGCAGTGAAGAAGATGTGCACACCGTCCAGTTGGTGTAAACAGTGGACCCCTGGCTACCCC 959
QY 287 GluThrGlnGluAlaLeuLeuProGlnValThrTrpSerTrpAspGlnLeuProSerArg 306
Db 960 GAGACCCAGAGAGCGCTGTCGCCGAGGTGACATGCTCTGGGACCAAGTTGCCACACAGA 1019
QY 307 AlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySerProAla 326
Db 1020 GCTCTTGGGCCCCGCTGCTGCTGCCACACTCTGCCACAGTCCCCACCGCGCTGCGCAGCC 1079
QY 327 MetMetLeuGlnProGlyProGlnLeuTyrrAspValMetAlaAspAlaValProAlaArgArg 346
Db 1080 ATGATGCTGCACCGCGCCCGCAGCTCTACGAGTGTATGAGCGGGGTCCACAGCGGGCGCC 1139
QY 347 TrpTyrGlnPheValArgThrLeuGlyLeuArgGluAlaGlnIleGluAlaValGluVal 366
Db 1140 TGGAGAGATTTGTGTGCGCACGCTGGGGCTGGCGGAGGAGAAATGCAACCCGTGGAGGGTG 1199
QY 367 GluIleGlyArgPheArgAspGlnGlnIleTyrrGluMetLeuLysArgTrpArgGlnGln 386
Db 1200 GAGATGCGCGCTTCCGACACAGCAGTACGATGCTCAACCGCTGGCGCCACGACAGCAG 1259
QY 387 ProAlaGlyLeuGlyAlaValTyrrAlaAlaLeuGluArgMetGlyLeuAspGlyCysVal 406
Db 1260 CCCGGGGGCTTGGAGCGCTTTACGCGGGCCCTGGAGCGCATGAGGCTGGACGGCTGCGTG 1319
QY 407 GluAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 1320 GAAAGCTTGGCAGCGCGCTGTGACGCGGGCGCCG 1352

RESULT 12
LOCUS AR119656 1783 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6153402.
ACCESSION AR119656
VERSION AR119656.1 GI:14102355
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1. (bases 1 to 1783)
  YU, G.-L., NI, J., GENTZ, R.L. and DILLON, P.J.
  Death domain containing receptors
  Patent: US 6153402-A 1-28-NOV-2000;
  Location/Qualifiers
  source
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    /organism="Unknown"

BASE COUNT 330 a 562 c 564 g 327 t
Alignment Scores:

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Pred. No.: 3,45E-111 Length: 1783
Score: 2267.00 Matches: 409
Percent Similarity: 97.39% Conservative: 1
Best Local Similarity: 97.15% Mismatches: 5
Query Match: 97.59% Indels: 6
DB: 6 Gaps: 1

US-09-993-234-6 (1-417) x AR119656 (1-1783)
QY 3 GlnArgProArgGly-----CysAlaAlaValAlaAlaLeuLeu 16
Db 219 GAGGCCCCACAGTGGGACAGCTGGCGGAGAGTCAAGCAGCACCTGTCCGCCAGCGGCTCTTC 278
QY 17 LeuValLeuLeuGlyAlaAlaArgAlaGlnGlnGlyThrArgSerProArgCysAspCysAla 36
Db 279 CTGGTCTGCTGGGGGCCCGGGGCCAGGGGGGACCTGTAGCCCAAGGAGGTGACTGTGGC 338
QY 37 GlyAspPheHisIleCysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisIleTyrr 56
Db 339 GGTGACTTCACAAAGAAGATGTGTCTGTTTGTGACAGAGGCTGCCACCGGGGCACTTAC 398
QY 57 LeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAsp 76
Db 399 CTGAAGGCCCTTGGCAGCGAGCGCTGGCACAATCCACCTGCTGTGTCTCCCAAGAC 458
QY 77 ThrPheLeuAlaTrpGluAsnHisIleAsnSerGluCysAlaArgCysGlnAlaCysAsp 96
Db 459 ACCTCTTGGCTGGGAGAACCAACCAATTAATTTGAAATGGCCCGCTGGCAGGCTGTGAT 518
QY 97 GluGlnAlaSerGlnValAlaLeuGluAsnCysSerAlaAlaAlaAspThrArgCysGly 116
Db 519 GAGCAGGCTCCACAGTGGCGCTGGAGAACTGTTCAGGAGTGGCGGACACCGCGCTGGC 578
QY 117 CysLysProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerSerProPhe 136
Db 579 TGTAAAGCAAGGCTGTGTGTGTGGAGTGCAGGTCCAGTCAATGTGTGACGAGTTCACCTTC 638
QY 137 TyrCysGlnProCysLeuAspCysGlyAlaLeuHisIleAsnHisThrArgLeuLeuCysSer 156
Db 639 TACTGCCAACAATGGCTAGACTGCGGGGCCCTGCACCGCCACACACGCGTACTCTGTTCC 698
QY 157 ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrrGluHisGlyAspGlyCys 176
Db 699 CGCAGAGATACGACTGTGGGACCTGCTGCTGCTCTGTAGAACATGGCGATGGCTGC 758
QY 177 ValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGly 196
Db 759 GTGTCTGCCCCACAGACACCCCTGGGGAGCTGTCCAGAGCCTGTGGCGTGTGTGGC 818
QY 197 TrpArgGlnMetPheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuLeu 216
Db 819 TGGAGGAGATGTTCTGGGTCCAGAGTGTCTCTGGCTGGCTGTGTGTGCTCCCTCTGCTT 878
QY 217 GlyAlaThrLeuThrTyrrThrArgHisIleCysTrpProHisIleCysProLeuValThrAla 236
Db 879 GGGGCCACCTGACCTTACATACCGCCACATGCTGGCTCCCAAGCCCTGTTACTGTCA 938
QY 237 AspGluAlaGlyMetGluAlaLeuThrProProAlaThrHisIleuSerProLeuAsp 256
Db 939 GATGAAGCTGGAGTGGAGGCTCTGACCCACACCGGGCCACCAATGTCTACCTTGTGAC 998
QY 257 SerAlaHisThrLeuLeuAlaProProAspSerSerGlyIleCysThrValGlnLeu 276
Db 999 AGCGCCACACCTTCTAGCAGCTCTGACAGCAGTGAAGAATCTGCACCGTCACTTG 1058
QY 277 ValGlyAsnSerTrpThrProGlyTyrrProGluThrGlnGluAlaLeuCysProGlnVal 296
Db 1059 GTGGTAAACAGCTGAGCCCTGCTGCTACCCCGAGAGCCAGAGGGCGCTGTGCCCCAGAGTG 1118
QY 297 ThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeu 316
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Oy	317	SeProgiuserProLaigLYseProLaImethLeuInProgiLProgiLeuNyr	336
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Oy	337	AspValmeAspAlaValaProLaArArgrTprlySGluPheValArgThrLeuGlyLeu	356
Db	1239	GACGTGATGGAGCGGGCTCCAGCGGGGCGTGGAGAGATTCTGCGCACCTGGGGCTG	1298
Oy	337	ArgGluAlaGluIleGluAlaValaGluValaGluIleGlyArgPheArgAspGlnInTyr	376
Db	1299	CGCGGCGACAGATCCAGACCGCTGGAGGTGGAGATGATCGCGCCCTTCCGACACGACATAC	1358
Oy	377	GluWetLeuysArGrTprArgGlnGlnInProLaagLYleuGlyAlaValaTyrAlaAla	396
Db	1359	GAGATGCTCAAGCGCTGGCGGCACAGACGCGCGGGCTTCGGAGCGTTTACCGGGCC	1418
Oy	397	LeuGluArgMetGlyLeuAspGlyCysValaGluAspLeuArGrSerArgLeuGlnArgGly	416
Db	1419	CTGGAGCGCCATGGGGCTGAGCGGCTGCTGGAAAGACTTGCCGACGCGGCTGCAGCGGCG	1478
Oy	417	Pro	417
Db	1479	CCG	1481
RESULT 13			
LOCUS	AX331947	1743 bp	DNA
DEFINITION	Sequence 2456 from Patent WO0194629.	linear	PAT 09-JAN-2002
ACCESSION	AX331947		
VERSION	AX331947.1	GI:18122581	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1		
AUTHORS	Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,		
	Horrigan,S., Soppet,D.R. and Weaver,Z.		
	Cancer gene determination and therapeutic screening using signature		
	gene sets		
JOURNAL	Patent: WO 0194629-A 2456 13-DEC-2001;		
	Avalon Pharmaceuticals (US)		
FEATURES	Location/Qualifiers		
source	1..1743		
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BASE COUNT	347 a 543 c 549 g 304 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	1.53e-110	Length:	1743
Score:	2254.50	Matches:	413
Percent Similarity:	91.57%	Conservative:	0
Best Local Similarity:	91.57%	Mismatches:	4
Query Match:	97.05%	Indels:	35
DB:	6	Gaps:	1
US-09-993-234-6 (1-417) x AX331947 (1-1743)			
Oy	1	MetGluGlnaGrProLaArgGlyCysAlaAlaValaAlaAlaLeuLeuValLeuLeu	20
Db	69	ATGGAGCGACGGCGCGGGCTGGCGGGCTGGGGGGGCGGCTCTCTGCTGCTG	128
Oy	21	GlyAlaArGrAlaGlnGlyGlyThrArGrSerProArGrCysAspCysAlaGlyAspPheHis	40
Db	129	GGGGCGCCGGCCGACGGCGGCGCACTGTAGCCCAAGTGTGACTGTGCTCCAC	188
Oy	41	LysLYsIleGlyLeuPheCysCysArGrGlyCysProLaGluYHisTyrLeuLYsAlaPro	60
Db	189	AAGAAGATTGGTCGTGTTGTTGTCGAGAGCGTCCACAGGGGGGCACTGTAAGGCCCT	248
Oy	61	CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla	80

[illegible]

QY	407	GI:AspIeuArGSeRrArGLeuGInrArGcYlPpRo	417
DB	1388	GAAGACTTCGCCGACGCCCTCCACAGCGTGGCCCG	1420
RESULT 14			
LOCUS	HSWSL1	1743 bp	mRNA
DEFINITION	H.sapiens mRNA for WSL-LR, WSL-S1 and WSL-S2 proteins.		linear
ACCESSION	U09392		PRI 16-DEC-1996
VERSION	U09392.1	GI:1669690	
KEYWORDS	WSL-1 gene; WSL-LR protein; WSL-S1 protein; WSL-S2 protein.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1743)		
TITLE	Kitson,J., Raven,T., Jiang,Y.P., Goeddel,D.V., Gilles,K.M., Pun,K.T., Grimham,C.J., Brown,R. and Farrow,S.N.		
JOURNAL	A death-domain-containing receptor that mediates apoptosis		
MEDLINE	Nature 384 (6607), 372-375 (1996)		
PUBMED	97088617		
REFERENCE	8934525		
AUTHORS	2 (bases 1 to 1743)		
TITLE	Kitson,J.		
JOURNAL	Submitted (12-NOV-1996) J. Kitson, GLAXO-Wellcome, Medicines Research Centre, Gunnels Wood Road, Stevenage, SG1 2NY, UK		
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Qy 207 LeuAlaGlyLeuValAlaProLeuLeuLeuGlyAlaThrLeuThrTyThrArgHis 226
Db 788 CTGGCTGGCTTGTGTGCTCCCTCTGCTTGGGGCCACCTGACATACATACCCGAC 847
Qy 227 CysTTPProHisLysProLeuValThrAlaAspGluAlaGlyMetCysLysAlaThrPro 246
Db 848 TCGTGCCCTCACAMAGCCCTGTGTTACTGACAGAAAGAGTGGGTGAGGCTCTGACCCCA 907
Qy 247 ProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAsp 286
Db 908 CCACCGGACCAACCATCTGTACACCTTGACAGAGGCCACACCTTCTAGACCTCTGAC 967
Qy 267 SerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTyPro 286
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Qy 307 AlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySerProAla 326
Db 1088 GCTCTTGCCCGCTGCTGCGCCACACTCTGCGCCAGAGTCCCGACCGCGCTGCCAGCC 1147
Qy 327 MetMetLeuGlnProGlyProGlnLeuTyAspValMetAspAlaValProAlaArgArg 346
Db 1148 ATGATGCTGCACGCGGGCGCGAGCTCTAGACGTATGAGCGGGTCCACAGCGCGCG 1207
Qy 347 TrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValGluVal 366
Db 1208 TGGAGAGAGTGTGCTGCGACAGCTGGGGCTGCGCGAGCGAGATCGAAGCCGCGAGAG 1267
Qy 367 GluIleGlyArgPheArgAspGlnGlnIleTyGluMetLeuLysArgTrpArgGlnGln 386
Db 1268 GAGATGGCTCTCTCCGACACACAGCATGAGATGCTCAAGCACAGCGCGCCAGCAG 1327
Qy 387 ProAlaGlyLeuGlyAlaValTyAlaAlaLeuGluArgMetGlyLeuAspGlyCysVal 406
Db 1328 CCGGGGGGCTGGAGCGCTTAAACGGGGCCCTGGAGCGCATGGGGCTGGAGCGCTCG 1387
Qy 407 GluAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 1388 GAAGACTGCGCAGCGCGCTGCAAGCGTGGCCG 1420

RESULT 15
AF026070 1669 bp mRNA linear PRI 28-JAN-1998
LOCUS Homo sapiens death receptor 3 beta (DR3) mRNA, complete cds.
DEFINITION AF026070
ACCESSION AF026070.1 GI:2570830
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1669)
AUTHORS Marzocha,K., Ribelto,P., Charlot,C., Renard,N., Colflier,B. and
Salles,G.
TITLE A new death receptor 3 isoform: expression in human lymphoid cell
lines and non-Hodgkin's lymphomas
JOURNAL Biochem. Biophys. Res. Commun. 242 (2), 376-379 (1998)
MEDLINE 98113360
PUBMED 9446802
REFERENCE 2 (bases 1 to 1669)
AUTHORS Marzocha,K., Ribelto,P., Renard,N., Charlot,C., Colflier,B. and
Salles,G.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-1997) Hematology, CTR Hospitalier Lyon-Sud,
Chemin du Grand Revolet, Pierre Benite 69495, France
FEATURES
source 1..1669

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CDS
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Mieliki"
/note="Identified in human pre-B cell line Mieliki and in
patients with non-Hodgkin's lymphoma"
1..1669
/gene="DR3"
/note="Apo-3; TRAMP; LARD"
69..1349
/gene="DR3"
/note="DR3 beta: TNF receptor family member; alternatively
spliced product; contains 28 amino-acid extension to the
extracellular domain of the ordinary DR3 molecule"
/product="death receptor 3 beta"
/protein_id="AAC39556.1"
/db_xref="GI:2570831"
/translation="MEQPRGCAVAALLLVLCARAGGTRSPRCDAQDFHKKIG
LFCRGGCPAGHYLAKPTEPCGNSYLCVCPDPTFLAMENHNHSEARCAQDEASQV
ALENCASAVADTRFGCKPGWFEQVSOCSVPYCOPLDGLAHRLRLCSRDY
DCGTCLPGFEHGDGCVSCPTEPPSLAGPMGAVOSAVPLSVAGRGVFWYVLLAG
LVVPLLGATLTYYRHCMPIKPLVTADEAGMEALTPPAATLSPLDSHTLLAPDS
SKRTVQVGVGSMTPGYETGDEALCPQYTNMSDPLPSALPAPATLSPSPAGSP
AMLDPPQLVDMDVAVPARMKKEFVRTGLDEALEAVEIEIGLFRDQYBLKHMW
Q00PAGLAVVALERMGIDGVEDLRSLDRGP"

BASE COUNT 329 a 532 c 513 g 295 t
ORIGIN

Alignment Scores:
Pred. No.: 6,68e-110 Length: 1669
Score: 2242.00 Matches: 412
Percent Similarity: 96.72% Conservative: 1
Best Local Similarity: 96.49% Mismatches: 4
Query Match: 96.51% Indels: 11
DB: 9 Gaps: 2

US-09-993-234-6 (1-417) x AF026070 (1-1669)

Qy 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
Db 69 ATGAGACAGCGCGCGGGGCTCGCGGCGGTGGCGGGCGGTCTCTCTGCTGCTG 128
Qy 21 GlyAlaArgAlaGlnGlyLysThrArgSerProArgCysAspCysAlaAspPheHis 40
Db 129 GGGGCCCGGGCCAGAGGCGGCACTGTAAGCCCAAGGTGACTGTCGGGTGACTTCC 188
Qy 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
Db 189 AAGAGATGGTCTGTGTTGTTCCAGAGGCTGCCAGCGGGGCACATACGAGGCCCT 248
Qy 61 CysThrGluProCysGlnAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 249 TGCACGAGAGCTTCGCGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTGGCC 308
Qy 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSer 100
Db 309 TGGAGAACACCATATATCTGTAATGCCCGCTGCCAGGCGCTGATAGCAGGCTCC 368
Qy 101 GlnValAlaLeuGlnAsnSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
Db 369 CAGGTGGCCCTGGAGAACTGTTGACGACAGTGGCCGACACCGCTGTGGCTGAAGCCAGGC 428
Qy 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
Db 429 TGGTTTGTGAGTGCACAGGTACACCAATGTGTACAGAGTTCACTTCTACTCCANCA 488
Qy 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 489 TGCCTAGACTGCGGGGCCCTGCACCGCCACACAGCGGTACTGTGTTCCCGCAGAGTACT 548
Qy 161 AspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysPro 180
Db 549 GACTGTGGGACGTCCTGCTGTATGAACATGGGCGATGGCTGCGTCTGCCCC 608

QY 181 ThrSer-----ThrLeuGlySerCysProGluArgCysAlaAla 193
|||
Db 609 ACCGCC-ACCCCGCTCCCTTGCAAGACACCTGGGGAGCTGTCCAGACGCGTGGCCGT 667
QY 194 ValCysGlyTrpArgGln-----MetPheTrpValGlnValLeuAlaGlyLeuVa 211
|||
Db 668 GTCTGTGGCTGGAGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 727
QY 211 lValProLeuLeuLeuGlyAlaThrLeuThrTrpTrpArgHisCysTrpProHisLy 231
|||
Db 728 GGTCCCGCTCTGTGTGTGGGGCCACCTGACCTACACATACCCGACCTGTGGCTCACAA 787
QY 231 sProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrProProProAlaThrH 251
|||
Db 788 GCCCTGTGTACTGACGATGAGTGGATGAGGCTGTGACCCCGACCGGCCACCA 847
QY 251 sLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAspSerSerGluLysTr 271
|||
Db 848 TCTGTACCCCTTGACAGCGCCACACCTCTGTAGACCTCTGTACAGCAGTGAAGAT 907
QY 271 eCysThrValGlnLeuValGlyAsnSerTrpTrpProGlyTrpProGluThrGlnGluAl 291
|||
Db 908 CTGCACCGCTCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 967
QY 291 aLeuCySProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAl 311
|||
Db 968 GCTGTGCCCGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1027
QY 311 aAlaAlaProThrLeuSerProGluSerProAlaGlySerProAlaMetMetLeuGlnPr 331
|||
Db 1028 TGTGTGGGCCACACTCTGCCAGAGTCCCGACCGGCTGTGCCACCAATGATGTGTGAGCC 1087
QY 331 oGlyProGlnLeuTrpAspValMetAspAlaValProAlaArgTrpIysGluPheVa 351
|||
Db 1088 GGGCCCGCAGCTCTAGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1147
QY 351 lArgThrLeuGlyLeuArgGluAlaGlnIleGluAlaValGluValGluIleGlyArgPh 371
|||
Db 1148 GCGCAGCTGGGGCTGTGGCGAGAGATCGAACCCGTGGAGTGTGAGATCGTCTCTT 1207
QY 371 eArgAspGlnGlnTrpGluMetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGl 391
|||
Db 1208 CCGAGACACGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1267
QY 391 yAlaValTrpAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSe 411
|||
Db 1268 AGCGCTTACGGGGCTGTGGAGCGCATGGGGCTGTGGAGCGCTGTGGAAGACTTGTGCGCAG 1327
QY 411 fArgLeuGlnArgGlyPro 417
|||
Db 1328 CCGCTGTGACGCGTGGCCCG 1346

Search completed: April 6, 2003, 21:07:27
Job time : 4876.17 secs

FT mat-peptide 73..1251
 XX /*tag- b
 PN MO9733904-A1.
 XX
 PD 18-SEP-1997.
 XX
 PF 17-OCT-1996; 96WO-US16849.
 XX
 PR 12-MAR-1996; 96US-0013285.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX (UNMT) UNIV MICHIGAN.
 PI Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
 DR WPI: 1997-470812/43.
 DR P-PSDB; AAW31517.
 XX
 PT Death domain containing receptor polypeptide(s) DR3 and DR3-V1
 PT for activation of apoptosis and NF-kappaB, antagonists can be used
 PT to treat inflammatory diseases
 PS
 PS Claim 6; Page 75-77; 108pp; English.

CC This cDNA clone codes for human death domain containing receptor
 CC DR3 (see AAW31517), a novel member of the tumour necrosis factor
 CC receptor family. It was isolated from a HUVEC cDNA library.
 CC Related death domain containing receptor DR3-V1 cDNA (see AAT89426)
 CC was isolated from a human testis tumour cDNA library. The genes
 CC have also been identified in cDNA libraries of foetal liver,
 CC foetal brain, tonsil and leukocyte. Nucleic acids encoding full-
 CC length or mature DR3, or the extracellular, transmembrane,
 CC intracellular or especially the death domain of DR3, can be used to
 CC produce recombinant polypeptides in transformed host cells. These
 CC polypeptides can be used to treat diseases and disorders associated
 CC with the inhibition of apoptosis. Antagonists can be used to treat
 CC diseases and disorders associated with increased apoptosis and for
 CC treating inflammatory diseases and disorders.

SO Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:
 Pred. No.: 5,32e-122 Length: 1254
 Score: 2323.00 Matches: 417
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-09-993-234-6 (1-417) x AAT89427 (1-1254)

QY 1 MetGIuGlnAtrProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeuLeu 20
 DB 1 ATGGAGCAGCGCGCGCGGGGCTGCGCGGGGCGGGGCGCTCTCTGTTGCTG 60
 QY 21 GlyAlaAtrGAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
 DB 61 GGGGCCCCGGGCGCGAGGCGCCTGTAGTGTGACTGTGCGGCGCTTCCAC 120
 QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
 DB 121 AAGAGATTTGGCTCTTTTGTTCGAGAGGCTGCCAGCGGGGCACTTACCTGAAGCCCT 180
 QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
 DB 181 TGCACGGAGCCCTGGGCACTCCACCTGCTGTGTCCTCCCAAGACACTTCTGGCC 240
 QY 81 TrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
 DB 241 TGGGGAACCAACCAATTTGGAATGTCGCCGTCGCGGCTGTGATGACAGGCTCC 300
 QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysValProGly 120

DB 301 CAGTGGCGCTGGAGAACTTTAGCAGTGGCCGAGACCGCGTGGCTGAAGCCAGGC 360
 QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
 DB 361 TGGTTGTGGAGTGCAGAGGTACACCAATGTGTAGAGATTCAACCTTCTACTGCCAACCA 420
 QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
 DB 421 TGCCTAGCTGGGGGCGCGCTGCACCGCCACACAGCGCTACTCTGTCCCGCAGAGTACT 480
 QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
 DB 481 GACTGGGAGACCTCCCTGCTGCTCTTGTGAACATGAGCGATGCTGCTGTCTGCCCC 540
 QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrArgGlnMet 200
 DB 541 ACGAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGCGGCTGTGTGGGTGGAGGCAGATG 600
 QY 201 PheTrpValGluValLeuLeuAlaGlyLeuValAlaProLeuLeuGlnGlyAlaThrLeu 220
 DB 601 TTCTGGGTCCAGTGTCTCTGCTGCTGCTGTGGTCCCTTGTCTCTGGGGCCACCTG 660
 QY 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly 240
 DB 661 ACCTACACATACCGCCACTGCTGGCTCAGAGCCCTGTGTTACTGCAATACACTGGG 720
 QY 241 MetGluAlaLeuThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
 DB 721 ATGGAGGCTCTACCCACCCACCGCCGCCACCATCTGTACCTTGGAGACGCCCCACACC 780
 QY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280
 DB 781 CTTTACAGACCTCTCTGACAGCGATGAGAGATCTACCGCTCACTTGTGGTAAACAGC 840
 QY 281 TyrThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTyrSerTrp 300
 DB 841 TGGACCCCTGGCTACCCCGAGACCCAGAGGGGGCTCTCCGCGAGTACATGTGCTGG 900
 QY 301 AspGluLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
 DB 901 GACCGTTGCCAGAGAGCTCTTGGCCCCCTGCTGGCCACACTCTCCAGAGATCC 960
 QY 321 ProAlaGlySerProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
 DB 961 CCAGCCGGCTGCGCAGCATGATGTGACAGCGGGCCGCAAGCTCTACGACGTATGGAC 1020
 QY 341 AlaValProAlaArgArgTyrLysGluPheValArgThrLeuGlyLeuAlaGlu 360
 DB 1021 GCGTCCAGCGCGCGCTGGAGAGATTCTGTGGCAGCGCTGGGGCTGCCGAGGCAGAG 1080
 QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnIleTyrGluMetLeuLys 380
 DB 1081 ATCAGAGCGGTGGAGTGAATGCGCGCTTCCGAGACAGCATGTGAGATCTCTAAG 1140
 QY 381 ArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
 DB 1141 CGCTGGCGCCAGAGAGAGCCCGGGGCGCTGGAGCCGTTTACGGCGCCCTGGAGCCGATG 1200
 QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
 DB 1201 GGGTGGAGCGGCTGCTGGAAGACTTGGCAGCGCTGACAGCGGCGCG 1251

RESULT 2
 ID AAX00925 standard; cDNA; 1254 BP.
 AC AAX00925;
 XX
 DT 25-MAR-1999 (first entry)
 XX
 DE Death domain containing receptor polypeptide (DR3) encoding cDNA.
 XX

KM Death domain; receptor; DR3-V1; DR3; recombinant; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1254
FT sig_peptide /product= "death domain containing receptor DR3"
FT mat_peptide 1..72
FT 73..1251
FT /*tag- b
FT /*tag- c
PN JP11000170-A.
PD 06-JAN-1999.
XX 12-MAR-1997; 97JP-0057503.
XX 06-FEB-1997; 97US-0037341.
PR 12-MAR-1996; 96US-0013285.
PR 17-OCT-1996; 96US-0028711.
XX (HDMN-) HDMN GENOME SCI INC.
PA (DNM1) UNIV MICHIGAN.
XX WPI: 1999-124390/11.
DR P-PSDB; AAW95538.
XX New death domain containing leader sequence and recombinant vector -
PT optionally comprising leader sequence
XX Claim 6; Fig 3; 50pp; Japanese.
PS The invention provides nucleotide sequences encoding death domain
CC containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are
CC used for the recombinant production of the proteins. The present
CC sequence represents a cDNA encoding the death domain containing
CC receptor polypeptide (DR3).
XX
SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other:

Alignment Scores:
Pred. No.: 5.32e-122 Length: 1254
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-993-234-6 (1-417) x AAX00925 (1-1254)
QY 1 MetGlnAlaArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
DB 1 ATGGACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
QY 21 GAlaAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 40
DB 61 GGGGGCCCGGGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
DB 121 AAGAAATATGGTCTGTTTGTTCAGAGGCTGCCAGCGGGGACACTGAAAGGCCCT 180
QY 61 CysThrGlnProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
DB 181 TGCACGAGGAGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACTTCTGGCC 240
QY 81 TTRGlnAsnHisIleAsnSerGlyCysAlaArgCysGlnAlaCysArgGlnAlaSer 100

DB 241 TGGAGAACCCACATATTTCTGATGTGCCCGCTGCCAGGCTGTATGACAGGCTCC 300
QY 101 GlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysProGly 120
DB 301 CAGGTGGCGCTGGAGAACTGTTCAGCAGGTGGCGGACACCGCGTGTGCTATGACGAGG 360
QY 121 TrpPheValGlyCysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnPro 140
DB 361 TGGTTTGTGAGTGCACAGGACCAATGTGTGAGAGTTCACCCCTTCTACTCCCAACA 420
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisSerThrArgLeuLeuLeuSerArgAspThr 160
DB 421 TGCCTAGACTGGGGGCGCTGCACCGCACACAGGCTACTGTTCGCGAAGACT 480
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspLysCysValSerCysPro 180
DB 481 GACTGTGGGACCTGGCTGCTGTATGAAACATGGCATGGCTGCTGCTGCTGCTGCTG 540
QY 181 ThrSerThrLeuGlySerCysProGlnArgCysAlaAlaValCysGlyTyrPargGlnMet 200
DB 541 ACAGACACCTGGGAGAGCTGTCCAGAGCGCTGTGCGGCTGTGTGTGTGTGTGTGTGT 600
QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValProLeuLeuLeuGlyAlaThrLeu 220
DB 601 TTCTGGGTCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 221 ThrTyrThrTyrArgHisCysTyrProHisLysProLeuValThrAlaAspGlnAlaGly 240
DB 661 ACCTACACATACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
QY 241 MetGlnAlaLeuThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
DB 721 ATGAGAGGCTGTGACCCACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
QY 261 LeuLeuAlaProProAspSerSerSerGlyLysIleCysThrValGlnLeuValGlyAsnSer 280
DB 781 CTCTTGACCTCTCTGACAGCTGAGATGTGACCTGACCTGACCTGACCTGACCTGACCTG 840
QY 281 TrpThrProGlyTyrProGlnThrGlnAlaLeuCysProGlnValThrTyrSerTyr 300
DB 841 TGGACCCCTGCGTACCCCGAGACCCAGAGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGG 900
QY 301 AspGlnLeuProSerAlaAlaLeuGlyProAlaAlaAlaProThrLeuSerProGlnSer 320
DB 901 GACCACTGGCCGACAGAGCTTGGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960
QY 321 ProAlaGlySerProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
DB 961 CCAAGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020
QY 341 AlaValProAlaArgTyrTrpLysGlnPheValArgThrLeuGlyLeuArgGlnAlaGln 360
DB 1021 GCGGTCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
QY 361 IleGlnAlaValGlnValGlnIleGlyArgPheArgAspGlnGlnTyrGlnMetLeuLys 380
DB 1081 ATCGAAGCCGTGGAGGTGGAGATCGGCGGCTCGGAGACAGAGATGAGATGAGATGAG 1140
QY 381 ArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlnAlaGln 400
DB 1141 CGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1200
QY 401 GlyLeuAspGlyCysValGlnAspLeuArgSerArgLeuGlnArgGlyPro 417
DB 1201 GGGCTGGAGGCGTGGTGGAGAACTTGGCGAGCGGCTGAGCGGCGGCGGCGGCGGCGG 1251

RESULT 3
AAC68777
ID AAC68777 standard; cDNA; 1254 BP.
XX AAC68777;
AC
XX 20-FEB-2001 (first entry)
DT

XX DE Human death domain containing receptor DR3 coding sequence.
 XX KW Human; death domain containing receptor; DR3; cancer;
 KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
 KW neurodegenerative disease; angiogenesis; ss.
 XX OS Homo sapiens.
 XX PN WO200064465-A1.
 XX PD 02-NOV-2000.
 XX PF 21-APR-2000; 2000MO-US10741.
 XX PR 22-APR-1999; 99US-0130488.
 XX PR 28-MAY-1999; 99US-0136741.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 PA (UNMI) UNIV MICHIGAN.
 PA (YUGG/) YU G.
 PA (NIJ/) NI J.
 PA (GENT/) GENTZ R L.
 PA (DILL/) DILLON P J.
 PA (DIXI/) DIXIT V M.
 PI YU G, NI J, Gentz RL, Dillon PJ, Dixit VM;
 DR WPI: 2000-687263/67.
 DR P-PSDB; AAB36265.
 XX PT Treating graft-versus-host disease, cancer, immunodeficiency or an
 PT autoimmune disease comprising administering an antibody to Death Domain
 PT Containing Receptor proteins and a second therapeutic agent -
 XX PS Example 2B; Fig 2; 273pp; English.
 CC The present invention provides the protein and coding sequences for two
 CC death domain containing receptors, designated DR3 and DR3-V1. These
 CC receptors are involved in apoptosis, and the sequences given can be used
 CC in the treatment of cancers, infections, cardiovascular disorders such as
 CC arhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
 CC and congenital heart defects, neurodegenerative diseases including
 CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
 CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
 CC and to promote angiogenesis and wound healing.
 XX SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;
 Alignment Scores:
 Pred. No.: 5,32e-122 Length: 1254
 Score: 2323.00 Matches: 417
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0
 US-09-993-234-6 (1-417) x AAC68777 (1-1254)
 QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaAlaLeuLeuValLeuLeu 20
 DB 1 ATGGAGCAGCGCGCGCGCGCGCTGGCGCGCGCTGCTCTCTCTGCTGCTG 60
 QY 21 GlyAlaArgAlaGlnGlnGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
 DB 61 GGGGCGCGCGCGCGCGCGCGCTGAGCCCGAGGTGTGCTGCTGCGGTGACTTCCAC 120
 QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisLysLysLysAlaPro 60
 DB 121 AAGAGATTGCTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCGACTACCTGAAGCCCT 180
 QY 61 CysThrGlnProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
 |||||||

DB 181 TGCAGGAGCCCTGGCGGCAATCCACCTGCTGTGTGTGCCCAAGACACTTCTGGCC 240
 QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluAlaSer 100
 DB 241 TGGGAGAACACCACTAATTTCTGAATGTGCCCTGCCAGGCTGTGATGACGAGCCCTCC 300
 QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
 DB 301 CAGGTGGCCCTGAGAACACTGTTACACAGTGGCCGACACCCGCTGTGGTGAAGCCAGGC 360
 QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheThrCysGlnPro 140
 DB 361 TGGTTGTGAGTGGCAGAGTGCACCAATGTGTACAGATTACCTTGTACTGACCAACA 420
 QY 141 CysLeuAspCysGlyAlaLeuHisArgHisLysThrArgLeuLeuCysSerArgArgAspThr 160
 DB 421 TGCCTAGACTGGGGGCGCTGACCGCCAGACACGCGTACTGTCTCCGAGACATPACT 480
 QY 161 AspCysGlyThrCysLeuProGlyPheThrGluHisGlyAspGlyCysValSerCysPro 180
 DB 481 GACTGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyThrArgGlnMet 200
 DB 541 ACGACACACCTGGGGAGCTGTCCAGAGCGCTGTGCGCTGTGTGTGTGGAGGAGATG 600
 QY 201 PheThrValGlnValLeuLeuAlaGlyLeuValAlaProLeuLeuLeuGlyAlaThrLeu 220
 DB 601 TTCTGGTTCAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 QY 221 ThrThrThrThrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly 240
 DB 661 ACCTACACATACCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 QY 241 MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
 DB 721 ATGGAGGCTGTGACCCACACACCGGCGCCATCTGTCTACCTTGGACAGCGCCACACC 780
 QY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280
 DB 781 CTCTAGACCTCTCTGACAGCAGTAGANAGTCTGACCGCTGCTGCTGCTGCTGCTGCTG 840
 QY 281 TrpThrProGlyThrProGluThrGlnGluAlaLeuCysProGlnValThrThrSerTrp 300
 DB 841 TGGACCCCTGTGCTACCCCGAGACCCAGAGAGCGCTGCGCCGCGAGTGACATGCTCTCG 900
 QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
 DB 901 GACCAAGTGGCCAGCAGAGCTCTTGGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuThrAspValMetAsp 340
 DB 961 CCAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
 QY 341 AlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
 DB 1021 GCGGTCCAGCGCGCGCTGGAAGAGTCTGTGGCAGCGCTGGGGCTGCGGAGGAGAG 1080
 QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnThrGluMetLeuLys 380
 DB 1081 ATCCAAAGCCGAGGAGGAGGAGATGCGCGCTTCCGAACACAGCATGTGAGATGCTCAAG 1140
 QY 381 ArgTrpArgGlnGlnProAlaGlyLeuGlyValAlaValThrAlaAlaLeuGluArgMet 400
 DB 1141 CGCTGGGCGCAGAGCAGCGCCGCGGCGCTGTGAGACCTTTACCGCGGCTGTGAGCGCATG 1200
 QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
 DB 1201 GGGCTGACCGCTGCTGGAAGACTTGCAGCCGCTGACGCGGCGGCGCG 1251
 RESULT 4
 AAT91180
 ID AAT91180 standard; cDNA; 1634 BP.

XX	AAT91180:
XX	14-APR-1998 (first entry)
DT	Human apoptosis protein Apo-3 cDNA clone FH20.57.
XX	
DE	Apo-3; apoptosis; human; therapy; drug screening; ss.
XX	
KW	Homo sapiens.
OS	
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	89..1342
FT	/**tag= a
FT	s1g_peptide
FT	89..160
FT	/**tag= b
FT	/note= "determined by hydrophathy analysis"
FT	mat_peptide
FT	161..1339
FT	/**tag= c
XX	
XX	W09737020-A1.
PN	
XX	
PD	09-OCT-1997.
XX	
PE	31-MAR-1997; 97MO-US05230.
XX	
PR	23-SEP-1996; 96US-0710802.
PR	01-APR-1996; 96US-0625328.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Ashkenazi AJ;
DR	
XX	WPI: 1997-503105/46.
XX	
PT	Poly peptide(s) Apo-3 and Apo-2L1 - useful for regulating apoptosis
PT	in mammalian cells
XX	
PS	Example 1; Page 45-46; 70pp; English.
CC	
CC	cDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see
CC	W26709), designated Apo-3, that stimulates or induces apoptotic
CC	activity in mammalian cells. It was isolated from a human foetal
CC	heart cDNA library by screening with probes (see T91183-84) based
CC	on an EST sequence (GenBank locus W1984) that showed homology to
CC	the intracellular domain of human TNFR1 and CD95. Amino acid
CC	residues 1-181 of Apo-3 are identical to another novel apoptosis
CC	polypeptide, Apo-2L1 (see W26708). Nucleic acids encoding Apo-3
CC	can be used diagnostically for tissue-specific typing and to
CC	produce recombinant Apo-3 polypeptides, especially the
CC	extracellular domain (amino acids 1-198) or death domain (amino
CC	acids 338-417). Apo-3 can be used to induce apoptosis or
CC	NF-kappa-N- or JNK-mediated gene expression for therapeutic
CC	purposes. Non-human transgenic animals containing cells that
CC	express Apo-3 nucleic acid, and knockout animals containing
CC	cells that have an altered Apo-3 gene, can be used in drug
CC	screening and development.
XX	
SO	Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;
Alignment Scores:	
Pred. NO.:	7.06e-122
Score:	2323.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	18
US-09-993-234-6 (1-417) x AAT91180 (1-1634)	
Oy	1 MetctuglnatrgproarvglycysalatalavalalalaaleuleValleuleu 20
Dh	89 ATGGAGCGACGCCGCGCGGTGCAGCGCGTGCAGCGCGTGCCTCCTGTCGTCGCTG 148

QY	21	GLYALATRGALAGLNGLYLTHRAASERPROALGASASCSYALGLYASPHETIS	40
Db	149	GGGGCCCCGGCCAGGGGGCCACTGCTAGCCACCAGGTGATGTGCCGGTACTTCAC	208
QY	41	LYSLYSILEGLLEUPHETCYSAARGLYCYSPROALAGLYNISTYTLLEULYSALPRO	60
Db	209	AMGAAAGATTGGTGTGTTTTGTCAGAGGCTGCCACGGGGGCACTTGAAGGCCCT	268
QY	61	CYSHTRCILUPROCSGLYANSETRPCYSLEUVALCYSPROGLIAPHRPHLEULA	80
Db	269	TGCACGGAGCCCTCGGCCAACTCCACTGCTGTGTGTCCCAAGAACCTTTTGGCC	328
QY	81	TRPLEUSNHNISHANSETRGLUCYSALAARGCYSGIALACYSASPGLUGLNASER	100
Db	329	TGGGAGAACCCATATCTGTAATGTGGCCGGTGGCAGAGCTGTGATGAGAGGCCCTC	388
QY	101	GLNVALALEUGLUANSYSSERIALAVALALASPRTHATGCSGLYCYSLYSPROGLY	120
Db	389	CAGGTGGCGGTGGGAACCTGTTCAGAGAGGGCCGACACCCGCTGTGGCTGAAGCCAGC	448
QY	121	TRPHEVALGLUCYSGLNVALSERGLNCYSVALSERSESPROPHETCYSGINPRO	140
Db	449	TGGTTTTGGAGTCCCAAGTCAACCAATGTGTACAGATTCACCTTCTACTGCCAACCA	508
QY	141	CYSLEUASPCYSGLYALALEUHNISARHNISSTRATGLEULEUCYSSETRATGTRAPHTR	160
Db	509	TGCCCTAAGCTGGGGGGCCCTGCACCCCAACACAGGCTACTGTGTCCCGCAGAGATCT	568
QY	161	ASPRCSGLYTHRCYSLEUPROGLIPIETRYGLHNISGLYASGLYCYVALSERCYSPRO	180
Db	569	GACTGTGGAGACTCCCTGGCTGGCTTCTATGAACAATGGGGAATGGCTGTCCGGCC	628
QY	181	THSERTHTRLEUGLYSERCYSPROGLIATRGCSYALALAVALCYSGLYTRPRAGLINAT	200
Db	629	ACGAGACACCCGTGGGAGACTGTCCAGAGCGGTGGCCGCTGTGGCTGAGAGGCAATG	688
QY	201	PHETRPVALGLNVALLEULEUALAGLYLEUVALALPROLEULEUENGLYALATHREU	220
Db	689	TTTCGGGTCCAGGTGCTTCCTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	748
QY	221	THTRTHTRTHTRAGHNSCYSTRPROHLISYSPROLEUVALTHRALASPGULIACLY	240
Db	749	ACCTACACATACCGCACTGCTGTGCTTCACACACCCCTGTACTGCATATGAACCTGG	808
QY	241	METGLUALAETHTRPROPROPROALATHRHISLEUSERPROLEUASPERALATHISTR	260
Db	809	ATGAGAGCTCTGACCCCAACCCAGCCACCAATCTGTACACCTTGAGAGCCCAACAC	868
QY	261	LEULEUALAPROPRADSPERSERGLUYLSILECYSTRVALGLNLEUVALGLYNSNER	280
Db	869	CTTTACACACTCTGTACACACAGTGAAGATGTGCACCTGCACAGTGGTGGTAACGC	928
QY	281	TRPHTRPROGLYTRPROGLIUTHRGLNGLUALALEUCYSPROGLIVALTHTRSPSETRP	300
Db	929	TGGACCCCTGGCTACCCCGAGACCACAGAGGGCTGTGCCGACAGGTGACATGTCRGG	988
QY	301	ASPLEINLEUPROSERATGALALEUGLYPROALALALAPROTHLEUSERPROGLUSER	320
Db	989	GACCAAGTGGCCACACAGACTCTTGGCCCGCGCTGCACCCCACTCTCCGCAAGATCC	1048
QY	321	PROALAGLYSERPROALAMETMETLEUGLINPROGLIPIEUTRYASPRALMETASP	340
Db	1049	CCACCGCGCTCGCAGCAATGATGTGTGCACCGGGGCCGACACTCTACGACCTGATGAC	1108
QY	341	ALAVALPROALATGATGTRPLYSGLIUPHEVALATGTHTRLEUGLYLEUATRGSLUALGLU	360
Db	1109	GGCGTCCCAAGCGCGCTGTGAAGAGATTCGTCCGACCTGGGGCTGGCGCAGAGCAGAG	1168
QY	361	ILEGLIUALVALGLIUALGLIUEGLYATGPRPHATGASGLINGLTYGSLMETLEUUS	380
Db	1169	ATTCGAACCGCGGAGGAGTGTGGCGGCTTCCGAGACCAAGTACAGATGCTCTCAG	1228

QY 381 ArgTPrAArgInGInGInProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
DB 1229 GCGTGGCGCCAGCAGACCCCGCGCGCTGAGACCGCTTACGGCGCCCTGAGACCGCATG 1288
QY 401 GlyLeuAspGlyCysValGlyAspLeuArgSerArgLeuGlnArgGlyPro 417
DB 1289 GGGCTGGAGCGCTGCTGGAGAACTTGTGAGCGCGCTGAGCGCGCGCCG 1339
RESULT 5
AAH27782
ID AAH27782 standard; DNA; 1634 BP.
AC AAH27782;
XX
DT 15-AUG-2001 (first entry)
XX
DE Human genomic DNA encoding a rheumatoid arthritis associated protein.
XX
KW Rheumatoid arthritis; transmembrane protein; human; ds.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 89..1342
FT /tag=a
FT /product="Rheumatoid arthritis associated protein"
XX
PN WO200132921-A2.
PD 10-MAY-2001.
XX
PE 01-NOV-2000; 2000WO-JP07690.
XX
PR 01-NOV-1999; 99JP-0310805.
XX
PA (SHIO/) SHIOZAWA S.
PI Shiozawa S, Konishi Y;
XX
DR MPI: 2001-308750/32.
XX
DR P-PSDB; AAB97370.
XX
PT Diagnosing rheumatoid arthritis by probing digested human genomic DNA
PT or comparing expression of mRNA or polypeptide of a region of
PT transmembrane protein
XX
PS Claim 1: Page 14-18; 21pp; Japanese.
XX
CC This invention relates to a method of diagnosing chronic rheumatoid
CC arthritis by digesting human genomic DNA with EcoRI and hybridizing it
CC with a probe containing a fragment of the present sequence which
CC represents DNA encoding a transmembrane protein. The method is used for
CC the diagnosis of chronic rheumatoid arthritis, and for developing new
CC treatments.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;
Alignment Scores:
Pred. No.: 7.06e-122 Length: 1634
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-993-234-6 (1-417) x AAH27782 (1-1634)
QY 1 MetGluAlaArgProAlaGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
DB 89 ATGAGAGCGCGCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCTGCTGCTG 148
QY 21 GlyAlaAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
|||||

DB 149 GGGCGCCCGCCAGCGCGCGCTGTACCCCAAGGTGTGACTGTCCGCTTCAC 208
QY 41 LysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisIleTyrLeuLysAlaPro 60
DB 209 AAGAAATTTGCTCTGTTTGTTCAGAGCGCTGCCAGCGGGGCGACTGTGAAGGCCCT 268
QY 61 CysThrGluProCysGlyLysSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
DB 269 TGCACGAGCCCTCGCGGCACTCCACCTGCTGTGTCTCCCAAGACACCTTCTTGCC 328
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAspSer 100
DB 329 TGGAGAAACCAACATATATCTGAATGTGCGCCCTGTCCAGGCTGTGATGAGCGACTTC 388
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
DB 389 CAGGTGCGCTGAGAACTGTTCAGCAGGCGGACACCCGCTGTGGCTGTGAAGCCAGGC 448
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnPro 140
DB 449 TGTGTTGTGAGTGTCCAGGTCCAGCCAAATGTTCAGCAGTTCACCTTCTACTGTCCAAACA 508
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisIleThrArgLeuLeuCysSerArgArgAspThr 160
DB 509 TGCCTAGACTGCGGGGCGCTGTGACCGCCACACAGCGCTACTCTGTTCGCCAGATACT 568
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
DB 569 GACTGTGGAGCTGCTCTGCTGCTGTATGAACTGCGATGCGTGTGCTGCTGCTGCTGCTG 628
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyThrArgGlnMet 200
DB 629 ACGACACACCTGGGGAGCTGTCCAGAGCGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGT 688
QY 201 PheTyrValGlnValLeuLeuAlaGlyLeuValAlaProLeuLeuGlyAlaThrLeu 220
DB 689 TTCTGGGTCCAGGTGCTCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 748
QY 221 ThrTyrThrTyrArgHisCysThrProHisLysProLeuValIleThrAlaAspGluAlaGly 240
DB 749 AACTACACATACCCCGCACTGTGTGCTCACAAGCCCTGTGTGTGTGTGTGTGTGTGTGTGT 808
QY 241 MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
DB 809 ATGAGGCTGTGACCCCAACACCGCCACCATCTGTACACCTGTGACACGCGCCACACCC 868
QY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280
DB 869 CTCTAGACACTCTGTACAGAGTGAAGAAATGTGCACCGCTGTGTGTGTGTGTGTGTGTGTGT 928
QY 281 TrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValIleThrTyrPheTyr 300
DB 929 TGGACCCCTGTGCTACCCCGAGACCCAGAGAGCGCTGTGCGCGAGGTGATGATGCTCTGG 968
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
DB 989 GACCAGTTGCCAGACAGAGCTGTGGCCCGCTGTGCGCCACACACTCTGCCAGAGCTCC 1048
QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
DB 1049 CAGCGCGCTGCGCGAGCAAGATGTGTGACCGCGCGCGCTGTACGACAGCTGTGATGGAGC 1108
QY 341 AlaValProAlaArgArgTyrGlyGluPheValArgThrLeuGlyLeuArgGlyValGln 360
DB 1109 GCGGTCCACAGCGCGCGCTGGAAGGAGTGTGTGCGACGCTGTGGGCTGTGGCGAGGAGAG 1168
QY 361 IleGluAlaValAluValGluIleGlyArgPheArgAspGlnIleTyrGluMetLeuLys 380
DB 1169 ATCGAAGCCCTGTGAGGTGTGAGATGCGCGCTGTCCGAGACAGAGATACGATGCTCAAG 1228
QY 381 ArgTPrAArgInGInGInProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
DB 1229 GCGTGGCGCCAGCAGACCGCGCGCTGAGACCGCTTACGGCGCCCTGAGACCGCATG 1288
|||||

QY 401 GtLLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
|||||
Db 1289 GGGCTGAGCGGCTGCTGGAGACTGTGGCAGCGCGCTGAGCGGCCG 1339
RESULT 6
MAL47186
ID MAL47186 standard; cDNA; 1634 BP.
XX
AC MAL47186;
XX
DT 22-ADG-2002 (first entry)
XX
DE Human rheumatoid arthritis associated DR3 gene related cDNA #1.
XX
KW Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH CDS 89..1342
FT /*tag= a
FT /product= "AA017879"
XX
PN WO200234912-A1.
XX
PD 02-MAY-2002.
XX
PF 24-OCT-2001; 2001WO-JP09313.
XX
PR 24-OCT-2000; 2000JP-0324296.
PR 27-MAR-2001; 2001JP-0090546.
PR 30-MAR-2001; 2001JP-0099990.
XX
PA (NEUT-) NEW IND RES. ORG.
PA (SHIO/) SHIOZAMA S.
XX
PI Shiozawa S, Konishi Y;
XX
DR WPI: 2002-417132/44.
DR P-PSDB; AA017879.
XX
PT Genomes, particularly DR3 genomic DNA, participating in rheumatoid
PT arthritis via mutation, useful in evaluating disease onset and its
PT possibility and providing therapy and remedies -
XX
PS Example 1; Page 66-69; 84pp; Japanese.
XX
CC The present invention relates to the human DR3 gene, which is associated
CC with rheumatoid arthritis. Certain mutations in the gene can be linked to
CC the disease. The sequences can be used to evaluate disease onset and its
CC possibility and to provide therapy and remedies. The present sequence is
CC a coding sequence described in the exemplification of the invention.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:
Pred. No.: 7, 06e-122 Length: 1634
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-993-234-6 (1-417) x MAL47186 (1-1634)
QY 1 MetGtLglnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeuLeu 20
|||||
Db 89 ATGAGACACCGCGCGCGGCTGCGCGGCTGCGCGGCTGCTCTGCTGCTGCTG 148
QY 21 GtYAlaArgAlaGlnGlnGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
|||||

Db 149 GGGCCCCGGGGCCAGGGCGGCGACTGTAAGCCCGAGGTGTGACTGTGCGGCTGCTCCAC 208
QY 41 LysLysLleGlyLeuPheCysArgGlyCysProAlaGlyHisThrLeuLysAlaPro 60
|||||
Db 209 AAGAAGATTGGTCTGTTTGTTCAGAGGCTGCGCCAGGGGCACTACCTGAAAGGCCCTT 268
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 269 TGCACGAGGCCCTGGCGCACTCCACCTGCGCTTGTGTGCCCAAGACACTTCTTGCC 328
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSer 100
Db 329 TGGAGAACCCACCATTAATTGTGAATGCCCCGCTGCGAGCCCTGTGATGAGAGGCCCTCC 388
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysProGly 120
Db 389 CAGGTGGCGCTGAGAACTTTCAGCAGTGGCCGACACCCGCTGTGCTTAAAGCCAGGC 448
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTrpCysGlnPro 140
Db 449 TGGTTTGTGAGTGCAGGTCAGCAATGTGTGACAGAGTTTCACCTTCTACTGCAACCA 508
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgAspPhe 160
Db 509 TGCCTAGACTGCGGGGCCCTGCACCCGACACAGGCTACTCTGTTCCCGAGAGTACT 568
QY 161 AspCysGlyThrCysLeuProGlyPheThrGluHisGlyAspGlyCysValSerCysPro 180
Db 569 GACTGTGGAGCTGCTGCTGCTGCTTCTATGAACATGCGATGCGCTGCTGCTGCTGCTG 628
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMet 200
Db 629 ACAGAGACCCCTGGGAGAGCTGCCAGAGCGGTGTCGCGCTGTGCTGCTGAGGACAGATG 668
QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeu 220
Db 689 TTCTGGGTCCAGGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 748
QY 221 ThrTrpThrTyrrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly 240
Db 749 ACCTACACATACCGCCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 808
QY 241 MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
Db 809 ATGAGAGCTGTGACCCACACAGCGCCACCACTGTGCACCTTGAGACAGCGCCACAC 868
QY 261 LeuLeuAlaProProAspSerSerGluLysLleCysThrValGlnLeuValGlyAsnSer 280
Db 869 CTCTAGACACTCTCTGACACAGCTGAGAMAGATCTGCACCTCCAGTTGTTGGGTAAACAGC 928
QY 281 TrpThrProGlyTrpProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrp 300
Db 929 TGAACCCCTGGCTACCCCGAGACCCAGAGGCGCTGTGCGCCGAGGTGACATGTGCTTGG 968
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
Db 989 GACCAGTTGCCAGCAGAGCTTTGGCCCGCGCTGCGCCACACTCTGCGCCAGAGTCC 1048
QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTrpAspValMetAsp 340
Db 1049 CCAGCCGGCTCGCCAGCAGATGCTGCACCCGCGCCGCTTACAGCAGTGAATGTGAC 1108
QY 341 AlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
Db 1109 GCGGTCCACAGCGCGCCCTGGAAGAGTTGTGTGCGCACGCTGGGGCTGCGCGAGCGAG 1168
QY 361 IleGluAlaValGluValGluLleGlyArgPheArgAspGlnGlnTrpGluMetLeuLys 380
Db 1169 ATGGAAGCCGTGAGAGTGAGATCGGCCGCTTCCGAGACAGATGAGATGCTCAAG 1228
QY 381 ArgTrpArgGlnGlnGlnProProAlaGlyLeuGlyAlaValTrpAlaAlaLeuGluValGmet 400
Db 1229 CGCTGGCGCCAGCAGAGCCCGCGGCGCTGAGCCGTTTACGCGCGCTGAGAGCGCATG 1288

QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
DB 1289 GGGCTGACGGCTGCGTGGAAAGACTTGGCCAGCGCGCTGAGCGCGGCCG 1339
RESULT 7
AAC91477
ID AAC91477 standard; cDNA; 1662 BP.
XX
XX AAC91477;
AC
XX
XX 21-MAR-2001 (first entry)
DT
XX
XX Human PRO779 cDNA.
DE
XX
XX Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW antineumatic; cardiant; antinaemic; immunosuppressive; antithyroid;
KW antiabetic; nootropic; neuroprotective; hepatocytic; virucide;
KW antiallergic; antiasthmatic; immune related disorder;
KW hepatobiliary disease; autoimmune disease; allergy; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200073452-A2.
PN
XX
XX 07-DEC-2000.
PD
XX
XX 02-JUN-2000; 2000WO-US15264.
PF
XX
XX 02-JUN-1999; 99WO-US12252.
PR 20-JUL-1999; 99US-0144732.
PR 20-JUL-1999; 99US-0144758.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28634.
PR 09-DEC-1999; 99US-0170262.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08438.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
XX
XX (GETH) GENENTECH INC.
PA
XX
XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL,
PI Hebert C, Henzel W, Kabakoff KC, Shelton DL, Tumas D, Watanabe CK,
PI Wood WI;
XX
XX WPI: 2001-025253/03.
DR P-PSDB; AAB50918.
XX
XX
XX Thirty three nucleic acids encoding PRO polypeptides which are useful
PT in the diagnosis and treatment of immune related disorders, e.g.
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
PT thyroiditis and diabetes mellitus -
XX
XX
XX Claim 48; Fig 33; 218pp; English.
XX
XX The present sequence is one of thirty three nucleic acids encoding PRO
CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and

CC antagonists are useful for treating and diagnosing immune related
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases
CC (such as infectious, autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC disease, autoimmune or immune-mediated skin diseases (such as bullous
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC food hypersensitivity and urticaria), immunological diseases of the
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
CC and hypersensitivity pneumonitis), transplantation associated diseases
CC including graft rejection and graft-versus-host diseases.
XX
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;
Alignment Scores:
Pred. No.: 7,19e-122 Length: 1662
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-993-234-6 (1-417) x AAC91477 (1-1662)
QY 1 MetGluGlnArgProArgGlyCysAlaAlaAlaAlaAlaLeuLeuValLeuLeu 20
DB 103 ATGGAGACGGCGCGCGGGCTGCGCGGGTGGCGGGCGGCTCTCTGCTGCTG 162
QY 21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
DB 163 GGGGCGCGGGCGCGAGCGGCGACATCTGACCCCGAGCTGACGTGGCGGACTCTCCAC 222
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlnIleIleIleValAlaPro 60
DB 223 AAGAGATTGGCTGTTTGTTCAGAGGCTGCCAGCGGGGACTACCTGAAGCCCT 282
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspPheLeuAla 80
DB 283 TGCAGGAGCCCTCGGCACTCCACCTGCTGTGTGCCAAGACACCTCTTG6CC 342
QY 81 TrpGluAsnHisAsnSerGluCysAlaAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
DB 343 TGGGAGAACCAACATAATTCGATGTGCCCGCTGCCAGGCTGTATGACAGGCTCC 402
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
DB 403 CAGGTGGCGCTGGGAACCTGTTCAGCAGTGGCCACACCCGCTGTGCTGAAGCCAGGC 462
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheProCysGlnPro 140
DB 463 TGGTTTGTGAGTCCAGGTCAGCCAAATGTCTCAGCAGTTCACCTCTTACTGCCAACCA 522
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
DB 523 TGCCTAGACTGGCGGGCCGCGACCGCCACACAGGCTACTGCTGCCGACAGAACT 582
QY 161 AspCysGlyThrCysLeuProGlyPheArgGlnHisGlyAspGlyCysValSerCysPro 180
DB 583 GACTGTGGAGCTGCTGCTGCTGTATGAAACATGGCATGGCTGCTGCTGCTGCTGCTG 642
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMet 200
DB 643 ACGAGCACCTGGGGAGCTGTCCAGAGCGCTGTGCGCTGTGTGGCGAGGAGATG 702

QY 201 PheTTPValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeu 220
 Db 703 TTTGGGTTCAGAGTGTCTCTGGGCTGTGGTCTCCCTCCCTGCTGGGGCCACCTG 762
 QY 221 ThrTyrThrTyrArgHisCysTyrProHisLysProLeuValThrAlaAspGluAlaGly 240
 Db 763 ACCACACATACCCGCACTGCTGCTCACAAGCCCTGGTACTGCAAGATGAAGCTGG 822
 QY 241 MetGluAlaLeuThrProProAlaThrHisLysSerProLeuAspSerAlaHisThr 260
 Db 823 ATGAGAGCTGTGACCCACACAGCGGCCACCATCTGTACACCTTGGAGAGGCCACACC 882
 QY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280
 Db 883 CTCTGTACACCTCTCTGACAGAGTGAAGATCTGCACCGCTCCAGTGTGGTAAACAGC 942
 QY 281 TrpThrProGlyTyrProGlyuThrGlnGluAlaLeuCysProGlnValThrTrpSerTrp 300
 Db 943 TGGACCCCTGGCTTACCCCGACACCCAGAGGCGCTGTGCGCCAGGTGACATGGTCTGG 1002
 QY 301 AspGlnLeuProSerArGAlaLeuGlyProAlaAlaAlaProThrLysSerProGlyLys 320
 Db 1003 GACCAAGTTGCCACACAGAGCTTGGCCCGCTGCTGCGCCACACTCTGCCAGAGTCC 1062
 QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
 Db 1063 CCAGCCGCTGCGCAGCATGATGCTCAGCGCGCCGCGCAGCTCTACAGAGTATGGAC 1122
 QY 341 AlaValProAlaArgArGTPLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
 Db 1123 GCGGTCCACAGCGCGCCCTGGAAGAGTCTGCGCAGCGCGGCTGCGCGAGGACAG 1182
 QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
 Db 1183 ATGGAACCCGTGGAGGTGGAGATGGCGGCTTCGGAACACAGCATGAGATCTCAAG 1242
 QY 381 ArgTTPArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
 Db 1243 CGGTGGCGCAGCAGCAGCGCGCGGCTGCGACCGCTTTCAGCGCGCTTGGAGCGCATG 1302
 QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
 Db 1303 GGGCTGACAGGCTCTCGTGAAGACTTCCGACGCCCTGACGCCGCGGCCG 1353
 RESULT 8
 ABK40265
 ID ABK40265 standard; cDNA; 1662 BP.
 AC ABK40265;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE cDNA encoding human PRO779 polypeptide.
 XX
 KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
 KW Leukemia; neuronal disorder; stromal disorder; blastocellular disorder;
 KW Inflammatory disorder; immune disorder; angiogenic disorder;
 KW gene therapy; cytostatic; neuroprotective; gene; ss.
 XX
 OS Homo sapiens.
 PN MO200153486-A1.
 PD 26-JUL-2001.
 XX
 PF 11-FEB-2000; 2000MO-US03565.
 XX
 PR 08-MAR-1999; 99MO-US05028.
 PR 11-MAR-1999; 99US-123972P.
 PR 11-MAY-1999; 99US-133459P.
 PR 02-JUN-1999; 99MO-US12252.
 PR 22-JUN-1999; 99US-140650P.
 PR 22-JUN-1999; 99US-140653P.

PR 20-JUL-1999; 99US-144758P.
 PR 26-JUL-1999; 99US-145698P.
 PR 28-JUL-1999; 99US-146222P.
 PR 17-AUG-1999; 99US-149395P.
 PR 31-AUG-1999; 99US-151689P.
 PR 01-SEP-1999; 99MO-US20111.
 PR 15-SEP-1999; 99MO-US21090.
 PR 30-NOV-1999; 99MO-US28313.
 PR 01-DEC-1999; 99MO-US28301.
 PR 01-DEC-1999; 99MO-US28634.
 PR 05-JAN-2000; 2000MO-US00219.
 XX
 PA (GENENTECH INC.
 XX
 PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
 PI Masters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
 PI Watanabe CK, Wood WI;
 XX
 DR WPI; 2002-205567/26.
 DR P-PSDB; AAU86139.
 XX
 PT Thirty five nucleic acids encoding PRO polypeptides, useful for
 PT treating benign or malignant tumours, leukemias and lymphoid
 PT malignancies, inflammatory, angiogenic and immunologic disorders -
 XX
 PS Claim 50; Fig 23; 302pp; English.
 CC
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides and the polynucleotide sequences encoding them. The
 CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
 CC useful for treating benign or malignant tumours (e.g. renal, kidney,
 CC bladder, breast, etc), leukemias and lymphoid malignancies, other
 CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
 CC macrophagal, stromal and blastocellular disorders, inflammatory, immune
 CC and angiogenic disorders. The polynucleotide sequences are also
 CC useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
 CC polypeptides of the invention.
 XX
 SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;
 Alignment Scores:
 Pred. No.: 7,19e-122 Length: 1662
 Score: 2323.00 Matches: 417
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0
 US-09-993-234-6 (1-417) x ABK40265 (1-1662)
 QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeuLeu 20
 Db 103 ATGAGACAGCGCGCGCGGCTGCGCGGCTGCGCGGCTGCTCTGCTGCTG 162
 QY 21 GAlaAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
 Db 163 GGGGCGCGCGCGCGAGGCGGCGCATGAGCCAGGTGTGACTGTGCGCGGTGACTTCAC 222
 QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
 Db 223 AAGAAGATGTGCTGCTTTTGTTCAGAGGCTGCCACGCGGCGCACTACCTCAAGGCCCT 282
 QY 61 CysThrGlnProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
 Db 283 TGCACGAGCCCTCGCGCACTCCACTGCTGTGTGTCCCAAGACACTTCTGTGCC 342
 QY 81 TTPGLuAsnHisLysAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
 Db 343 TGGAGAGAACCACTAATTTGTGAATGTGCCCGCTGCAGGCTGTGATGACAGAGGCTCC 402
 QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
 Db 403 CAGGTGGCGCTGAGAACTGTTACAGAGTGGCCGACACCCCGCTGTGCTTAAGCCAGGC 462

QY	121	TRPHEVALGLUCYGLINVALSERGLINCYSVALSERSERPROPHETRYCSGLINPRO	140
Db	463	TGGTTTGTGGAGATGGCCAGCTGACGCCAAGGTGCAGAGTTCCACCTTCTACTGCCAACCA	522
QY	141	CYSLEASPCCYSGLVALALEUHIISARGTISITHRARGLEUCYSSERATGATGAPTHR	160
Db	523	TGCCTAGACTGGGGGGCCCTGCACGCCACACAGGCTACTCTGTCCCGAAGATACT	562
QY	161	ASPCYSGLYTHRYSLEUPROGLYPHERTRYGLUHSISGLYSPGLYCSVALSERCYSPRO	180
Db	583	GACTGTGGAGACCTGGCTCTCCGTGGCTTCTATACATGATGCGATGGCTGCTGTGCTCGCCGCC	642
QY	181	THRSERTHLEUGLYSERCYSPROGLIARGLYSVALALVALYCSGLYTPRPAAGINMET	200
Db	643	ACGACACACCTGGGAGCTGTCCAGAGCGCTGTCCCTGTCTGTGGCTGGAGCGAATG	702
QY	201	PHERTPVALGLINVALLEULEUALAGLYLEUENVALAIPROLEULEULEUGLYALATPHLEU	220
Db	703	TTCCTGGTCCAGAGTCTCTGCTGGCCCTTGCTGCCCTCCGTCGTGGGGCACCTCG	762
QY	221	THRTYRTHRYTPRARGHISCYSTPRPROHISYSSTROLEUENVALTHRALASPGLUALAGLY	240
Db	763	ACCTACACATACCGGCACCTGTGGCTCTCACAGGCCCTGTGTTACTGACATGTAAGCTGGG	822
QY	241	METGLUALALEUTHRPROPROALATATHRHSILEUSERPROLEUASPSPERALAHSRTHR	260
Db	823	ATGGAGGCTGTGACCCCCACACCGGCCACCCATCTGTACACCTTGACAGCGCCACAC	882
QY	261	LEULEUALAPROPROASPSSERSERGLINLYSILECYSTHYVALGLINLEUVALGLYASNSER	280
Db	883	CTTCTAGCACTCTCTGCAGAGTGAAMAATCTGCACCGTCCAGTTGGTGGTTACACAC	942
QY	281	TPRTHRPROGLYTYRPROGLUPTHGGLIALALEUCYSPROGLINALTHRTTPSERTPR	300
Db	943	TGGACCCCTGGCTACCCCGAGACCAGAGAGCCCTGTGCCCGCAGGTGACATGTCTTG	1000
QY	301	ASPGINLEUPROSERATGALALEUGLYPROALALALALAPROTHREUSERPROGLUSER	320
Db	1003	GACCAAGTGGCCACACAGCTCTTGGCCCCGCGCTGGCCCCACACTCTGCGCAGAGTCC	1060
QY	321	PROIAGLYSERPROALAMETLEUGINPROGLIYPROGLINLEUYRASPVALMETAP	340
Db	1063	CCAGCGCGCTGGCCAGGCATGATGTCTGCACCGGGCCCGCATGCTTACACATGATGAC	1122
QY	341	ALAYALPROIALATARGATGTPPLYSGLINPHEVALARGTHREUGLYLEUARGGLUALAGLI	360
Db	1123	GGCGTCCAGCGCGCCCTGTGAAGAGATTGTCTGCACACTGGGGCTGGCGGAGGAGAG	1182
QY	361	ILEGLUALAYALGLINVALGLIUILEGIARGYPHARGLASPGLINTRYRILMETLEULYS	380
Db	1183	ATCCAAACCCGTGGAGGTGGAGATTCGGCCGCTTCCGAGACCAAGATGACAGATGTCTCAAG	1242
QY	381	ARGTPRARGLINGLINGLINPROIAGLYLEUGLYALAYALTYRVALALALEUULARGMET	400
Db	1243	CGCTGGCGCCAGCGACGACCCCGGGGCGCTGGAGCCGTTTACGGCGGCCCTGGAGGCGATG	1302
QY	401	GLYLEUASPGLYCSVALGLIASPLEUARGSERATRGLEUGINARGGLYPRO	417
Db	1303	GGGCTGACAGCGCTGTGGTGAAGACTTGGCAGCGCTGTCCACGCGGGCCG	1353

	RESULT 9
AAV28700	
ID	AAV28700 standard; cDNA, 1847 BP.
XX	
XX	
AC	AAV28700;
XX	
DT	20-AUG-1998 (first entry)
XX	
DE	Human apoptosis inducing receptor coding sequence.
XX	
KM	Apoptosis inducing receptor; AIR protein; human; cell death regulator;
XX	type I transmembrane protein; tumour cell death; autoimmune disease;

KW	therapy; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	236..1489	
FT		/*tag= a	
FT		/product= AIR	
XX			
PN	W09814565-A1.		
XX			
PD	09-Apr-1998.		
XX			
PF	03-Oct-1997;	97WO-US17876.	
XX			
PR	04-Oct-1996;	96US-0044456.	
XX			
PA	(IMMV) IMMUNEX CORP.		
XX			
PI	Perkins PA;		
XX			
DR	WPI; 1998-240077/21.		
DR	P-PSDB; AAW57045.		
XX			
PT	DNA encoding apoptosis inducing receptor - which is Type I		
PT	transmembrane protein, useful for regulating cell death		
XX			
SS	Claim 2; Page 28-30; 45pp; English.		

Sequence 1847 BP; 316 A; 605 C; 579 G; 347 T; 0 other;

Alignment Scores:	
Pred. No.:	8.05e-122
Score:	2323.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	19
Length:	1847
Matches:	417
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-993-234-6 (1-417) x AAV28700 (1-1847)

QY 1 MeluGlnArpProArgIgcYcysAlaAlaValAlaAlaAlaLeuLeuValLeuLeu 20
Db 236 ATGGAGCAGCGGGCGGGGGCTCGCGGGGGGGGGGGCGTCCTCGTCTCTG 295
QY 21 G1yAlaArpAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 296 GGGGCGCGGGCGGAGGGCGCAGCTGGTAGCCCGCAGCTGTGACTGCGGGACTTCAC 355
QY 41 LysLysIleGlyLeuPheCysCysArgIgcYcSProAlaGlyHisTyrLeuLysAlaPro 60
Db 356 AATAAATTTGGTCGTGTTTGTGTGCAGAGGCTGCCAGCGGGGCACTGAAAGGCCCT 415
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValLysProGlnAspTrpPheLeuAla 80
Db 416 TGCACGGAGCCCTCGCGCACTCCACCTGCTGTGTCTCCCAAGACACCTTCCTGGCC 475
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
Db 476 TGGGAGAACCACACATATTCTGAATGTGCCCGGCTGCCAGGCGCTGTGATGACAGGCCCTCC 535
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120

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Db 536 CAGGTGGCGCTGGAGAACTGTTGACAGAGTGGCCGACACCCGGCTGTGCTTAAGCCAGGC 585
Qy 121 TRPPhenylGluCysGlnValSerGlnCysValSerSerSerProPheTyCysGlnPro 140
Db 596 TGGTTTGTGGAGTGGCCAGGTCACCAATGTGTGACAGATTACACCCCTTACTTCCCAACCA 655
Qy 141 CysLeuAspCysGlyAlaLeuHisArgHisIsthrArgLeuLeuCysSerArgArgaPthr 160
Db 656 TGGCTGTAGACTGGGGGGCCCTGCACCCGACACAGGCTACTGTGTGCCGACAGATTAAT 715
Qy 161 AASPcysGlyThrCysLeuProGlyPheTyGlnHisGlyAspGlyCysValSerCysPro 180
Db 716 GACTGTGGAGCTGCTGCTGCTGCTGTATGAACATGGGATGGCTGCTGCTGCTGCTGCTGCT 775
Qy 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTTPArgGlnMet 200
Db 776 AGSAGACCCCTGGGGAGAGTGTCCAGAGCCCTGTGCGGCTGTCTGTGTGGCTGGAGCAGATG 835
Qy 201 PheTPrValGlnValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeu 220
Db 836 TTCTGGGTCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 895
Qy 221 ThrTyThrThrArgHisCysTrpProHisIsthrProLeuValThrAlaAspGlyAlaGly 240
Db 896 ACCTACACATACCCGCACTGTGGCTGCACACACCCCTGTGTTACTGACAGTGAAGCTGGG 955
Qy 241 MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
Db 956 ATGGAGGCTGTGACCCCAACCCAGCCGACCCACCACTGTCAACCTTGGACAGCCGCCACAC 1015
Qy 261 LeuLeuAlaProProAspSerSerGlyIsthrIsthrValGlnLeuValGlyAsnSer 280
Db 1016 CTTCGTAGCACTCTCTACAGACAGTGAAGATGTGCACCGTCCAGTGGGGGTAAACAGC 1075
Qy 281 TTPThrProGlyTyrProGlyThrGlnGlnGlnAlaLeuCysProGlnValTTPTrpSerTrp 300
Db 1076 TGGACCCCTGGGTACCCCAAGACCCAGAGAGCGCTGTGCCGAGGTGACATGCTCTGTG 1135
Qy 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGlyUser 320
Db 1136 GACCAATTCGCCAGACACTCTTGGCCCGCGCTGCGCCCACTCTGCCAGAGATCC 1195
Qy 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
Db 1196 CCAAGCCGCTGCCACGCACTGATGCTGACAGCCGCGCCGACGCTACAGCATGATGAGAC 1255
Qy 341 AlaValProAlaArgArgTrpIsthrIsthrValArgThrLeuGlyLeuArgGlyAlaGln 360
Db 1256 GCGGTCCAGCGCGCGCTGGAGAGTTCGTGCGACAGCTGGGGCTGCGCGAGGACAG 1315
Qy 361 IleGluAlaValGlnValGlnIleGlyArgPheArgAspGlnGlnTyrGlnMetLeuLys 380
Db 1316 ATCGAAGCCGTGGAGGTGGAGATCGGCCCTTCCGAGACAGACAGATGACGATGCTCAAG 1375
Qy 381 ArgTPrArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlnArgMet 400
Db 1376 CGCTGGCGCCAGACAGACGCGCGCGCTGAGCGCTTACCGCGCCCTGAGAGCATG 1435
Qy 401 GlyLeuAspGlyCysValGlnAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 1436 GGGCTGGACGGCTGCTGGAGAACCTTGGCGAGCGCTGACGCGGCGCGC 1486

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KW Inflammation; NF-kappaB; ds.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH CDS 198..1484
FT sig_peptide 198..302
FT mat_peptide 304..1481
FT /tag= a
FT /tag= b
FT /tag= c
PN W09733904-A1.
XX
PD 18-SEP-1997.
XX
PF 17-OCT-1996; 96MO-US16849.
XX
PR 12-MAR-1996; 96DS-0013285.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
PI Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
DR WPI: 1997-470812/43.
DR P-PSDB; AAW31516.
XX
PT Death domain containing receptor polypeptide(s) DR3 and DR3-V1 -
PT for activation of apoptosis and NF-kappaB, antagonists can be used
PT to treat inflammatory diseases
PS
XX Claim 2; Page 71-73; 108pp; English.
CC This cDNA clone, deposited as ATCC 97456, codes for human death
CC domain containing receptor DR3-V1 (see AAW31516), a novel member of
CC the tumor necrosis factor receptor family. It was isolated from a
CC cDNA library derived from cells of a human testis tumour. Related
CC death domain containing receptor DR3 cDNA (see AAT89427) was isolated
CC from a HUVEC cDNA library. The genes have also been identified in
CC cDNA libraries of foetal liver, foetal brain, tonsil and leukocyte.
CC Nucleic acids encoding full-length or mature DR3-V1 can be used to
CC produce recombinant polypeptides in transformed host cells. These
CC polypeptides can be used to treat diseases and disorders associated
CC with the inhibition of apoptosis. Antagonists, such as antibodies
CC raised against DR3-V1, can be used to treat diseases and disorders
CC associated with increased apoptosis and for treating inflammatory
CC diseases and disorders.
XX
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;
XX
Alignment Scores:
pred. No.: 1,08e-118 Length: 1783
Score: 2267.00 Matches: 409
Percent Similarity: 97.39% Conservative: 1
Beet Local Similarity: 97.15% Mismatches: 5
Query Match: 97.59% Indels: 6
DB: 18 Gaps: 1
US-09-993-234-6 (1-417) x AAT89426 (1-1783)
Qy 3 GlnArgProArgGly-----CysAlaAlaValAlaAlaAlaLeuLeu 16
Db 219 GAGGCCCCAGCTGGCGACGTCGCGGAGAGTCAACAGACACTGTCCCCAGCGGCTCTCTC 278
Qy 17 LeuValLeuLeuGlnAlaAlaGlnGlyGlyThrArgSerProArgCysAspCysAla 36
Db 279 CTGGTCTCTGCTGGGGCCCGCGCCAGGCGCGCACTGTAGCCCAAGGTGTGACTGGCC 338
Qy 37 GlyAspPheHisIsthrIsthrIleGlyLeuPheCysCysArgGlyIsthrProAlaGlyHisTyr 56
Db 339 GGTGACTTCCACAAGAAAGATTGTGTGTTGTGACAGAGGCTCCACAGCGGGGCACTAC 398

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QY 57 LeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAsp 76
    |||
Db 399 CTGAAGCCCTTGGACGAGGAGCCCTGGCCACTCCACTGCTGTGTGTCCTCCCAAGAC 458
QY 77 ThrPheLeuAlaIrrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAsp 96
    |||
Db 459 ACCTTTTGGCCCTGGAGAAACCACTTAATTTGAAATGTGCGCGCTGCAAGGCTGTGAT 518
QY 97 GluGlnAlaSerGlnValAlaLeuGluAsnGlySerAlaValAlaAspThrArgCysGly 116
    |||
Db 519 GAGCAGGCTCCAGAGTGGCGCTGAGAACTGTTTCAGCAGTGGCCGACACCGCTGTGGC 578
QY 117 CysLysProGluThrPheValGluCysGlnValSerGlnCysValSerSerProPhe 136
    |||
Db 579 TGTAAAGCCAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 638
QY 137 TyrCysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuSer 156
    |||
Db 639 TACTGCCAACATGCTTACACTGCGGGGCGCTGCACCGCCGACACAGGCTACTGTGTC 698
QY 157 ArgAlaArgPheThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCys 176
    |||
Db 699 CCGAGAGATGACTGACTGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 758
QY 177 ValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGly 196
    |||
Db 759 GTGTCTGCTCCCAAGACAGACCCCTGGGAGCTGTCCAGAGCGCTGTGTGTGTGTGTGT 818
QY 197 TrpArgGlnMetPheTrpValGlnValLeuAlaGlyLeuValValProLeuLeuLeu 216
    |||
Db 819 TCGAGGCAAGATGTCTGGGTCCAGGTCCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 878
QY 217 GlyAlaThrLeuThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAla 236
    |||
Db 879 GGGGCGACCCCTGACATACATACCGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 938
QY 237 AspGluAlaGlyMetGlnAlaLeuThrProProProAlaThrHisLeuSerProLeuAsp 256
    |||
Db 939 GATGAAGCTGGATGAGAGCTGTGACCCACACCGCCGACCCACTGTGACCTTGGAC 998
QY 257 SerAlaHisThrLeuLeuAlaProAspSerSerSerGluLysIleCysThrValGlnLeu 276
    |||
Db 999 AGCGCCACACCCCTTCTAGCACCTCTGACAGACTGAGAAATGTGCACCTCCAGTTG 1058
QY 277 ValGlyAsnSerTrpThrProGlyTyrProGluThrGlnAlaLeuCysProGlnVal 296
    |||
Db 1059 GTGGTAAACAGCTGAGACCCCTGCTACCCCGAGACCCAGAGGCGCTGCGCCGAGGTG 1118
QY 297 ThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeu 316
    |||
Db 1119 ACATGCTCTGGAGACATTTGCCAGCAGAGCTTGGCCCGCTGCTGCGCCACACTTC 1178
QY 317 SerProGluSerProAlaGlySerProAlaMetLeuGlnProGlyProGlnLeuTyr 336
    |||
Db 1179 TCGCCAGAGTCCCGCCAGCGCTCCGACCATGATGTGACAGCGGCGCCGACAGTCTAC 1238
QY 337 AspValMetAspAlaValProAlaArgTrpTrpLysGluPheValArgThrLeuGlyLeu 356
    |||
Db 1239 GACGATGAGAGCGGCTCCAGCGCGCTGAGAGGAGTTCGTGCGCACCTGCGGCTG 1298
QY 357 ArgGluAlaGluIleGluAlaValAlaGluValGluIleGlyArgPheArgAspGlnGlyTyr 376
    |||
Db 1299 CGCGAGGAGAGATCGAAGCCGTGAGAGTGTGAGATCGGCCCTTCCGAGACACAGTAC 1358
QY 377 GluMetLeuLysArgTyrPArgGlnGlnGlnProAlaGlyLeuGlnAlaValTyrAlaAla 396
    |||
Db 1359 GAGATGCTCAAGCGCTGCGCCAGCAGACAGCGCGGCGCTCGGAGCGCTTACGCGGCC 1418
QY 397 LeuGluArgMetGlyLeuAspGlyCysValGluLysLeuArgSerArgLeuGlnArgGly 416
    |||
Db 1419 CTGAGAGCGCATGGGGCTGAGAGCGCTGCTGAGAACTTGGCAGACCGCTGACGCGGC 1478
QY 417 Pro 417

```

```

Db 1479 CCG 1481
    |||
RESULT 11
AAK00924
ID AAK00924 standard; cDNA, 1783 BP.
AC AAK00924;
XX
AC AAK00924;
XX
DT 25-MAR-1999 (first entry)
XX
DE Death domain containing receptor polypeptide (DR3-V1) encoding cDNA.
XX
KW Death domain; receptor; DR3-V1; DR3; recombinant; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 198..1484
FT /tag= a
FT /product= "Death domain containing receptor DR3-V1"
FT /tag= b
FT mat_peptide 301..1481
FT /tag= c
XX
PN JP11000170-A.
XX
PD 06-JAN-1999.
XX
PE 12-MAR-1997; 97JP-0057503.
XX
PR 06-FEB-1997; 97US-0037341.
PR 12-MAR-1996; 96US-0013285.
PR 17-OCT-1996; 96US-0028711.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI) UNIV MICHIGAN.
XX
DR WPI: 1999-124390/11.
DR P-PSDB: NAM95537.
XX
XX
XX New death domain containing receptor and recombinant vector -
XX optionally comprising leader sequence
XX
XX Claim 2; Fig 1, 2; 50pp; Japanese.
XX
XX The invention provides nucleotide sequences encoding death domain
XX containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
XX is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
XX contained in ATCC deposition No. 97757. Recombinant vectors comprising
XX the nucleic acid sequences and optionally the leader sequences are
XX used for the recombinant production of the proteins. The present
XX sequence represents a cDNA encoding the death domain containing
XX receptor polypeptide (DR3-V1).
XX
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

```

Alignment Scores:

```

Pred. No.: 1.08e-118 Length: 1783
Score: 2267.00 Matches: 409
Percent Similarity: 97.39% Conservative: 1
Best Local Similarity: 97.15% Mismatches: 5
Query Match: 97.59% Indels: 6
DB: Gaps: 1

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US-09-993-234-6 (1-417) x AAK00924 (1-1783)

```

QY 3 GlnArgProArgGly-----CysAlaAlaValAlaAlaAlaLeu 16
    ::| |||||
Db 219 GAGGCCCAAGTGGGAGAGTCCGCGAGAGTACAGACACTGTCCCGCAGCGCTCTC 278
QY 17 LeuValLeuGlnGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAla 36

```

Db 279 CTGGTCTCTGGGGCCGGGGCCAGGGGGGACCTGTAAGCCCGAGGTGTGCTGTGGC 338
 Oy 37 GLYAspPheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyr 56
 Db 339 GGGATCTTCACAGAAAGATGTGTCTGTTGTGTGAGAGAGCGCCAGCGGGGACATAC 338
 Oy 57 LeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAsp 76
 Db 399 CTGAAGGCCCTTGCACAGGAGCCCTGGCAACTCCACCTGCTGTGTGTCTCCCAAGAC 458
 Oy 77 ThrPheLeuAlaTropGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAsp 96
 Db 459 ACCTTCTTGCTGGGAGAACCAACCAATATCTGAATGTGCCCGCGCCAGGCTGTGAT 518
 Oy 97 GLUGlnAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGly 116
 Db 519 GAGCAGGCTCCAGAGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGC 578
 Oy 117 CysLysProGlyTyrPheValGluCysGlnValSerGlnCysValSerSerProPhe 136
 Db 579 TGTAAACCCAGGCTGTTGTGTGAGTGCAGTCCAGTCAATGTGTGACAGTTCACCCCTTC 638
 Oy 137 TyrCysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSer 156
 Db 639 TACTGCCAACATGCTTACACTGCGGGGCTGACCGCCACACAGCGCTACTCTGTCC 698
 Oy 157 ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCys 176
 Db 699 CGCAGAGATACACTGACTGTGGAGCTGCTGCTGCTGTCTATGAACTGGCGATGTGCTGC 758
 Oy 177 ValSerCysProThrSerThrLeuGlySerCysProGlnArgCysAlaValCysGly 196
 Db 759 GGTCTGCTGCCCGCAGCAGCAACCTGGGAGCTGTCCAGAGCGCTGCTGCTGTGCTGCG 818
 Oy 197 TrpArgGlnMetPheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuLeu 216
 Db 819 TGGAGGCAATGTGTGGGTCCAGGTGCTGCTGGCTGTGCTGCTGCTGCTGCTGCTGCT 878
 Oy 217 GlyAlaThrLeuThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAla 236
 Db 879 GGGGCCACCTGACCTACACATACCCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 938
 Oy 237 AspGluAlaGlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAsp 256
 Db 939 GATGAAGCTGGGATGAGAGCTGTGAGCCACACCGCCACCATCTGTACACCTTGAGAC 998
 Oy 257 SerAlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeu 276
 Db 999 ACGGCCACACCTTCTACACCTCTGACAGCAGTGAAGATGTGACACCTGTCCAGTTG 1058
 Oy 277 ValGlyAsnSerThrPheProGlyTyrProGluThrGlnGluAlaLeuCysProGlnVal 296
 Db 1059 GTGGGTAAAGCTGGAGCCCTGGCTTACCCCGAGACCCAGAGAGCGCTGTGCGCAGGTG 1118
 Oy 297 ThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeu 316
 Db 1119 ACATGTCTCTGGGACCAAGTGTGCCACAGAGCTCTTGCCCGCTGCTGCGCCACACATC 1178
 Oy 317 SerProGluSerProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyr 336
 Db 1179 TCGCCAGATCCCGACCGCTGCGCCAGCAGATGCTGACGCGGCGCGCGCTGAC 1238
 Oy 337 AspValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeu 356
 Db 1239 GACGTATGAGACCGGTCCACGCGCGCGCTGGAGAGATGTGCTGCGCAGCGTGGGCTG 1298
 Oy 357 ArgGluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyr 376
 Db 1299 CCGAGAGCAGAGATCGAACCGGTGAGGTGAGATGCGCGCTGCGAGACAGCAGGTAC 1358
 Oy 377 GluMetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyValAlaValTyrAlaAla 396

Db 1359 GAGATCTCAAGCGCTGGCGCCAGCAGACCCCGGGGCTTGGAGCCGTTTACGGCGCC 1418
 Oy 397 LeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGly 416
 Db 1419 CTGAGCGCATGGGCGCTGGAGCGCTGCTGTGAAGACTTGGCGACCGCCCTGACGCGCGC 1478
 Oy 417 Pro 417
 Db 1479 CCG 1481
 RESULT 12
 AAC68776 standard; cDNA: 1783 BP.
 AAC68776;
 20-FEB-2001 (first entry)
 Human death domain containing receptor DR3-VI coding sequence.
 Human: death domain containing receptor; DR3-VI; cancer;
 autoimmune disorder; inflammation; cardiovascular disorder; infection;
 neurodegenerative disease; angiogenesis; ss.
 Homo sapiens.
 WO200064465-A1.
 02-NOV-2000.
 21-APR-2000; 2000MO-US10741.
 22-APR-1999; 99US-0130488.
 28-MAY-1999; 99US-0136741.
 (HUMA-) HUMAN GENOME SCI INC.
 (UNMI) UNIV MICHIGAN.
 (YUGG/) YU G.
 (NIJ/) NI J.
 (GENT/) GENTZ R L.
 (DILL/) DILLON P J.
 (DIXI/) DIXIT V M.
 YU G, NI J, Gentz RL, Dillon PJ, Dixit VM;
 WPI: 2000-687263/67.
 P-PSDB: AAB36264.
 Treating graft-versus-host disease, cancer, immunodeficiency or an
 autoimmune disease comprising administering an antibody to Death Domain
 Containing Receptor proteins and a second therapeutic agent -
 Example 1; Fig 1; 273pp; English.
 The present invention provides the protein and coding sequences for two
 death domain containing receptors, designated DR3 and DR3-VI. These
 receptors are involved in apoptosis, and the sequences given can be used
 in the treatment of cancers, infections, cardiovascular disorders such as
 arrhythmias, ischemia, aneurysms, arterial occlusive diseases, embolisms
 and congenital heart defects, neurodegenerative diseases including
 Alzheimer's and Parkinson's diseases, autoimmune diseases such as multiple
 sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
 and to promote angiogenesis and wound healing.
 Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other:
 Alignment Scores:
 Pred. No.: 1,08e-118 Length: 1783
 Score: 2267.00 Matches: 409
 Percent Similarity: 97.39 Conservative: 1
 Best Local Similarity: 97.158 Mismatches: 5
 Query Match: 97.598 Indels: 6
 DB: 21 Gaps: 1

Db	1239	GACGTGATGAGACGGCGGTCCACACGGGGCGCGCTGGAGAGACTTCGTCCGACGCTGGGGCTG	1298
QY	357	ArgGluAlaIGluIleGluAlaValGluValGluIleGlyIleArgpheArgAspGlnGlnTyr	376
Db	1299	CGGAGGAGCAGAAATCGAACCCCTGGAGGAGTGAGATCGGCCCTTCCTCCGAGACCACGATAC	1358
QY	377	GIuMeIleuLysArgTyrPargGlnGlnGlnProIaGlyIleuGlyAlaValTyrIlaAla	396
Db	1359	GAGATGCTCAACCGCTGGCGGCCACGACGACGCCCGCGGCGCTTCGAGGCCGTTTACGGGGCC	1418
QY	397	IleuGluIleuMetGlyIleuAspGlyCysValGluAspIleuArgSerArgIleuGlnIleArgGly	416
Db	1419	CTGAGACCGCATGGGGCTGGACGCTGCTGCGAAGACTTGGCAGACCGCGCTCAGCGGGGC	1478
QY	417	Pro 417	
Db	1479	CCG 1481	
RESULT 13			
ABL64119			
ID	ABL64119	standard; DNA; 1743 BP.	
XX			
AC	ABL64119;		
DT			
XX	15-MAY-2002	(first entry)	
DE	Breast cancer related gene sequence SEQ ID NO:2456.		
XX			
KW	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;		
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;		
KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;		
XX	gene; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	W0200194629-A2.		
XX			
PD	13-DEC-2001.		
XX			
PF	30-MAY-2001; 2001WO-US10838.		
XX			
PR	05-JUN-2000; 2000US-209473P.		
PR	05-JUN-2000; 2000US-209531P.		
PR	18-SEP-2000; 2000US-233133P.		
PR	18-SEP-2000; 2000US-233617P.		
PR	20-SEP-2000; 2000US-234009P.		
PR	20-SEP-2000; 2000US-234034P.		
PR	20-SEP-2000; 2000US-234052P.		
PR	22-SEP-2000; 2000US-234509P.		
PR	22-SEP-2000; 2000US-234567P.		
PR	25-SEP-2000; 2000US-234923P.		
PR	25-SEP-2000; 2000US-234924P.		
PR	25-SEP-2000; 2000US-235077P.		
PR	25-SEP-2000; 2000US-235082P.		
PR	25-SEP-2000; 2000US-235134P.		
PR	25-SEP-2000; 2000US-235280P.		
PR	26-SEP-2000; 2000US-235637P.		
PR	26-SEP-2000; 2000US-235638P.		
PR	27-SEP-2000; 2000US-235711P.		
PR	27-SEP-2000; 2000US-235720P.		
PR	27-SEP-2000; 2000US-235840P.		
PR	27-SEP-2000; 2000US-235863P.		
PR	28-SEP-2000; 2000US-236028P.		
PR	28-SEP-2000; 2000US-236032P.		
PR	28-SEP-2000; 2000US-236033P.		
PR	28-SEP-2000; 2000US-236034P.		
PR	28-SEP-2000; 2000US-236109P.		
PR	28-SEP-2000; 2000US-236111P.		
PR	29-SEP-2000; 2000US-236842P.		
PR	29-SEP-2000; 2000US-236849P.		
PR	02-OCT-2000; 2000US-237112P.		
PR	02-OCT-2000; 2000US-237113P.		
PR	02-OCT-2000; 2000US-237173P.		
PR	02-OCT-2000; 2000US-237278P.		

RESULT 14
AAFB3770
ID AAFB3770 standard; DNA; 1250 BP.
XX
AC AAFB3770;
XX
DT 06-NOV-2001 (first entry)
XX
DE Nucleotide sequence of human TR3 gene.
XX
KW TR3; cell proliferation; leukemia; immunosuppressive; cytostatic;
KW dermatological; antiarthritic; antidiabetic; neuroprotective; cardiac;
XX antihypertoid; antiinflammatory; antiallergic; T cell-inhibitor; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1250
FT /tag= a
FT /transl_except= "(pos:481..482, aa:Asp)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except= "(pos:558..559, aa:Cys)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except= "(pos:638..639, aa:Leu)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except= "(pos:718..719, aa:Met)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT sig_peptide 1..72
FT /tag= b
FT mat_peptide 73..1247
FT /tag= c
XX
XX WO200135995-A2.
XX
XX 25-MAY-2001.
XX
XX 17-NOV-2000; 2000MO-US31692.
XX
XX 19-NOV-1999; 99US-0166583.
XX
XX (TITV) TITVLE T V.
XX (WEGM) WEGMANN K W.
XX
XX Title TV, Wegmann KW;
XX
XX WPI: 2001-343711/36.
XX P-PSDB: AAB84941.
XX
XX Composition for treatment of T-cell mediated disease e.g. arthritis,
XX cancer comprises a biologically active TR3-specific binding agent
XX especially a monoclonal antibody -
XX
XX Disclosure: Page 72; 77pp; English.
XX
XX The invention relates to a composition comprising a biologically active
XX TR3-specific binding agent (I) that binds to TR3 and inhibits the
XX proliferation of cells expressing TR3. (I) identified by the methods are
XX useful for treating a subject suspected of having a disease associated
XX with a proliferation of cells expressing TR3 especially leukemias or
XX lymphomas or a T-cell mediated disease especially autoimmune diseases
XX such as myasthenia gravis, systemic lupus erythematosus, rheumatoid
XX arthritis, diabetes, multiple sclerosis, sarcoidosis, myocarditis,
XX thyroiditis and tumours. (I) is also useful for treating a subject
XX suspected of having graft-versus-host disease, rejection of a
XX transplanted organ such as heart, liver, lung, kidney, pancreas, bowel,
XX skin or an appendage, or inflammatory diseases, allergies and contact
XX dermatitis. The present sequence represents the nucleotide sequence of
XX human TR3 gene.

SQ Sequence 1250 BP; 201 A; 419 C; 406 G; 224 T; 0 other:
Alignment Scores:
Pred. No.: 1.52e-115 Length: 1250
Score: 2208.00 Matches: 413
Percent Similarity: 99.04% Conservative: 0
Best Local Similarity: 99.04% Mismatches: 4
Query Match: 95.05% Indels: 4
DB: 22 Gaps: 0
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OY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeuLeu 20
DB 1 ATGGAGCAGCAGCGCGGGGGCTGCGGGGGTGGCGGGCCCTCTCTGCTGCTG 60
OY 21 GlyAlaArgAlaGlnGlyCysArgSerProArgCysAspCysAlaGlyAspPheHis 40
DB 61 GGGGCGCGGGCGCGAGCGCGACCTGCTAGCCCGAGGTGACTGTGCGGTGCTCCAC 120
OY 41 LysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
DB 121 AAGAGATTTGCTGTTTGTGTCAGAGGCTCCAGCGGGGACTACTGTAAGCCCTT 180
OY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
DB 181 TGCAGAGAGCCCTGGGGGACATCCACCTGCTGTGTGTCGCCAAGACACCTTCTGGCC 240
OY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluAlaSer 100
DB 241 TGGGAGAACCAACATTAATTCGATGTCGCCCTCCAGGCGCTGTGATGAGCAGCCTCC 300
OY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
DB 301 CAGGTGGCGCTGAGAACTGTCAGACAGTGGCGGACCCCGCTGTGTGTAAGCAGGC 360
OY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
DB 361 TGGTTTGTGAGATGCCAGGTGACCAATGTGCACATTCACCTTCTACTGCCAACCA 420
OY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
DB 421 TGCCTAGACTGGGGGGCCCTGCACGCCACACGCGCTACTGTTCCCGCAGAGATAC- 479
OY 161 AspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysPro 180
DB 480 GACTGTGGGACTGCTGCTCTGCTTATGAACTGCGGATGGCTGCTGCTGCTGCTG 539
OY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrPArgLmet 200
DB 540 ACGAGCACCTGGGGAGCGT-CCAGAGCGCTGTGCCGTGCTGTGGCTGGAGGCACATG 598
OY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValAlaProLeuLeuGlyAlaThrLeu 220
DB 599 TTCTGGGTCAGGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657
OY 221 ThrTyrThrTyrArgHisCysTyrProHisLysProLeuValAlaAlaAspGluAlaGly 240
DB 658 ACCTACACATACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
OY 241 MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
DB 718 TG-GAGGCTGACCCACCCACCGCCACCCATCTGTACCTGTGACAGGCCACACC 776
OY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280
DB 777 CTCTTACACCTCTCTGACAGAGTGAAGATCTGACCCGCTGCTGCTGCTGCTG 836
OY 281 TrpThrProGlyTyrProGluThrGlnGluAlaLeuGlyProGlnValAlaTrpPserTrp 300
DB 837 TGGAGCCCTGGCTACCCCGAGACCCAGAGAGGCGCTGTGCCGAGGTGATGGTCTGG 896
OY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320

[illegible][illegible]

[illegible]

Db	2802	GTGCTGGGGATGCAACAGGGGGACAAAATAGGCAAAATCCCTCTCTTTGGGGTTGACAT	2861
Qy	182	-----	182
Db	2862	TCTAGTACTCTTCANTAGTAGTACAGAAAGACTCAAGTAATAGTCTGTGGTTGTATAC	2921
Qy	182	-----	182
Db	2922	AGGGACACATGACAGCAACATTCTTGGGTAGAGTAGAGGCGCTGGGGAGGAAGGCTCT	2981
Qy	182	-----	182
Db	2982	CTAGATGAGAGACAGATGCTGGGCAAGTCTTAGGGAGCCCTCCTGGGATGACCCCTCAT	3041
Qy	183	-----ThrLeuGlySerCysProGluIaVal	192
Db	3042	CCCTACAGCCACCCCGCTCCCTTCGAGAGACACCTGGGGAGCTGTCAGAGCGCTGGGC	3101
Qy	192	aAlaValCysGlyTyrPArg-----	198
Db	3102	CCCTGCTGTGTGGCTGGAGGCGAGAGTAGGTGTGTGCTGGGAATGCGAGTGGAGAACTGG	3161
Qy	198	-----	198
Db	3162	GATGGACCGAGGGGAGGGGTAGGAGGGGGGCAACCAACCAACCCACAGCTGCTT	3221
Qy	199	-GlnMetPheTyrValGlnValLeuLeuAlaGlyLeuValProLeuLeuGluIaVal	218
Db	3222	TCAGTGTGCTGGGTCCAGGCTGCTCCCTGGCTGGCCCTTGGTGTGCCCTCTGCTGGGGC	3281
Qy	218	aThrLeuThrTyrThrTyrTrpHisIscysTyrProHisIysProLeuValThr-----	235
Db	3281	CACCTGACCTACACATACATACCGCACCTGCTGCCCTCACAAAGCCCTGGTTACTGTAACTA	3340
Qy	235	-----	235
Db	3341	CACACACCCACACACGACACCCACAAACCTGGGTGACAGTGGGTAGCCACAGTCTACTC	3400
Qy	235	-----	235
Db	3401	AACCCGTATACAGAGGGGAAACTGAGAGCAGGAGTGTGGGTGCAGAGAACCTTAGAG	3460
Qy	235	-----	235
Db	3461	GAGCTGTACCAGCACCCAGGCTCCAGGAGCGCTGCTGGTGTGACCCGCAATCTCTGTCT	3520
Qy	236	-----AlaAspGluAlaGlyMetGluAlaLeuThrProPro-----	247
Db	3521	GTCGTGACGACGATGAAGAGCTGGGATGTGAGGCTGTGACCCACACCGGTAAAGAACTCAC	3581
Qy	247	-----	247
Db	3581	TGTGTATTCCTGGGCTGCTCTTCTGAGCTGGAAAGATCAAGCCTTAATATGATCCCTGGAG	3640
Qy	247	-----	247
Db	3641	CTTGGCAGCGGGCCAGCACCGGGTAGCCCTAGTGGACAGAGGTGTGGAGCAGAGTCAT	3700
Qy	247	-----	247
Db	3701	CAGTGGATGAGACCAAGCAGACAGTCCCTGCTCAAGGGGTGCTCAGTCAAGCTGGAAGTCAAG	3760
Qy	247	-----	247
Db	3761	ATTTCGTACACAGAGAGCTAACAGTTCAATGGAAGAGAGGCCCATGGTGTGGGGGACAAG	3820
Qy	247	-----	247
Db	3821	AGGAAGAGGCGGGGCGAGGGAGCTCAAGGACAGAAACAAAGAGTGTCTGGGCTACAGTG	3880
Qy	247	-----	247
Db	3881	AGAGCAGGGCCAACTGTGGGAGGTGTCAATTCGCGGGGTTCTGTCTGACTGAACACAGGAC	3940

[illegible]

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Job time : 420.274 secs

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GenCore version 5.1.4-p5-A578
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 6, 2003, 21:08:18 ; Search time 158.782 Seconds

(without alignments)
2303.655 Million cell updates/sec

Title: US-09-993-234-6

Perfect score: 2323
Sequence: 1 MEORPCCAAVAALLVLL.....ERMGLDGCVEDLRSLRQGP 417

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2323	100.0	1254	10	US-09-333-966-3
2	2323	100.0	1634	9	US-10-081-280-9
3	2323	100.0	1634	9	US-10-112-793-9
4	2323	100.0	1634	9	US-10-112-193-11

5	2323	100.0	1634	10	US-09-993-234-9	Sequence 9, Appl1
6	2267	97.6	1783	10	US-09-333-966-1	Sequence 1, Appl1
7	2254.5	97.1	1743	9	US-09-954-531-1389	Sequence 1389, Ap
8	1556.5	67.0	10797	9	US-10-092-154-1577	Sequence 1577, Ap
9	1556.5	67.0	10797	10	US-09-764-847-1577	Sequence 1577, Ap
10	1066	45.9	1438	9	US-10-081-280-5	Sequence 5, Appl1
11	1066	45.9	1438	9	US-10-112-793-5	Sequence 5, Appl1
12	1066	45.9	1438	9	US-10-112-793-5	Sequence 5, Appl1
13	1066	45.9	1438	10	US-09-884-733-5	Sequence 5, Appl1
14	1066	45.9	1438	10	US-09-993-234-5	Sequence 5, Appl1
15	1039.5	44.7	816	10	US-09-964-824A-292	Sequence 292, App
16	692	29.8	433	9	US-10-081-280-2	Sequence 2, Appl1
17	692	29.8	433	9	US-10-112-793-2	Sequence 2, Appl1
18	692	29.8	433	10	US-10-112-793-2	Sequence 2, Appl1
19	692	29.8	433	10	US-09-884-733-2	Sequence 2, Appl1
20	692	29.8	433	10	US-09-993-234-2	Sequence 2, Appl1
21	394.5	17.0	2130	10	US-09-917-860A-1601	Sequence 1601, Ap
22	387.5	16.7	2440	10	US-09-970-532-1	Sequence 1, Appl1
23	380.5	16.4	2173	9	US-09-898-234-14	Sequence 14, Appl
24	380.5	16.4	2173	9	US-09-898-429A-24	Sequence 24, Appl
25	380.5	16.4	2173	9	US-09-792-356-14	Sequence 14, Appl
26	380.5	16.4	2173	10	US-09-899-422-14	Sequence 14, Appl
27	374	16.1	1368	9	US-09-898-234-1	Sequence 1, Appl1
28	374	16.1	1368	9	US-09-899-429A-1	Sequence 1, Appl1
29	374	16.1	1368	9	US-09-792-356-1	Sequence 1, Appl1
30	374	16.1	1368	10	US-09-899-422-1	Sequence 1, Appl1
31	374	16.1	2111	10	US-09-880-107-2360	Sequence 2360, Ap
32	374	16.1	2141	9	US-09-898-234-16	Sequence 16, Appl
33	374	16.1	2141	9	US-09-899-429A-26	Sequence 26, Appl
34	374	16.1	2141	9	US-09-792-356-16	Sequence 16, Appl
35	374	16.1	2141	10	US-09-899-422-16	Sequence 16, Appl
36	374	16.1	2141	10	US-10-120-397-1	Sequence 1, Appl1
37	330	14.2	191	9	US-09-796-692-2549	Sequence 2549, Ap
38	261	11.2	1334	9	US-09-898-234-11	Sequence 11, Appl
39	261	11.2	1334	9	US-09-792-356-11	Sequence 11, Appl
40	261	11.2	1334	10	US-09-899-429A-21	Sequence 21, Appl
41	256	11.0	1334	10	US-09-899-429A-21	Sequence 21, Appl
42	233	10.0	1704	12	US-10-020-787-1	Sequence 1, Appl1
43	230.5	9.9	1724	10	US-09-924-231-1	Sequence 1, Appl1
44	230.5	9.9	1724	10	US-09-934-289A-14	Sequence 14, Appl
45	220.5	9.5	1334	10	US-09-934-289A-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-09-333-966-3
Sequence 3, Application US/09333966
Patent No. US2002009773A1
GENERAL INFORMATION:
APPLICANT: YU, Guo-Liang
APPLICANT: MI, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:

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1  PRIOR APPLICATION DATA:
2  APPLICATION NUMBER: US/08/815,469
3  FILING DATE:
4  APPLICATION NUMBER: NO. US20020009773A1 Yet Assigned
5  FILING DATE: 06-FEB-1997
6  PRIOR APPLICATION DATA:
7  APPLICATION NUMBER: US
8  FILING DATE: 17-OCT-1996
9  PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 60/013,285
11 FILING DATE: 12-MAR-1996
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Steffe, Eric K.
14 REGISTRATION NUMBER: 36,688
15 REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: 202-371-2600
18 TELEFAX: 202-371-2540
19 INFORMATION FOR SEQ ID NO: 3:
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 1254 base pairs
22 TYPE: nucleic acid
23 STRANDEDNESS: double
24 TOPOLOGY: both
25 MOLECULE TYPE: cdna
26 FEATURE:
27 NAME/KEY: CDS
28 LOCATION: 1..1251
29 US-09-333-966-3

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[illegible]

Db	689	TTCTGGGCTCCAGGTCGCTCCTGGCTGGCTTGTGGTCCCCCTCTGCTTGGGGCCACCCTTG	748
QY	221	ThrTyrThrTyrArgHisCysTyrProHisIleProLeuValThralaAspGluAlaGly	240
Db	749	ACGTACACATACGCCCACTGTGGCTCTACAAAGCCCTGTGTACTGTAGATGAAGCTGGG	808
QY	241	MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr	260
Db	809	ATGAGAGGCTGTGACCCCAACCCACCCGCCACCACTGTGCACCTGTGGACACGGCCACACC	868
QY	261	LeuLeuAlaProProAspSerSerGluIleGlySerValGlnLeuValGlyAsnSer	280
Db	869	CTTCTAGCACTCTCTGACAGAGTGAAGAAGTCTGCACCGTCCAGTTGGTGGTAAACAGC	928
QY	281	TyrThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTyrSerTyr	300
Db	929	TGGAACCCCTGGCTACCCCGAGAACCCAGAGAGCGCTGTGCCCGCAGGTGACATGTGCTGG	988
QY	301	AspGlnLeuProSerArgAlaLeuGlyProAlaAlaIleProThrLeuSerProGluSer	320
Db	989	GACCAAGTGGCCACAGACAGCTCTTGGCCCGCTGCTGCCCCACACTCTGCCAGAGTCC	1048
QY	321	ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp	340
Db	1049	CCACCCGGCTGCCACGACCATGTACTCTGCACCCGGGCCCGCAGCTTACGACGAGATGGAC	1108
QY	341	AlaValProAlaArgArgTyrPlyGluPheValArgThrLeuGlyLeuArgGluAlaGlu	360
Db	1109	GGGGTCCACAGCCGGCCGCTGGAGAGAACTGTGTGCCAGCTGGGGGCTGGCCGAGCGAG	1168
QY	361	IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys	380
Db	1169	ATCGAAGCCGTGGAGGTGGAGATCGGCGGCTGTCCGACACGACAGAGTACGAGATGCTCAAG	1228
QY	381	ArgTyrPargGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaLeuGluIleArgMet	400
Db	1229	CGCTGGGGCCGACGACGCCCGCGGGCTGTGCACCTTACCGCGGGCTGGAGCGCATG	1288
QY	401	GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro	417
Db	1289	GGGCTGGACGGCTCGTGGAAAGATTGGCGACCGGCTGTGACGCGCGGCGCCG	1339
RESULT 3			
US-10-112-793-9			
Sequence 9, Application US/10112793			
Publication No. US2002019272A1			
GENERAL INFORMATION:			
APPLICANT: Ashkenazi, Avi J.			
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES			
NUMBER OF SEQUENCES: 28			
CORRESPONDENCE ADDRESSES:			
ADDRESSEE: Genentech, Inc.			
STREET: 1 DNA Way			
CITY: South San Francisco			
STATE: California			
COUNTRY: USA			
ZIP: 94080			
COMPUTER READABLE FORM:			
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Winpatin (Genentech)			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/10/112.793			
FILING DATE: 28-Mar-2002			
CLASSIFICATION: <Unknown>			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US/08/828,683A			
FILING DATE: 31-Mar-1997			
APPLICATION NUMBER: 08/625328			
FILING DATE: 1-Apr-1996			
APPLICATION NUMBER: 08/710802			

TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1634 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-112-193-11
Alignment Scores:
Pred. No.: 2 07e-198 Length: 1634
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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QY 21 GlyAlaArGlaGlnGlyGlyThrArgSerProArGlyCysAlaGlyAspPheHis 40
Db 149 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 208
QY 41 LysAlaIleGlyLeuPheCysArgGlyCysProAlaGlyHisIleuValPro 60
Db 209 AAGAGAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 268
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 269 TGCACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 328
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluAlaSer 100
Db 329 TGGAGAGACCACTAATTTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 388
QY 101 GlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysValProGly 120
Db 389 CAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 448
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheIleuValPro 140
Db 449 TGGTTTGTGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 508
QY 141 CysLeuAspCysGlyAlaLeuHisAsnGlnHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 509 TGCCTAGACTGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 568
QY 161 AspCysGlyThrCysLeuProGlyPheIleuGlnHisGlyAspGlyCysValSerCysPro 180
Db 569 GACGTGGGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 628
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMet 200
Db 629 ACGAGCACCTGGGGAGCTGCCAGACGCGCTGTCCCTGTGTGTGTGTGTGTGTGT 688
QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValProLeuLeuGlyAlaThrLeu 220
Db 689 TTTCTGGGTCCAGGTGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 748
QY 221 ThrTrpThrIleArgHisCysTrpProHisIlePheProLeuValThrAlaAspGlnAlaGly 240
Db 749 ACCTACACATACCGCACCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 808
QY 241 MetGlnAlaLeuThrProProAlaThrHisIleuSerProLeuAspSerAlaHisIleThr 260
Db 809 ATGAGAGCTGTGACCCAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 868
QY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280

Db 869 CTTCCTACACCTCTCTGACAGCAGTGAAGAATCTGCACCGCTCCAGTTGTGGTAAACAGC 928
QY 281 TrpThrProGlyIleTrpProGlnThrGlnGlnAlaLeuCysProGlnValThrTrpSerTrp 300
Db 929 TGCACCGCTGAGTACCCCGAGACCGAGAGCGGCTGTGCGCGCGAGTACATGTCTCTGG 988
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluIle 320
Db 989 GACCAAGTTGCCACAGACAGCTTGTGGCCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1048
QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuIleuTrpAspValMetAsp 340
Db 1049 CCACCGCGCTGCGCGAGCATATGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1108
QY 341 AlaValProAlaArgArgTrpIleGlyPheValArgThrLeuGlyLeuArgGlnAlaGlu 360
Db 1109 GCGGTCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1168
QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnIleuTrpGluMetLeuLys 380
Db 1169 ATGACAGCGCGTGAAGTGTGAATGTGGCGCTCCGAGACCAAGCATGAGATGCTCAAG 1228
QY 381 ArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValIleuValAlaLeuGluArgMet 400
Db 1229 CGCTGGCGCGCGAGCAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1288
QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 1289 GGGCTGAGCGCGCTGTGTGAAGACTTGTGCGACGCGCGCTGACGCGCGCGCGCGCG 1339
RESULT 5
US-09-993-234-6
; Sequence 9, Application US/09993234
; Patent No. US20020146768A1
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/993,234
; FILING DATE: 19-NO. US20020146768A1-2001
; CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,683
; FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1634 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-993-234-9

Alignment Scores:

Pred. No.:	2,07e-198	Length:	1634
Score:	2323.00	Matches:	417
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-993-234-6 (1-417) x US-09-993-234-9 (1-1634)

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QY 21 GlyAlaArgAlaGlnGlnGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
DB 149 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 208
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
DB 209 AAGAGATGGTGCTGTTTGTGGAGAGCGTCCACGCGGCGCGCGCGCGCGCG 268
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
DB 269 TGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 328
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSer 100
DB 329 TGGGAGAACCCACATATCTGATGTGCCGCGTGCAGCGCTGTATGAGCGCTCC 388
QY 101 GlnValAlaLeuGlnAsnGlySerSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
DB 389 CAGGTGGCGCTGGAAGACCTGTTCAGAGTGGCGGACACCGCTGTGTGCTTAAGCCAGGC 448
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
DB 449 TGGTTTGTGGAGTGCAGCGTGCACCAATGTGTGACGATTCACCTTCTTACGCCAACCA 508
QY 141 CysLeuAspCysGlyAlaLeuHisAsnGlnHisThrArgLeuLeuCysSerArgArgAspThr 160
DB 509 TGGCTTGTGGAGTGCAGCGTGCACCGCGCTACTGTGTGCCGAGAGTACT 568
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyLysValSerCysPro 180
DB 569 GACTGTGGGACCTGCTGCTGCTTCTTATGAACTGGGATGGCTGCTGCTGCC 628
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrPheArgGlnMet 200
DB 629 ACGAGACACCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGCTGTGGAGGCGAGATG 688
QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValProLeuLeuLeuGlyAlaThrLeu 220
DB 689 TTTCTGGGTCCAGATGCTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 748
QY 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGlnAlaGly 240
DB 749 ACCTACACATACCGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 808
QY 241 MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
DB 809 ATGGAGGCTGTGACCCACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 868
QY 261 LeuLeuAlaProProAspSerSerLysLysIleCysThrValGlnLeuValGlyAsnSer 280
DB 869 CTTCTAGACACCTCTGACAGCAGTAGAAGATCTGACCGCTGCTGCTGCTGCTGCTGCTG 928
QY 281 TrpThrProGlyTyrProGluThrGlnGlnAlaLeuCysProGlnValThrTrpSerThr 300
DB 929 TGGACCGCTGGGTACCGCGAGACCGAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 988
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGlnSer 320

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DB 989 GACCAATTGCCACAGACGCTTGCGCCCGCGCTGCTGCGCCACACTCTGCCAGAGTCC 1048
QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
DB 1049 CCACCGCGCTGCGCGACGACATGATGCTGACCGCGCGCGCGCGCGCGCGCGCGCG 1108
QY 341 AlaValProAlaArgArgTyrPlyGlnPheValArgThrLeuGlyLeuArgGlnAlaGlu 360
DB 1109 GCGGTCCACCGCGCGCGCTGGAAGAGTCTGTGCGACGCTGCGCGCGCGCGCGCGCG 1168
QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlnMetLeuLys 380
DB 1169 ATCGAAGCGCTGAGAGTGCAGATCGCGCGCTTCCGAGACCGACAGTACGATGCTCAAG 1228
QY 381 ArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
DB 1229 CGCTGGCGCGAGCAGCAGCGCGCGCGCTGCGAGCGCTTACCGCGCGCTGCGAGCGCATG 1288
QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
DB 1289 GGGCTGAGCGCTGCTGCTGGAAGACTTGCAGCGCGCTGCGAGCGCGCGCGCG 1339

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RESULT 6

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US-09-333-966-1
Sequence 1, Application US/09333966
Patent No. US20020009773A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
APPLICATION NUMBER: No. US20020009773A1 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488, 0310003/EKS/RRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
Type: nucleic acid

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STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 198..1481
US-09-333-966-1

Alignment Scores:
Pred. No.: 2,27e-193 Length: 1783
Score: 2267.00 Matches: 409
Percent Similarity: 97.33% Conservative: 1
Best Local Similarity: 97.15% Mismatches: 5
Query Match: 97.59% Indels: 6
Gaps: 1

US-09-993-234-6 (1-417) x US-09-333-966-1 (1-1783)

QY 3 GlnAtrProArGly-----CysAlaAlaValAlaAlaLeuLeu 16
DB 219 GAGGCCCCACGTGGCGAGCTGCGGAGAGTCAAGACCTGCCCCAGCGCTCTC 278
QY 17 LeuValLeuLeuGlyAlaArgAlaGlyGlyThrArgSerProArGlyAspCysAla 36
DB 279 CTGGTCTGCTGGGGCCCGGGCCAGGGCGGACTGTAGCCCCAGGTGTGACTGTGCC 338
QY 37 GlyAspPheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisLys 56
DB 339 GGTGACTTCCACAGAAGATGTGTCTGTTTGTTCAGAGGCTGCCACAGGGGGCACTAC 398
QY 57 LeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAsp 76
DB 399 CTGAAGCCCCCTGTGCACGAGGAGCTGCGGCACTCCACCTGTGTGTGCCCAAGAC 458
QY 77 ThrPheLeuAlaThrPheLysHisAsnSerGluCysAlaArgCysGlnAlaCysAsp 96
DB 459 ACCCTTTGGCTGGGAGAACCACTAATCTGAATGTGCGCGCCAGCGCTGTGAT 518
QY 97 GluGlnAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGly 116
DB 519 GAGCAGCGCTCCAGGTGGCGGTGGAGAACTGTTCAGCACTGCCACACCCCTGTGGC 578
QY 117 CysLysProGlyLThrPheValGlyCysGlnValSerGlnCysValSerSerProPhe 136
DB 579 TGTAAAGCCAGGCTGTGTGTGGAGTCCAGGTCAAGCAATGTGTCAAGACTTCAACCTTC 638
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DB 639 TACTGCCAACCAATGCTAGACTGGGGCCCTGCACCCGACACAGGCTACTCTGTTC 698
QY 157 ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCys 176
DB 699 CCGAGAGATACATGACTGTGGAGACTGCGCTGCTCATATAACATGGCGATGGCTGC 758
QY 177 ValSerCysProThrSerThrLeuGlySerCysProGlnArgCysAlaAlaValCysGly 196
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QY 197 TrpArgGlnMerPheThrValGlnValLeuLeuAlaGlyLeuValProLeuLeu 216
DB 819 TGGAGGCAATGTTCTGGGTCCAGGTGTCTGCTGGCTTGTGGTCCCTCCCTGCTT 878
QY 217 GlyAlaThrLeuThrTyrThrTyrArgHisCysTyrProHisLysProLeuValThrAla 236
DB 879 GGGGCAACCTGATGACATACATACCCCACTGTGGCTCACAAGCCCTGGTTACTGCA 938
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QY 257 SerAlaHisThrLeuLeuAlaProProAspSerSerGlnLysLysThrValGlnLeu 276
DB 999 AGGGCCACACCTTCTAGACCTCTCTGACAGCAGTGAAGATGTGCACCGTTCAGTTG 1058

QY 277 ValGlyAsnSerThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnVal 296
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QY 297 ThrTrpSerThrAspGlnLeuProSerArgAlaLeuGlyProAlaAlaProThrLeu 316
DB 1119 ACATGTCTCTGGGACAGTGTGGCCAGCAGACTTGTGGCCCCCTGCTGTGGCCACACTC 1178
QY 317 SerProGluSerProAlaGlySerProAlaMetMetLeuLeuProGlyProGlnLeuTyr 336
DB 1179 TCGCCAGAGTCCCGACGCGGCTGCGCAGCATATGCTGTGAGCGGGCCCGCAGCTTAC 1238
QY 337 AspValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeu 356
DB 1239 GACGTATGAGCCCGGTGCCAGCGCGCGCTGGAAGAGTCTGTGCCACAGCTGGGGCTG 1298
QY 357 ArgGluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyr 376
DB 1299 CGCGAGGCAAGATCGAAGCCGTGGAGGTGAGATCGGCCGTTCCGAGACACAGACTAC 1358
QY 377 GluMetLeuLysArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAla 396
DB 1359 GAGATGCTCAAGCGCTGCGCCAGCAGACAGCCCGGGCTCGGAGCGGCTTACGGGGCC 1418
QY 397 LeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGly 416
DB 1419 CTGGAGCGCATGGGGCGTGGAGCGGCTGTGTGAAGACTTGGCGCAGCCGCTGCAGCGGGC 1478
QY 417 Pro 417
DB 1479 CCG 1481

RESULT 7

US-09-954-531-1389
Sequence 1389, Application US/09954531
Patent No. US20020165180A1
GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/09/954, 531
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233, 133
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234, 009
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234, 034
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234, 509
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234, 567
NUMBER OF SEQ ID NOS: 1392
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1389
LENGTH: 1743
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-531-1389

Alignment Scores:

Pred. No.: 2,88e-192 Length: 1743
Score: 2254.50 Matches: 413
Percent Similarity: 91.57% Conservative: 0
Best Local Similarity: 91.57% Mismatches: 4
Query Match: 97.05% Indels: 35
Gaps: 1

US-09-993-234-6 (1-417) x US-09-954-531-1389 (1-1743)

QY 1 MetGluGlnArgProArGlyCysAlaAlaValAlaAlaAlaLeuLeuValLeuLeu 20

Db	69	ATGGAGCAGCGCGCGGGGCTCGCGGGGGTGGCGGGCGCGCTCTCTGCTGCTCTG	128
Qy	21	GLYALAARGLAAGLNLGLYTHRARSERPROARGCYSAAPCYSAALAGLYASPHEHIS	40
Db	129	GGGGCCCCGGCCCCAGGCGCGCACTCGTACCCCCAGAGTGTCAGTGGCCGGGACTTCCAC	188
Qy	41	LYSLYSILLEGLYENPHECYSCYARGLYCYSPROALAGLHISTYRILEUVALAPro	60
Db	189	AAGAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	248
Qy	61	CYSPTHGLUPROCYSLYASNSERTHCYSEUVALCYSPROGINASPTHRPHELEUALA	80
Db	249	TGCACGAGAGCCCTGCGCGCACTCCACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT	308
Qy	81	TRPGIASNHIISHIASNSERGLUCYSVALARPGYSGINALACYSAAPGLUGINALSER	100
Db	309	TGGGAGAACACCATTATTTCTGAATGTGCCCCGCTGCCAGGCGCTGTGATGAGCAGGCTCC	368
Qy	101	GLINVALALEUGLUASNCYSSEVALAVALAASPTHRACGYSGILYCYLSPROGLY	120
Db	369	CAGGTGGCCCTGGAGAACTGTTCACACATGGCCGCACACCCGCTGTGCTTAAGCCAGCG	428
Qy	121	TRPPHEVALGLINUCYGLINVALSERGLINCYVALSERSERPROPHETRYCYSGINPro	140
Db	429	TGGTTTGTGAGATGTCAGAGTCAAGCCAAATGTGTACAGATTCACCCCTTCTACTCCACCA	488
Qy	141	CYSLEUASPQYSGILYALALEUHIISARGLHISARGLLEUCYSESERAGAGASPTHR	160
Db	489	TGCGCTAGACTGGGGGCGCCGTGACCGCCACACAGCGCTACTGTGTTCGCCAAGATACT	548
Qy	161	ASPPCYSGILYTHCYSEUPROGLYPHERYGLIHISGLYSPGLYCYVALSERCYSPRO	180
Db	549	GACTGTGGGACCTGCTCTCCGTGGCTTCTATATACATGCGATGGCTGCGTCTCTCCCC	608
Qy	181	THRSERTHLEUGLYSERCYSPROGLIARGLCYSAALALEUCYSGILYTPRAG-----	198
Db	609	ACGAGACCCCTGGGAGGCTGTCCAGAGCGCTGTCCGCTGTGTGTGTGTGTGTGTGTGTGT	668
Qy	198	-----	198
Db	669	AGGTGCTGCTGGGAATCCGCTGGGAGAACTGGATGGACGAGGGGAGGGGTGAG	728
Qy	199	-----GLMETHERRPYALGLINVALLEU	206
Db	729	GAGGGGGGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	787
Qy	207	LEUALAGLYLEUVALVALPROLEULEUENGLYALATHLEUTHRYTHRYTRARHIS	226
Db	788	CTGGCTGGCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	847
Qy	227	CYSTPRPROHISLYSPROLEUVALTHRALASGLIUALGLYMETGLIUALALEUTHPro	246
Db	848	TGCTGTGCTCAACAGCCCTGTACTGTCAAGATGAAGCTGGGATGGAGGCTGTGACCCCA	907
Qy	247	PROPROALATHRHSLEUSERPROLEUASPSEALAHISTHRLEUENVALPROPROASP	266
Db	908	CCACCGGCGCACCATCTGTACCTGTGACGAGCGCCACACCTTCTACACCTCTGTAC	967
Qy	267	SERSERGLYULYSILCYSTHINVALGLINLEUVALGLYASNSERTTPHTRPROGLYTRPro	286
Db	968	AGCATGTGAAGATCTCCACCGTCCAGATGGTGGTAAAGCTGGACCCCTGTGTAACCC	1027
Qy	287	GLUTHRGINGLINALALEUCYSPROGLINVALTHRTSPSERTRIPASGLINLEUPROSERARG	306
Db	1028	GAGACCCGAGGAGGCGCTCTGCCGAGGTGACATGTGCTGTGGACCAAGTGTGCCAGCAGA	1087
Qy	307	ALALEUGLYPROALAAALAPRTHRLEUSERPROGLIUSERPROALAGLYSERPROALA	326
Db	1088	GCTTTTGGCCCCGCTGTGTGGCCCAACTCTGCGCAGAGTCCACGCGGCGTCCGACCC	1147
Qy	327	METLEULEUGINPROGLYPROGLINLEUWYTRASPVALMETASPALAVALPROALARGARG	346

Db	1148	ATGATGCTGCAGCCGGGGCCGACACTTACGACGTATGTGACCGCGGTCCCAACGGCGGCC	1207
Qy	347	TrpLysGluPheValaIaGthrIleuGlyLeuArgGluAlaGluIleGluAlaValGluVal	366
Db	1208	TGGAAAGGATTCGTGGCCACGCTGGGGCTCCGGAGGACAGATGCAACCCGTGGAGGTG	1267
Qy	367	GluIleGlyArgPheArgAspGlnGlnIleTyrGluMetLeuLysArgTyrArgGlnIle	386
Db	1268	GAGATCGGTCTCTTCGACAGACACAGATACGATGATCTTAACACCTGGGGCCAGCAGAG	1327
Qy	387	ProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspIleCysVal	406
Db	1328	CCCCGGGGCTTCGGAGGCGTTTACGGCGCCCTTGAGCCGATGGGCTGAGCGGCTG	1387
Qy	407	GluAspLeuArgSerArgLeuGlnArgGlyPro	417
Db	1388	GAAAGCTTGGCGACACCGCTGCACGCGTGGCCG	1420

	RESULT	8
US-10-092-154-1577		
: Sequence 1577, Application US/10092154		
: Publication No. US20030054375A1		
: GENERAL INFORMATION:		
: APPLICANT: Rosen et al.		
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies		
: FILE REFERENCE: PC009C1		
: CURRENT APPLICATION NUMBER: US/10/092,154		
: NUMBER OF SEQ ID NOS: 2003		
: Prior Application removed - See File Wrapper or Palm		
: SOFTWARE: PatentIn Ver. 2.0		
: SEQ ID NO 1577		
: LENGTH: 10797		
: TYPE: DNA		
: ORGANISM: Homo sapiens		
US-10-092-154-1577		
Alignment Scores:		
Pred. No.:	4.34e-129	Length: 10797
Score:	1556.50	Matches: 405
Percent Similarity:	29.10%	Conservative: 1
Best Local Similarity:	29.03%	Mismatches: 9
Query Match:	67.00%	Indels: 984
DB:	9	Gaps: 9
US-09-993-234-6 (1-417) x US-10-092-154-1577 (1-10797)		
OY 3 GlnArgProArgSly-----CysAlaIalValAlaLalaLeuLeu 16 ::: Db 5184 GAGGCCACGCTGGCGAGCTGCATGAGTCAGCACGACACTGTCCCAAGCGCTTCTC 52433 OY 17 LeuValleuLeuGllyAlarGalaglIngLyglThrParSer-ProArGcysAspCysAla 36 Db 5244 CTGTGCTCTGTGGGGCCCCGGGCCCGGCGGCACACTCGTAGCGCCACAAGTGTCAGTGTGCC 53039 OY 37 GLyASPheHisLysLysILiegLYeuPheCysCysArgGLyCySProAla----- 53 Db 5304 GGIGACTTCCACAGAAGATTGCTCTGTTTGTTCAGAGGCTCCACCAGCGGTAA GTGG 53633 OY 53 ----- 53 Db 5364 CCACAGGGGTGGAGAGGCGCATGGGGCGAGGCGCTGGAGAGAGTGGCGGCCAGGCCCGGG 54233 OY 53 ----- 53 Db 5424 AGGTAAAGAGAGCTTGCGCAGGGAGGTAGGGGTAGCTGA CAGAGAAAGTAAGGAGCTTGA 54833 OY 53 ----- 53 Db 5484 GAGAAAAGAGGAGGAGGCGCAGGTGGAAGAACAGAGTCCGGGGGTTCGTGGCCAGCCCCTCT 55433 OY 54 ----- GlyHisTryleuLysAlaProCysThrGluPr 64		

Db 5544 GCGTCCGTGACCCCTGGCTGGTTCCACAGGGCACTACCTGAAGGCCCTTGCCACGGAGCC 5603
OY 64 OCys61LysAsnSerThrCysLeuValCysProGlnAspLhrPheLeuAlaTrpGluAsnI 84
Db 5604 CTGGGGCAACTCCACGCTGCTGGTGTGTGCCCAAGACACGCTTCTGGGCTGGGAGAACCA 5663
OY 84 sHlaAsnSerGluCysAlaArgCysGlnAlaCysAspGlu----- 97
Db 5664 CCAATAAATCTGAATGTCCCGCTGCGACGGCTGTGATGAGCAGGGTGAGGGGCTTTCAG 5723
OY 97 ----- 97
Db 5724 TGCTTGCGAGGAGTTCCTAAGACAGGCCCTTCTGAAGAGATGGCTGGCTGGGCCCA 5783
OY 97 ----- 97
Db 5784 AACTTGGGGTGTAGGGTCCGACCAACCCCTTGCCAGAACCCCTCAACCCGATCTCTCT 5843
OY 97 ----- 97
Db 5844 TCAGGGTGGCCCTTGGCCCTTCTCTCTCTGAGACCTTCCCATCTCTCATGTGCTTG 5903
OY 97 ----- 97
Db 5904 GCGCTGTGGGCTTAATCTGAGCTTCTCTTTTAAAGGAGCCCTGACCTGTG 5963
OY 97 ----- 97
Db 5964 TGTCTTTCGGCTATTTCTGTCTCCATATGCTGGGATATGCTGCTGCTCCATGGGA 6023
OY 98 -----GlnAlaSerG1 101
Db 6024 GCGTTTGGCCCTGACACTCTCCACTCCCATCTCCCTGACCCCAACAGCC-TCGCA 6082
OY 101 nValAlaLeuGlnAsnSerAlaValAlaAspLhrArgCysGlnCysLysProGlyTr 121
Db 6083 GGTGGCCCTGGAGAACTGTTCAGCAGTGGCGACACCGGCTGTGTAAAGCAGGCTG 6142
OY 121 pPheValGluCysGlnValSerGlnCysValSerSerProPheTrpCysGlnProCy 141
Db 6143 GTTTGTGAGTGGCAGGTCAGCCCAATGTGTGACAGTTCAACCTTCTATCTGCAACCATG 6202
OY 141 sLeuAspCysGlnAlaLeuHisArgHisThrArgLeuLeuCysSer----- 156
Db 6203 CCTGAGCTGGGGGCGCTGCACCGCACACAGCGCTACTCTGTGA-GTACCCCAACCCAG 6261
OY 156 ----- 156
Db 6262 GCGTCTCTACTCCAGACCCCTTCTCCGCTGACCCCACTCTGTCCATGGTGAGCC 6321
OY 157 -----ArgArgAspLhrAspCysGlnCysLeuProG1 168
Db 6322 ATGCGCTCTCCGATTTGACAGGTTCCGCGACAGATACAGCTGTGGACACCTGCTGCTGG 6381
OY 168 yPheTrpGluHisGlnAspGlnCysValSerCysProLhrSer----- 182
Db 6382 CTCTATGACACATGCGCATGTGCTGTCTGCCCAACGTA-ATTCCTAGCTGTCTG 6440
OY 182 ----- 182
Db 6441 GATGGAGGAAAGGGGCTGGAGACAGAGGGGCTGGGGTGGGGCAGGTGCTGTGG 6500
OY 182 ----- 182
Db 6501 TTTCAGAAATAGGAAGGGGATAGGAGAGAGGAGCTTGGCCCTGTGATGGTGGGCC 6560
OY 182 ----- 182
Db 6561 CACTTCAGGCAAACTAGATGGCAAAAGAGCAATCTGATCCGCTTAGCCAGATACATA 6620
OY 182 ----- 182
Db 6621 AGGGATTTGCTTCACTTTCAGCCAGCAATTCCTCCAGGAGATCTTACAGATATTACA 6680

OY 182 ----- 182
Db 6681 GATGATTTGTCACTTACACAGAGTCAATGATATAGCTTTAAACTTGGGCTGAAG 6740
OY 182 ----- 182
Db 6741 AGGTGAGGCTCAGTGAAGTATGATGCTGCCACTGCATTCAAGCTGGGCAAGCG 6800
OY 182 ----- 182
Db 6801 AGACCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 6860
OY 182 ----- 182
Db 6861 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 6920
OY 182 ----- 182
Db 6921 TGGCAAGTGCAGAAATTCGCTCTGATGTGTGTGCTTCTCAACATGGGATG 6980
OY 182 ----- 182
Db 6981 TTACAGCTAATTCACAGGCTTGTATCAGAGTAAGGACTTCTGTAGTATTCAGT 7040
OY 182 ----- 182
Db 7041 CTTTTTTTTTTTTTTTTTTTTTTTTTTTGTAGATGAGACCTTGCCTGTCCACCCAGGCTG 7100
OY 182 ----- 182
Db 7101 GAGTCAGTGCAGAACTTGTGCTCACTACAACTGTGCTGCTGCTCAAGTATCT 7160
OY 182 ----- 182
Db 7161 CTTGCTCAGCTCCCAAGTAGTGGGACTAGAGAGCCACACACCCCGGCTAAT 7220
OY 182 ----- 182
Db 7221 TTTGTATTTTACTAGAGAGGGGTTTCAACCGTTTACCCAAATGATGTCTTGATCACT 7280
OY 182 ----- 182
Db 7281 GACCTGTATCACCAGGCTTGGCTGCCAAAGTGTGGGATTACAGGATGAGCCACC 7340
OY 182 ----- 182
Db 7341 GCGCCGCGCTCATTCAGTCTTTAATTAATCTGCTATGTTCTACACAGTGTCTAG 7400
OY 182 ----- 182
Db 7401 GTGCTGGGATGCAACAGGGGACAAATATAGCAAAATCCCTGTCTTTGGGGTTGACAT 7460
OY 182 ----- 182
Db 7461 TCTAGTACTCTCATGTAGCTAGAAAGCTCAGTGAATAGTGTCTGTGTAC 7520
OY 182 ----- 182
Db 7521 AGGACACAAATGACAGGAACATCTTGGGTAGAGTGAAGAGGCTGGGAGGAAAGGCT 7580
OY 182 ----- 182
Db 7581 CTAGGATGAGCAATGCTGGCAGTCTTAGAGAGCCCTCTCGGATGACACCCCTCAT 7640
OY 183 -----ThLeuGlySerCysProGlnArgCysAl 192
Db 7641 CCTCAGGCAACCCCGCTCCCTTGCAGAGCACCTGGGAGAGTCTCAGAGGCTGTGC 7700
OY 192 aAlaValCysGlyTrpArg----- 198
Db 7701 CGCTGTGTGTGGTGGAGCAGAGTAGGTGTGTCTGGGAATGCGAGTGGGAGAACTGG 7760

[illegible]

QY	248	-----Pro-fAlaThrHisIeuSerProIleuAspSerAlaHisIleu	261
Db	8600	GGGGGCCCTCTTGGCTTCAGAGCCACCATCTGTACCTTTGGACAGCGCCACACCTTT	8655
QY	262	IeuAlaProIAspSerSerGluIuylIeCyThrValGluIeuValGluAsnSerTrp	281
Db	8660	CTAGCACTCTCTGACAGCAGTGAAGATCTGCACCGTTCAGTTGGTGGTAACTACTGG	8711
QY	282	ThrProGlyTrpProGluIuThrGluAlaIeuCysProGluValIhrTrpSerTrpAsp	301
Db	8720	ACCCCTGGCTACCCCGAGAACCCAGAGAGCGCTCTGGCCGAGGTGACATGCTCTGGAC	8777
QY	302	GluIeuProSerArgAlaIeu-----	308
Db	8780	CAGTTGCCACAGACGACGCTTGGTAAGGACATCAGTGGCTTAGAGCCCTTGACCCATTTC	8833
QY	308	-----	308
Db	8840	TCCTGTCTCGGGTGGGAAGTTGTGTTTCACAAAGTTCCTTCTGCCCCCTAACTGA	8899
QY	308	-----	308
Db	8900	CGGAGTCCGCCCTATGCCCTTGACCCACCGGATCCAGCGGAGCTTACAGCCCTGGGGTACCG	8955
QY	308	-----	308
Db	8960	CACGACGCCCTGACTGCTGCTCCCGACCGCGGCCACGATACCCCAATTGGCTCTCTCT	9019
QY	309	-----GlyProAlaAlaIaProThrIleuSerProGluSerProAlaGlySer	324
Db	9020	GGCCCTGCCCGACGGCCCGCTGGCTGGCGCCACACTCTGCGCAGAGTCCACACCGGCTCG	9079
QY	325	ProAlaMetIeuGluIuProGlyProGluIuLeuTyAspValMetAspAlaValProIa	344
Db	9080	CCACGCATGATGCTGCAGCGGGCGCGGACGCTACGAGTGATGGACCGGCTCCACGG	9139
QY	345	ArgArgTrpIysGluPheValaArgThrIleuGlyIleuArgGluAlaIuIleGluAlaVal	364
Db	9140	CGGGCTGGGAAGAGATTCGGCGCACGCTGGGGCTGCGGAGGACAGATGCTCAACCCGTG	9199
QY	365	GluValaIuIleGlyArgPheArgAspGlnIuTrpGluMetIeuIysArgTrpArgGln	384
Db	9200	GAGGTGAGATTCGGCGCTTCGAGACACGACGATGACGATCTCAAGCGCTGGCGGACG	9259
QY	385	GlnIuProAlaGlyIeuGlyAlaValTyrrAlaAlaIeuGluArgMetGlyIeuAspGly	404
Db	9260	CAGACGCCCGGGCGCTCGGAGCGCTTTCAGCGGGCCCTTGAGACGATGGGGCTGGACGGC	9319
QY	405	CysValaGluAspLeuArgSerArgIeuGluIuArgGlyPro	417
Db	9320	TGCCTGGAGAACTTGGCGACMACCGCTGCAGCGCGCGCCG	9358
RESULT	10		
US-10-081-280-5			
Sequence 5, Application US/10081280			
Patent No. US20020165157A1			
GENERAL INFORMATION:			
APPLICANT: Ashkenazi, Avi J.			
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES			
NUMBER OF SEQUENCES: 11			
CORRESPONDENCE ADDRESS:			
ADDRESS: Genentech, Inc.			
STREET: 460 Point San Bruno Blvd			
CITY: South San Francisco			
STATE: California			
COUNTRY: USA			
ZIP: 94080			
COMPUTER READABLE FORM:			
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: WinPatIn (Genentech)			
CURRENT APPLICATION DATA:			

APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-081-280-5

Alignment Scores:
Pred. No.: 2,32e-86 Length: 1438
Score: 1066.00 Matches: 187
Percent Similarity: 94.47% Conservative: 1
Best Local Similarity: 93.97% Mismatches: 3
Query Match: 45.89% Indels: 8
DB: 9 Gaps: 1

US-09-993-234-6 (1-417) x US-10-081-280-5 (1-1438)

QY 1 MetGlunArProArGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
Db 377 ATGAGACAGGCGCGCGGCTGCGGCGGCGGCGGCTCTCTGCTGCTG 436
QY 21 GYAlaArGlaInGlyIthrArgSerProArGcYsaPcYsaIaGlyAspPheHs 40
Db 437 GGGGCCCGGGCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 496
QY 41 LysLysIleGlyLeuPheCysArgGlyCysProAlaGlyIthrLeuLysAlaPro 60
Db 497 AAGAAATTTGGTGTGTTTGTTCAGAGGCTGCCACGGGCGGCGGCGGCGG 556
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 557 TGCACGAGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 616
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArGcYsaIaGlyAspGlnAlaSer 100
Db 617 TGGAGAACACCATTAATTTGTAATGCGCCGCGGCGGCGGCGGCGGCGG 676
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysProGly 120
Db 677 CAGGTGCGCTGAGAGACGTTTCAAGTGGCGGCGGCGGCGGCGGCGGCGG 736
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheThrCysGlnPro 140
Db 737 TGGTTTGTGAGAGTCCAGGTCAGCAATGTGTCAAGTTCAACCTTCTCTG 796
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArGAspThr 160
Db 797 TGCCTAGACTGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 856
QY 161 AspCysGlyIthrCysLeuProGlyPheThrGlnHisGlyAspGlyCysValSerCysPro 180
Db 857 GACTGTGGGCGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTG 916
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaValCysGlyTPArGln 199
Db 917 ACCTAATCTCTA-----GCTCTGTTGGATGGAGGAA 949

RESULT 11
US-10-112-793-5
Sequence 5, Application US/10112793
Publication No. US20020192729A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/7710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/225-5416

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-793-5

Alignment Scores:
Pred. No.: 2,32e-86 Length: 1438
Score: 1066.00 Matches: 187
Percent Similarity: 94.47% Conservative: 1
Best Local Similarity: 93.97% Mismatches: 3
Query Match: 45.89% Indels: 8
DB: 9 Gaps: 1

US-09-993-234-6 (1-417) x US-10-112-793-5 (1-1438)

QY 1 MetGlunArProArGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
Db 377 ATGAGACAGGCGCGCGGCTGCGGCGGCGGCGGCGGCTCTCTGCTGCTG 436
QY 21 GYAlaArGlaInGlyIthrArgSerProArGcYsaPcYsaIaGlyAspPheHs 40
Db 437 GGGGCCCGGGCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 496
QY 41 LysLysIleGlyLeuPheCysArgGlyCysProAlaGlyIthrLeuLysAlaPro 60
Db 497 AAGAAATTTGGTGTGTTTGTTCAGAGGCTGCCACGGGCGGCGGCGGCGG 556
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 557 TGCACGAGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 616

QY 81 TrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
Db 617 TGGGAGAACACCATTAATTCTGAAATGTGCCCGTCCAGCGCTGTGATGACAGCGCTCC 676
QY 101 GlnValAlaLeuGluAsnGlySerAlaValAlaAspThrArgCysGlyCysValSProGly 120
Db 677 CAGGTGGCGGTGGAGACTGTTCAGCAGTGGCCACACCCGCTGGCTGTAAACAGCGGC 736
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheArgCysGlnPro 140
Db 737 TGGTTTGGAGGTCCAGGTGACCATGTGTCCAGCATTCACCTCTCTCTCTCTCTCTCTCT 796
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuGlySerArgArgAspThr 160
Db 797 TGCCTAAGCTCCGGGGCCCTGCACCGCCACACAGCGCTACTGTCTCCGACAGATACT 856
QY 161 AspCysGlyThrCysLeuProGlyPheArgGlnHisGlyAspGlyCysValSPro 180
Db 857 GACGTGGAGACCTGCTCCCTGCTGTATGAAACATGGCGATGGCTGCTGCTGCTGCTGCTG 916
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGln 199
Db 917 ACGTAATTCCTA-----GCTGTGCTGGGATGGAGGAA 949

RESULT 12

US-10-112-193-5
Sequence 5, Application US/10112193
Publication No. US20030004313A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,193
FILING DATE: 28-Mar-2002
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/928,069
FILING DATE: 11-Sep-1997
APPLICATION NUMBER: 60/026943
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P105281

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-193-5

Alignment Scores:
Pred. No.: 2,32e-86 Length: 1438
Score: 1066.00 Matches: 187
Percent Similarity: 94.47% Conservative: 1

Best Local Similarity: 93.97% Mismatches: 3
Query Match: 45.89% Indels: 8
DB: 9 Gaps: 1

US-09-993-234-6 (1-417) x US-10-112-193-5 (1-1438)

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QY 21 GlnValAlaLeuGlnGlyArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 437 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 496
QY 41 LysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisThrLeuValSPro 60
Db 497 AAGAGATTGCTGCTGTTTGTGTCAGAGGCTCCACGCGGCGGCGGCGGCGGCGGCGG 556
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
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QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheArgCysGlnPro 140
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QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuGlySerArgArgAspThr 160
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QY 161 AspCysGlyThrCysLeuProGlyPheArgGlnHisGlyAspGlyCysValSPro 180
Db 857 GACGTGGAGACCTGCTCCCTGCTGTATGAAACATGGCGATGGCTGCTGCTGCTGCTGCTG 916
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGln 199
Db 917 ACGTAATTCCTA-----GCTGTGCTGGGATGGAGGAA 949

RESULT 13

US-09-884-733-5
Sequence 5, Application US/09884733
Patent No. US20020123116A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 Ligand Inhibitor
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/884,733
FILING DATE: 19-Jun-2001
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/304,003
FILING DATE: 14-JUNE-2000

ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-884-733-5
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-993-234-6 (1-417) x US-09-884-733-5 (1-1438)
Alignment Scores:
Pred. No.: 2,32e-86 Length: 1438
Score: 1066.00 Matches: 187
Percent Similarity: 94.47% Conservative: 1
Best Local Similarity: 93.97% Mismatches: 3
Query Match: 45.89% Indels: 8
DB: 10 Gaps: 1
US-09-993-234-6 (1-417) x US-09-884-733-5 (1-1438)
QY 1 MetGluGlnArpProArGlyCysAlaAlaValAlaLeuLeuValLeu 20
DB 377 ATGGAGACAGCGCGCGGCGCTGCGCGCGCGCGCGCTCTCTGCTG 436
QY 21 G1yAlaArGlaGlnGlyGlyThrArgSerProArGcysAspCysAlaGlyAspPheHis 40
DB 437 GGGGCCCGGGCCAGCGCGGCGCTGAGCCAGCGAGTGAGTGTGCGCGGAGATTCCAC 496
QY 41 LysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuValPro 60
DB 497 AAGAAGATTGCTGTTTGTTCAGAGGCTGCCAGCGGCGACCTGAAGGCCCT 556
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
DB 557 TGCACGAGCGCGCGCGGCGCTGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTG 616
QY 81 TrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
DB 617 TGGGAGAACCAACATATTTCTGAATGTGCCGCTGACAGGCTGTGATGAGAGGCTCC 676
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
DB 677 CAGGTGGCGCTGAGAACTGTTCAGAGTGGCGGACACCGCTGTGGCTGAAGCCAGGC 736
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
DB 737 TGGTTTGTGAGTGGCGCGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 796
QY 141 CysLeuAspCysGlyAlaLeuHisAsnGlnHisThrArgLeuLeuCysSerArgAspThr 160
DB 797 TGGCTAGACTGCGGCGCGCTGACCGGCGGCGGCGCTGCTGCTGCTGCTGCTGCTG 856
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysPro 180
DB 857 GACGTGGGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 916
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaCysGlyTyrTrpArgGln 199
DB 917 ACGTAATTCCTA-----GCTGTGCGGAGTGGAGGAA 949
RESULT 14
US-09-993-234-5
; Sequence 5, Application US/09993234
; Patent No. US20020146768A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/993,234
FILING DATE: 19-NOV-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,683
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-993-234-5
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-993-234-6 (1-417) x US-09-993-234-5 (1-1438)
Alignment Scores:
Pred. No.: 2,32e-86 Length: 1438
Score: 1066.00 Matches: 187
Percent Similarity: 94.47% Conservative: 1
Best Local Similarity: 93.97% Mismatches: 3
Query Match: 45.89% Indels: 8
DB: 10 Gaps: 1
US-09-993-234-6 (1-417) x US-09-993-234-5 (1-1438)
QY 1 MetGluGlnArpProArGlyCysAlaAlaValAlaLeuLeuValLeu 20
DB 377 ATGGAGACAGCGCGCGGCGCTGCGCGCGCGCGCTCTCTGCTGCTGCTGCTGCTGCTG 436
QY 21 G1yAlaArGlaGlnGlyGlyThrArgSerProArGcysAspCysAlaGlyAspPheHis 40
DB 437 GGGGCCCGGGCCAGCGCGGCGCTGAGCCAGCGAGTGAGTGTGCGCGGAGATTCCAC 496
QY 41 LysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuValPro 60
DB 497 AAGAAGATTGCTGTTTGTTCAGAGGCTGCCAGCGGCGACCTGAAGGCCCT 556
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
DB 557 TGCACGAGCGCGCGCGGCGCTGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 616
QY 81 TrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
DB 617 TGGGAGAACCAACATATTTCTGAATGTGCCGCTGACAGGCTGTGATGAGAGGCTCC 676
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
DB 677 CAGGTGGCGCTGAGAACTGTTCAGAGTGGCGGACACCGCTGTGGCTGAAGCCAGGC 736
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:19:54 ; Search time 2608.38 Seconds

(without alignments)
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Fgapop 6.0 , Fgapext 7.0
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Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-UNIT5-bits START=1 -END=1 -MATRIX=Diosum62 -TRAMS=human40.cdi -LIST=45
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: em_estlin : *
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7: em_estro : *
8: em_hlc : *
9: em_hlc : *
10: gD_estl2 : *
11: gD_hlc : *
12: gD_est3 : *
13: gD_est4 : *
14: gD_est5 : *
15: em_estfun : *
16: em_estlom : *
17: gD_gss : *
18: em_gss_hum : *
19: em_gss_inv : *
20: em_gss_pln : *
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22: em_gss_fun : *
23: em_gss_mam : *
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26: em_gss_pro : *
27: em_gss_rod : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1179	50.8	681	10 BE563566	BE563566 601334867
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8	1078	46.4	562	9 A1140043	A1140043 qe87a04.x
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ALIGNMENTS

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DEFINITION
AGENCOURT_6794093 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5770562
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ACCESSION
B0068309
VERSION
B0068309.1 GI:19897355
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1010)
NIH-MGC <http://mgc.ncl.nih.gov/>.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE

QY 136 heTyrCysGlnProCysLeuAspCysGlnAlaLeuHisArgHisThrArgLeuLeuCys 156
 Db 444 TTTACTGCCAACCACTGCTAGACTCGGGGCCCTGCACCGCCACACAGCGCTACTCTGTT 503
 QY 156 eArGATGAspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyC 176
 Db 504 CCGCCAGAGTACTGACTGTGGAGCTGCTGCTGCTGCTTATGAACATGGCGATGGCT 563
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 QY 196 lYrPrpArgGlnMetPheTrpValGlnValLeuLeuAlaGlyLeuValProLeuLeu 216
 Db 624 GCTGGAGGCAAGTGTCTGGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 683
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 Db 684 TTGGGGCCACCTG-ACCTACACATACGC-CACTGTGTGCT-CACAGAGCCCTGGTACT- 739
 QY 236 laAspGluAlaGlyMet 241
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 VERSION BE563566.1 GI:9807286
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 TITLE NIH-MGC http://mgc.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (ILNI)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNI at:
 http://image.llnl.gov
 Plate: LLCN382 row: f column: 18
 High quality sequence stop: 681.

FEATURES
 Source Location/Qualifiers

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 /db_xref="taxon:9606"
 /clone="IMAGE:3688721"
 /clone_1lb="NIH_MGC_39"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;
 Site: 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAGCAG(C). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin
 (University of California, Berkeley) using Zap-cDNA
 synthesis kit (Stratagene) and Superscript II RT (Life
 Technologies)."

BASE COUNT 110 a 236 c 220 g 115 t

Alignment Scores: 8.43e-89 Length: 681
 Pred. No.: 1179.00 Matches: 225
 Score:

Percent Similarity: 99.12% Conservative: 0
 Best Local Similarity: 99.12% Mismatches: 2
 Query Match: 50.73% Indels: 0
 Db: 10 Gaps: 0
 US-09-993-234-6 (1-417) x BE563566 (1-681)

QY 175 GlyValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaVal 194
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 QY 195 CysGlyTrpArgGlnMetPheTrpValGlnValLeuLeuAlaGlyLeuValProLeu 214
 Db 63 TGTGGGTGGAGGAGATGTTCTGTGGTCCAGTCTCTGCTGCTGCTGCTGCTGCTGCT 122
 QY 215 LeuLeuGlyAlaThrLeuThrTyrThrTyrArgHisCysTrpProHisCysProLeuVal 234
 Db 123 CTGCTTGGGGCCACCTGTACATACATACCGCCACTGTGCTGCTGCTGCTGCTGCTGCT 182
 QY 235 ThrAlaAspGluAlaGlyMetGluAlaLeuThrProProProAlaThrHisLeuSerPro 254
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 QY 335 LeuTyrAspValMetAspAlaValProAlaArgArgTrpGlnPheValArgThrLeu 354
 Db 483 CTCTACAGAGTATGAGCGGCTGCCAGCGCGGCTGTGAGAGTGTGTGCGACGCTG 542
 QY 355 GlyLeuArgGluAlaGlyLeuGluAlaValGluValGluLeuArgPheArgAspGln 374
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 QY 375 GlnTyrGlnMetLeuLeuArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyr 394
 Db 603 CAGTACGAGATGCTCAAGCGCTGCGCCAGCAGCAGCCCGG-GGCCCTGGAGCCGTTTAC 661
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RESULT 5 632 bp mRNA linear EST 03-JAN-2000
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 PRECUTSOR ;, mRNA sequence.

ACCESSION AW268610 GI:6655640
 VERSION AW268610
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)


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OY      44  GYLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGlu 63
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OY      64  ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsn 83
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OY      144  CysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGly 163
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OY      164  ThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThr 183
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OY      184  LeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrp 202
Db      542  CTGGGAGAGTCTCCAGAGAGGCTGCTGCCGTCTGTGCTGTAGAGCAGAGTAAAGTGG 598

RESULT 7
LOCUS   BM009354 651 bp mRNA linear EST 30-OCT-2001
DEFINITION 603629813p1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5443659 5',
ACCESSION BM009354
VERSION   BM009354.1 GI:16523708
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL    Contact: Robert Strausberg, Ph.D.
            Email: cga@bse-femail.nih.gov
            Tissue Procurement: DCTD/DFP
            CDNA Library Preparation: Ling Hong/Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNLN at:
            http://image.llnl.gov
            Plate: LCM1921 row: 1 column: 04
            High quality sequence stop: 649.
            Location/Qualifiers
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                /db_xref="taxon:9606"
                /clone="IMAGE:5443659"
                /clone_1db="NIH_MGC_41"
                /tissue_type="amelanotic melanoma, cell line"

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/lab_host="DH10B (phage-resistant)"
/Note="Organ: skin; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC library."
BASE COUNT 107 a 224 c 204 g 116 t
ORIGIN
Alignment Scores:
Pred. No.: 1,05e-80 Length: 651
Score: 1082.00 Matches: 210
Percent Similarity: 98.14% Conservative: 1
Best Local Similarity: 97.67% Mismatches: 2
Query Match: 46.58% Indels: 4
DB: 13 Gaps: 0
US-09-993-234-6 (1-417) x BM009354 (1-651)
OY      166  LeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeuGly 185
Db      4  CTGCTGCTCTTATGAAATGCGATGCGATGCTGCTGTC-TGCCCAAGAGACACCTGGGG 62
OY      186  SerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGlnVal 205
Db      63  AGCTGTCCAGAGAGCTGTGCGCTCTCTGTGGCTGGAAGCAATGTTGTGGGTCCAGGTG 122
OY      206  LeuLeuAlaGlyLeuValAlaProLeuLeuGlnGlyAlaThrLeuThrTyrThrArg 225
Db      123  CTCCGTGCTGGCTGTGTGCTGCCCTCTGCTGTGGGGCACCTGACCTTACATATACGC 182
OY      226  HisCysTrpProHisLysProLeuValThrAlaAspGlnAlaGlyMetGlnAlaLeuThr 245
Db      183  CACTGTGCTCTCAACAAACCCCTGTTACTCAGATGAAGCTGGGATGAGAGCTGTGACC 242
OY      246  ProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProPro 265
Db      243  CCACACAGCGGC-ACCCATCTGTACCTTGGACAGCGCCACACCTTCTTACACTTCT 301
OY      266  AspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTyr 285
Db      302  GACAGCACTGAGAGATGTCACCGTCCAGTTGGTGGTACACTGAGACCCCTGGGTAC 361
OY      286  ProGluThrGlnGlnAlaLeuCysProGlnValAlaThrTrpSerTrpAspGlnLeuProSer 305
Db      362  CCCGAGACCCAGAGAGGCGCTGTGCCGAGGTGACATGTCTTGTGGACCAAGTTGCCAGC 421
OY      306  ArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySerPro 325
Db      422  AGAGCTCTTGGCCCCGCTGTGCTGCCACACTCTCGGCAGAGTGTCCAGCGGCTGCCA 481
OY      326  AlaMetLeuGln-ProGlyProGlnLeuTyrAspValMetAspAlaValProAlaArg 345
Db      482  GCCATGATGTGCGAGCGCGCGCGCGAGCTCTACGAGATGATGAGCGGCTCCAGCGCG 541
OY      345  GATGTrpLysGlnPheValArgThrLeuGlyLeuArgGlnAlaGlnLeuAlaValG 365
Db      542  CGCGTGAAGAGAGTCTGTGCGCACAGCTGGGGCTGCGGAGAGATGAAAGCCGTGGA 601
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Db      602  GGTGAGATCGGGCGGCTTCCGAGACAGAGTACAGATT 642

RESULT 8
LOCUS   A1140043 562 bp mRNA linear EST 13-APR-1999
DEFINITION 9487404.x1 Soares-fetal_heart_BbNH19W Homo sapiens cDNA clone
IMAGE:1693710 3' similar to SW:MSL1_HUMAN Q93038 MSL-1 PROTEIN
PRECURSOR: "", mRNA sequence.
ACCESSION A1140043

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VERSION AT140043.1 GI:3647500
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 562)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
Tumor Gene Index
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaps-remail.nih.gov.
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1640 Std Error: 0.00
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 494.
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/sex="unknown"
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strand cDNA was primed with a Not I - oligo(dT) primer [5'
TCCTACCATCTGTAAGTGGAGCGCGCCGACATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Patino Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHL19W."
BASE COUNT 88 a 182 c 180 g 111 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 1.83e-80 Length: 562
Score: 1078.00 Matches: 186
Percent Similarity: 99.47% Conservative: 0
Best Local Similarity: 99.47% Mismatches: 1
Query Match: 46.41% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6 (1-417) x AT140043 (1-562)
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QY 44 GlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGlu 63
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QY 104 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal 123

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QY 124 GluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAsp 143
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Db 362 GAGTGGCCAGGTGACCAATGTGTAGACGATTACACCTTTCTACTGCCAACATGCTTGAC 421
QY 144 CysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgAspThrAspCysGly 163
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QY 164 ThrCysLeuProGlyPheTyrGlnHisGlyAspGlyValSerCysProThrSerThr 183
Db 482 ACCGTGCTGCTGCTCTATGAACATGGCGATGGCTGCTGCTGCCACGACGACC 541
QY 184 LeuGlySerCysProGluArg 190
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Db 542 CTGAGGAGCTGTCCAGAGCGC 562
RESULT 9
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LOCUS K-EST0076219 S22SN016n1 Homo sapiens cDNA clone S22SN016n1-48-G11
DEFINITION 5', mRNA sequence.
ACCESSION BM794760 GI:19142992
VERSION BM794760
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 647)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: Yongsung@mail.krrib.re.kr
Plate: 48 row: G column: 11
High quality sequence stop: 647.
FEATURES
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Site 2: NotI. The S22SN016 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."
BASE COUNT 110 a 229 c 203 g 105 t
ORIGIN
Alignment Scores:
Pred. No.: 2.06e-79 Length: 647
Score: 1066.50 Matches: 201
Percent Similarity: 99.51% Conservative: 1

GenCore version 5.1.4_p5-4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:28:24 ; Search time 70.3944 Seconds
(without alignments)
1816.682 Million cell updates/sec

Title: US-09-993-234-6
Perfect score: 2323
Sequence: 1 MEORRGCANVAALLLVLL.....ERMGDGVEDLRSLQRC 417

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BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Issued_Patents_NA :
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2323	100.0	1254	3	US-08-815-469-3 Sequence 3, Appl1
2	2323	100.0	1634	4	US-08-928-069-11 Sequence 11, Appl1
3	2323	100.0	1634	4	US-08-828-683A-9 Sequence 9, Appl1
4	2267	97.6	1783	4	US-08-815-469-1 Sequence 1, Appl1
5	1066	45.9	1438	4	US-08-928-069-5 Sequence 5, Appl1
6	1066	45.9	1438	4	US-08-828-683A-5 Sequence 5, Appl1
7	692	29.8	433	4	US-08-928-069-2 Sequence 2, Appl1
8	692	29.8	433	4	US-08-828-683A-2 Sequence 2, Appl1
9	404.5	17.4	1956	4	US-08-762-308-10 Sequence 10, Appl1
10	387.5	16.7	2440	4	US-09-513-007-1 Sequence 1, Appl1
11	376	16.2	2062	1	US-08-050-319B-24 Sequence 24, Appl1
12	376	16.2	2062	2	US-08-465-982-24 Sequence 24, Appl1

13	374	16.1	2161	3	US-09-106-038A-1 Sequence 1, Appl1
14	374	16.1	2161	4	US-09-505-250-3 Sequence 3, Appl1
15	374	16.1	2175	1	US-08-321-668-1 Sequence 1, Appl1
16	374	16.1	2175	1	US-08-837-941-1 Sequence 1, Appl1
17	374	16.1	2175	1	US-08-126-016-1 Sequence 1, Appl1
18	374	16.1	2175	4	US-08-054-970-1 Sequence 1, Appl1
19	231.5	10.0	1724	5	PCT-US96-12374-1 Sequence 1, Appl1
20	230.5	9.9	1724	4	US-08-509-024-1 Sequence 1, Appl1
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22	218.5	9.4	6889	4	US-08-286-740-2 Sequence 1, Appl1
23	218.5	9.4	6889	5	PCT-US95-09576-2 Sequence 2, Appl1
24	217	9.3	1049	4	US-08-804-166-1 Sequence 1, Appl1
25	217	9.3	1049	4	US-08-910-991-1 Sequence 1, Appl1
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28	216	9.3	1202	4	US-08-910-991-3 Sequence 3, Appl1
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33	210	9.0	6896	2	US-08-627-151A-6 Sequence 6, Appl1
34	203.5	8.8	1323	3	US-08-883-036A-1 Sequence 1, Appl1
35	203	8.7	1147	4	US-08-804-166-5 Sequence 5, Appl1
36	203	8.7	1147	4	US-08-910-991-5 Sequence 5, Appl1
37	200.5	8.6	483	4	US-09-326-394-1 Sequence 1, Appl1
38	200.5	8.6	1478	4	US-09-149-922-6 Sequence 6, Appl1
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41	199.5	8.6	2534	4	US-08-468-560C-1 Sequence 1, Appl1
42	199.5	8.6	2534	4	US-09-180-100-16 Sequence 16, Appl1
43	199.5	8.6	2531	4	US-09-290-640-1 Sequence 1, Appl1
44	197.5	8.5	1596	4	US-09-146-950-17 Sequence 17, Appl1
45	196	8.4	1480	4	US-09-290-640-65 Sequence 65, Appl1

ALIGNMENTS

RESULT 1
US-08-815-469-3
Sequence 3, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285

FILING DATE: 12-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Steffe, Eric K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1254 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1251
 US-08-815-469-3

Alignment Scores:
 Pred. No.: 1.79e-181 Length: 1254
 Score: 2323.00 Matches: 417
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 Query Match: 100.00% Indels: 0
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 Db 61 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
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 QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
 Db 481 GACTGTGGAGCTCGCTGCTGCTTATGAACATGCGCATGCTGCTGCTGCTGCTGCTG 540
 QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaValCysGlyTyrTrpArgLysMet 200
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 QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeu 220
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QY 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGlnAlaGly 240
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 QY 281 TrpThrProGlyTyrTrpProGluThrGlnGlnAlaLeuCysProGlnValThrTrpSer 300
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 QY 381 ArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
 Db 1141 CGGTGGCCCGAGCAGACACCGCGGCGCTCGAGACCGCTTACGCGGCGCTGGAGCG 1200
 QY 401 GlyLeuAspGlyCysValGluAspLeuAsnSerArgLeuGlnArgGlyPro 417
 Db 1201 GGGGTGGAGCGCTCGTGGAAAGACTTGGCAGGCCCTGCGAGCGGCGCGG 1251

RESULT 2
 US-08-928-069-11
 Sequence 11, Application US/08928069
 Patent No. 6462176
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 TITLE OF INVENTION: Apo-3 POLYPEPTIDE
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Minipact (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/928,069
 FILING DATE: 11-Sep-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/026943
 FILING DATE: 09/23/1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Marschang, Diane L.
 REGISTRATION NUMBER: 35,600
 REFERENCE/DOCKET NUMBER: P1052R1
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-928-069-11

Alignment Scores:

Pred. No.:	2,64e-181	Length:	1634
Score:	2323.00	Matches:	417
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-993-234-6 (1-417) x US-09-928-069-11 (1-1634)

QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
DB 89 ATGGAGCAGACGGCGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 148
QY 21 GAlaAlaArgAlaGlnGlnGlyLysThrArgSerProArgCysAspCysAlaGlnAspPheHis 40
DB 149 GGGGCGCGGGCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 208
QY 41 LysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisThrLeuValPro 60
DB 209 AGAGATTTGGTCTGTTTGTGTCAGAGCGTCCCGCGGGGCGGAGCTGAGAGGCGCCCT 268
QY 61 CysThrGluProCysGlyLysAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
DB 269 TGCAGGAGACCTCGGGCAATCTCAGCTGCTGTGTCCCAAGACACCTTCTGGGC 328
QY 81 TTPGluAsnHisHisAsnSerGlyCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
DB 329 TGGGAACACCCATTAATCTGAAATGTCCTGCGAGCGCTGTATGAGCGGCTCC 388
QY 101 GlnValAlaLeuGluAsnGlyCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
DB 389 CAGGTGGCGCTGGAGACTGTTTCAGCAGTGGCGGACCGCGCTGTGTAAAGCCAGCG 448
QY 121 TTPheValGluCysGlnValSerGlnCysValSerSerSerProPheThrCysGlnPro 140
DB 449 TGGTTTGTGAGAGTCCAGGTGCAAGCAATGTGTACAGCATCCCTTACTGCCAACA 508
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
DB 509 TGCCTAAGACTGGGGCGCTGCAACCGCACACAGCGCTACTCTGTCCCGCAGAGTACT 568
QY 161 AspCysGlyThrCysLeuProGlyPheThrGluHisGlyAspGlyCysValSerCysPro 180
DB 569 GACTGTGGAGACTGCTGCTGCTGCTTCTATGAACATGGGAGTGGCTGCTGCTGCC 628
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyThrArgGlnMet 200
DB 629 ACGAGACACCTGGGAGGCTGTCAGAGCGCTGCGCGCTGTGTGTGGTGGAGGAGGAG 688
QY 201 PheThrPvalGlnValLeuLeuAlaGlyLeuValProLeuLeuLeuGlyAlaThrLeu 220
DB 689 TTTCTGGGTCTCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 748
QY 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly 240
DB 749 ACCTACACATACCCGACACTGCTGGCTTCAAGAGCCCTGTACTGCAATGAGAGCTGG 808
QY 241 MetGluAlaLeuThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
DB 809 ATGGAGGCTCTGACCCACACCGGCGCACCATCTGTGACCGCTGGACAGCGCCACAC 868
QY 261 LeuLeuAlaProProAspSerSerGlyLysIleCysThrValGlnLeuValGlyLysSer 280

DB 869 CTTCAGACACCTCTCAGACAGCAGTGAAGATGCAACCTCCAGTTGGTGGTAAACAGC 928
QY 281 TTPThrProGlyLysProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrp 300
DB 929 TGGACCCCTGGCTACCCCGAGACCCAGAGAGCCCTTGTCCCGGAGGTGACATGCTCTGG 988
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
DB 989 GACCACTTGGCCAGAGAGCTTGGCCCGGCTGTGCGGCGCCACACTCTGCCAGAGTCC 1048
QY 321 ProAlaGlySerProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
DB 1049 CCAGCCGCTCGCCAGACCATGATGCTGACAGCCGCGCCCGCAGCTTACAGCATGATGAG 1108
QY 341 AlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
DB 1109 GCGGTCCAGCGCGCGCGTGGAAAGAGTTCGTGCGCACCTGGGCTGCGCGAGCAGAG 1168
QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
DB 1169 ATGGAAGCCGTGAGAGTGGAGATCGGCGCTTCCAGACAGCAGTACAGATGCTCAAG 1228
QY 381 ArgTPArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
DB 1229 CGGTGCGCGCAGCAGCAGCGCGCGGCTCGGAGCGGCTTACCGCGCCCTGAGCGCATG 1288
QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
DB 1289 GGGCTGACGCGCTGCGTGGAAAGACTTGGCGAGCGGCTGACGCGCGGCGCGCG 1339

RESULT 3

US-08-828-683A-9
Sequence 9, Application US/08828683A
Patent No. 6469144

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatlin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997

PRIOR APPLICATION DATA:
CLASSIFICATION: <Unknown>

APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 198..1481
US-08-815-469-1

Alignment Scores:
Pred. No.: 1.16e-176 Length: 1783
Score: 2267.00 Matches: 409
Percent Similarity: 97.39 Conservative: 1
Best Local Similarity: 97.154 Mismatches: 5
Query Match: 97.598 Indels: 6
Gaps: 1

US-09-993-234-6 (1-417) x US-08-815-469-1 (1-1783)

QY 3 GlnArgProArgGly-----CysAlaAlaValAlaAlaAlaLeu 16
Db 219 GAGGCCCGGCTGGGAGCTGGCGGAGAGTGCAGCAGCTGTGCCCCGCGGCTCTC 278
QY 17 LeuValLeuLeuGlyAlaAlaAlaGlnGlyAlaArgSerProArgCysAspCysAla 36
Db 279 CTGGTGTCTGTGGGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 338
QY 37 GlyAspPheHisLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 56
Db 339 GGTGATCTTCACAGAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 398
QY 57 LeuLysAlaLysProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAsp 76
Db 399 CTGAAGGCGGCTGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 458
QY 77 ThrPheLeuAlaIleProLysAsnHisAsnSerGluCysAlaAlaArgCysGlnAlaCysAsp 96
Db 459 ACCTTCTTGGCGCTGGGAGAGAACCAATATTCGATGTCGCCGCTGCTGAT 518
QY 97 GluGlnAlaSerGlnValAlaLeuGlnAsnSerGlnAlaValAlaAspThrArgCysGly 116
Db 519 GAGCAGAGCGCTCCGAGGTGGGCTGGAGAACTGTTGAGCAAGTGGCGGCGGCGGCTG 578
QY 117 CysLysProGlyLysPheValGluCysGlnValSerGlnCysValSerSerProPhe 136
Db 579 TGTAAACCGAGGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 638
QY 137 TyrCysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSer 156
Db 639 TACTGCCAACATGCTTACACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 698
QY 157 ArgValAspPheThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCys 176
Db 699 CGCAGAGATACGACTGCTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 758
QY 177 ValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGly 196
Db 759 GTTCTCTGCGGCGGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 818
QY 197 TrpArgGlnMetPheThrValGlnValLeuLeuAlaGlyLeuValValProLeuLeu 216
Db 819 TGGAGGCAATGTTCTGGGCTCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 878
QY 217 GlyAlaThrLeuThrTyrThrTyrArgHisCysTyrProHisLysProLeuValThrAla 236
Db 879 GGGGCGACCTGACATACATACGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 938
QY 237 AspGlnAlaGlyMetGlnAlaLeuThrProProProAlaThrHisLeuSerProLeuAsp 256
Db 939 GATGAAGCTGGGATGGAGCTGTGAGCCACACACCGGCGGCGGCGGCGGCGGCGGCG 998
QY 257 SerAlaHisThrLeuLeuAlaProProAspSerSerGlnLysLysLysThrValGlnLeu 276
Db 999 AGCGGCCACACCTTCTACACCTCTGACAGAGTACAGATCTGACCGCTGCGAGTTG 1058

QY 277 ValGlyAsnSerThrProGlyLysThrProGluThrGlnGlnAlaLeuCysProGlnVal 296
Db 1059 TGGGTGTAACAGCTGAGACCCCTGCTACCCGAGACCCAGAGGCGGCTGCTCCGCGAGT 1118
QY 297 ThrTrpSerThrPaspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeu 316
Db 1119 ACATGCTCTGGGAGCCAGTGGCCAGCAGAGCTTGGCCCCGCTGCTGCGCCACACTC 1178
QY 317 SerProGluSerProAlaGlySerProAlaMetLeuGlnProGlyProGlnLeuTyr 336
Db 1179 TCCGCAAGAGTCCCGCAGCGGCTGCGCAGCATATGTCAGCCGCGGCGGCGGCTTAC 1238
QY 337 AspValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeu 356
Db 1239 GACGTGATGAGCGGCGGCTCCAGCGGCGGCGGCTGGAAGAGATTGTCGCGCAGCGGCG 1298
QY 357 ArgGlnAlaGlnLeuGlnAlaValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 376
Db 1299 CGCGAGGACAGATCGAAGCCGTGGAGGTGAGATCGCGCTTCCAGACAGCAGACTAC 1358
QY 377 GluMetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlnAlaValTyrAlaAla 396
Db 1359 GAGATGCTCAAGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1418
QY 397 LeuGlnArgMetGlyLeuAspGlyCysValGlnAspLeuArgSerArgLeuGlnArgGly 416
Db 1419 CTGAGGCGCATGGGGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1478
QY 417 Pro 417
Db 1479 CCG 1481

RESULT 5
US-08-928-069-5
Sequence 5, Application US/08928069
Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-928-069-5


```

RESULT 7
US-08-928-069-2
; Sequence 2, Application US/08928069
; Patent No. 6462176
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinpacIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,069
; FILING DATE: 11-Sep-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/026943
; FILING DATE: 09/23/1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1052R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 433 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;
US-08-928-069-2

Alignment Scores:
Pred. No.: 1,74e-48 Length: 433
Score: 692.00 Matches: 133
Percent Similarity: 93.10% Conservative: 2
Best local Similarity: 91.72% Mismatches: 6
Query Match: 29.79% Indels: 5
DB: 4 Gaps: 0

US-09-993-234-6 (1-417) x US-08-928-069-2 (1-433)
Oy 19 LeuLengUyAlAaGyAlaGInGlyLThrArgSerProArGyCysAspCysAlaGlyAsp 38
Db 1 CTGGCGGGGGCCCGGGCCAGNGCGGCACTGTAAGCCCAAGGTGTGACTGTGCGGTGAC 60
Oy 39 PheHisIySLySLiEGlyLeuPheCysCysArGgLyCysProAla-0LyHsIyTLeuLy 58
Db 61 TTTCCACAAGAGATTTGGGTCTTTTGTGTGCGAGAGCGTCCCAAGGGGGCAACTACCTGAA 120
Oy 58 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysBProGlnAspThrph 78
Db 121 GGGCCCTTGGCAACGAGAGCCCTTCGCC-AACTCCACCTGCTGTGTGCCCAAGACACTT 179
Oy 78 eleuAlarPrpLusnHsHsAsnSerGluCysAlaArgCysGlnAlaCysAspGlu 98
Db 180 CTGGCCCTGGGAGAACCAACCTAATTTCTGAATGTGCCCGCTGCCAGGCGCTGTGATGACA 239
Oy 98 nAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLy 118
Db 240 GGGCTCCCAAGCTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTTAA 239
Oy 118 sPrGGLyTrpPheValGluCysGln-ValSerGlnCysValSerSer-SerProPheTyr 137

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Db      300  GCAGGGCTGTTGGAGTGCCAGAGGGTCACCAACCATGTCAGACGTTTACACCTTTTAA 359
|
QY      138  CysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCys-Ser 157
|
Db      360  TGCCACCATCTCTAGACTGCGGGGCCCTGCACACGCAACACACGCGTAATWTGTTCCCG 419
|
QY      157  gArGasp 159
|
Db      420  CAGAGAT 426
|
RESULT 8
US-08-828-683A-2
: Sequence 2, Application US/08828683A
: Patent No. 6469144
:
: GENERAL INFORMATION:
:   APPLICANT: Ashkenazi, Avi J.
:   TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
:   NUMBER OF SEQUENCES: 28
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Genentech, Inc.
:     STREET: 1 DNA Way
:     CITY: South San Francisco
:     STATE: California
:     COUNTRY: USA
:     ZIP: 94080
:
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: Winpatin (Genentech)
:
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/828,683A
:   FILING DATE: 31-Mar-1997
:   CLASSIFICATION: <Unknown>
:
: PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: 08/625328
:   FILING DATE: 1-Apr-1996
:   APPLICATION NUMBER: 08/710802
:   FILING DATE: 23-Sep-1996
:
: ATTORNEY/AGENT INFORMATION:
:   NAME: Marschang, Diane L.
:   REGISTRATION NUMBER: 35,600
:   REFERENCE/DOCKET NUMBER: P1007P1
:
: TELECOMMUNICATION INFORMATION:
:   TELEPHONE: 650/225-5416
:   TELEFAX: 650/952-9881
:
: INFORMATION FOR SEQ ID NO: 2:
:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 433 base pairs
:     TYPE: Nucleic Acid
:     STRANDEDNESS: Single
:     TOPOLOGY: Linear
:
:   SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-828-683A-2
|
Alignment Scores:
Pred. No.:      1,74e-48      length:      433
Score:          692.00      Matches:      133
Percent Similarity: 93.10%      Conservative: 2
Best Local Similarity: 91.72%      Mismatches: 6
Query Match:    29.79%      Indels:      5
DB:             4          Gaps:          0
|
US-093-234-6 (1-417) x US-08-828-683A-2 (1-433)
QY      19  LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 38
|
Db      1  CTGCTGGGGGGCCCGGGCCAGAGGCGGCACCTGTAGCCCAAGGTGTACTGTGCGCGTGAC 60
|
QY      39  PheHisLysLysIleGlyLeuPheCysArgGlyCysProAla-GlyHisTyrLeu 58
|
Db      61  TTCACAAGAAGATGTGCTCTTTTGTGTGCAGAGGCTGCCACGCGGGCAACTACTGAA 120
|

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QY      58  salaprocysThngluprocysgllynsbserhrcysleuValcysProglInasprhPh  78
Db      121  GGGCCCTTGACGAGAGCCCTGGCC  |||||CCCCCCCCCCCCCCCCCCCC  179
QY      78  elauaIatPrpGluaSNhIshIsasnsSerIuCYsaIlaarCYsgInaIaCYsaSPgluGl  98
Db      180  CTTGGCGCTGGAGAGAACACCATATATCTGAATGTGCCCGCTGCCGCTGTGATGACCA  235
QY      98  naIasergInValAlaLeuGluaSnCYsSerIaValAlaAsprhIarCYsgIuCYsLy  118
Db      240  GGGCTCCACAGGTGGCCCTGGAGAACTGTTCACACAGTGGCCGACACCCCTGTGGCTGAA  299
QY      118  sProglYTrpPheValGlucysGln-ValSerGInCYsValSerSer-serProPheTyr  137
Db      300  GCAGGCGCTGGTTGTGTGGATGTCCAGGGTCAAGCAATGTGTACGAGTTCACCCCTCTAA  359
QY      138  CysGlnProCYsLeuAspCYsGlgYalAlaEuNIshArGhIshTrArGleuCYs-SerAr  157
Db      360  TGGCAACACATGCTAGACTGCGGGGCGCTGCAGCCACACACACGGCTAATATGTTTCCCG  419
QY      157  gATgAsp 159
Db      420  CAGAGAT 426

RESULT 9
US-08-762-308-10
; Sequence 10, Application US/08762308
; Patent No. 5925548
; GENERAL INFORMATION:
; APPLICANT: Beutler, Bruce A.
; APPLICANT: Bazoni, Flavia M.
; TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY
; TITLE OF INVENTION: SIGNAL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,308
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 179
; FILING DATE: 05-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: TUSD:335--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 418-3000
; TELEFAX: 474-7577
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1956 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-762-308-10

Alignment Scores:
Pred. No.: 5.8e-24 Length: 1956
Score: 404.50 Matches: 127
Percent Similarity: 39.19% Conservative: 56

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QY 295 GlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaPro 314
|||:
DB 1104 ACCTCTGTTCCAGAAATGGAGAC----- 1127
QY 315 ThrLeuSerProGlnSerProAlaGlySerProAlaMetMetLeuGlnProGlyProGln 334
|||:
DB 1128 TCCGCCACCCCGACAGCTCTTGCATATGCAATGCAACCTTCGCAAT----- 1169
QY 335 LeuTrpAspValMetLeuAlaValProAlaArgArgTrpLeuGlnPheValArgThrLeu 354
|||:
DB 1170 CTGTATGCTGTGTGTGTATGGCTGCTTCCAGCCGCTCGAAGAGATTCATGCTTTCATG 1229
QY 355 GlyLeuArgGlnAlaGluIleGlnAlaValGluValGluIleGlyArg--PheArgAsp 373
|||:
DB 1230 GGGCTGAGGACGACGATCGAGAGCTGAGATGACAGAACGGCGCTGCGCGAG 1289
QY 374 GlnGlnTrpGlnMetLeuAspArgTrpArgGlnGlnGlnProAla-----GlyLeu 390
|||:
DB 1290 GCTCACTACAGCATGTGCGAAGCTGCGCGCCGACGCGCGGCGACGACGACGACGCTG 1349
QY 391 GlyAlaValAlaLeuAlaLeuGlnArgMetGlyLeuAspGlyCysValGluAspLeuArg 410
|||:
DB 1350 GAAGTAGTGGCGCTGCTTCCAGATGACCTGCTGGTGGTCTGCGAGATATCTTC 1409
QY 411 SerArgLeuGlnArgGlyPro 417
DB 1410 GAGGCTCTG--AGAAATCC 1427

RESULT 10

US-09-513-007-1
Sequence 1, Application US/09513007
Patent No. 6406907
GENERAL INFORMATION:
APPLICANT: Taylor, J. Michael
APPLICANT: Kehrl, Jr., Marcus
APPLICANT: Lee, Eun-Kyung
APPLICANT: Mwang, Simon
TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
FILE REFERENCE: 08411-018001
CURRENT APPLICATION NUMBER: US/09/513,007
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 60/122,156
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2440
TYPE: DNA
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: CDS
LOCATION: (294)...(1706)
US-09-513-007-1

Alignment Scores:

Pred. No.: 1,98e-22 Length: 2440
Score: 387.50 Matches: 130
Percent Similarity: 36.57% Conservative: 47
Best Local Similarity: 26.86% Mismatches: 186
Query Match: 16.68% Indels: 121
Gaps: 18

US-09-993-234-6 (1-417) x US-09-513-007-1 (1-2440)

QY 11 ValAlaAlaLeuLeuValLeuLeuGlyAlaArgAlaGlnGlyThrArgSer 30
|||
DB 333 GTGCTTCCAGCTCTGTGTGACATGTATCCCGCAGGGGTTCCAGGGCTGATCCTC 392
QY 31 ProArgCysAspCysAlaGlyAspPhe----- 39
DB 393 CCC-----GGGACCTGGAGAAAGAGAGAGATCTCTCTCCCAAGGAAAA 437

QY 40 -----HisLeuLysIleGlyLeuPheCysArgGlyCysProAlaGlnHisTrpLeu 57
|||:
DB 438 TATTAACACCCCGCAATAATACACCATTTGCTGACCAAGTGCACCAAGATACCTATCTG 497
QY 58 LysAlaProCysThrGlnProCysGlyAsnSerThrCysLeuValCysProGlnAspThr 77
|||:
DB 498 TACAAATGACATCTCGGGGTCCAGGCGGACACACAGCTGAGGTGTCTGCTCCCTGACCC 557
QY 78 PheLeuAlaTrpGlnAsnHisAsnSerGlnCysAlaArgGlyGlnAlaCysAspGln 97
|||:
DB 558 TACACTGCTTGGAGAACCTCTCAGA--CGATGCTGAGCTGCCAGCTCCGGAG 614
QY 98 GlnAlaSerGlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyAsp 117
|||:
DB 615 GAATATTCAGATGAGATTTGCTGCTGTGTATGAGTGCACCGGACACTGTGTGCTGCTG 674
QY 118 LysProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTrp 137
|||:
DB 675 AGGAGAAC-----CAGTACCGGGAATACTGGGTGAAACTGGCTTCCCG 719
QY 138 CysGlnProCysLeuAspCys-----GlyAlaLeuHisArgHisThrArgLeuLeuCys 155
|||:
DB 720 TGTCTGAATGCAAGCTCTGTCCCAATGGACAGTGAAAT-----ATCCCTGCTG 767
QY 156 ---SerArgArgAspThrAspCysGlyThrCysLeuProGlyPheTrpGlnHisGlyAsp 174
|||:
DB 768 CAGAGAGACAGACACACATCTGC---CACTGCATATGAGGCTTCTTTCTTAAAGCGCC 824
QY 175 GlyCysValSerCysProThrSerThrLeuGlySerCysProGluArg---CysAlaAla 193
|||:
DB 825 AACTGATCTCTCTGCT-----CATGATTTGAAGAACAGAGTCCGAGAG 869
QY 194 ValCysGlyTrpArg-----GlnMetPhe 201
|||:
DB 870 TTATGTCCAAACCCGACCTTCACTGTAAGACTCTCAGAGCCAGGACACTACAGTACTA 929
QY 202 TrpValGlnValLeuLeuAlaGlyLeuValAlaProLeuLeuGlnGlyAlaThrLeuThr 221
|||:
DB 930 TTACCCCTGTGATTTGCTTGGGGCTTGTGCTGACATCTTCCCTCTGTGCTTACGA 969
QY 222 TyrThrTyrArgHisCysTrpProHisLys----- 231
|||:
DB 990 TGTGCTTACACGCG--TGGAAAGCCCAAGCTTACTCATCATTTGGGGCAGTGCAGT 1046
QY 231 ----- 231
DB 1047 CTGCTAAGAGGGGAGCCAGACCTCTGCTCCGCGCCAGGCTTCAACCCACCCACC 1106
QY 232 -----ProLeuValThr 235
|||:
DB 1107 ACCATCTGCTTACGCTCCACCCCAAGTTCACAGCTCTGTCCATTTCCCTTACATCTGC 1166
QY 236 AlaAspGlnAlaGlyMetGlnAlaLeuThrProProProAlaThrHisLeuSerProLeu 255
|||:
DB 1167 TGTGACCCGCTCAACTTCGAGCGCTGCGCATCTCCACAGAGAGGCGCCGCCCAT 1226
QY 256 AspSerAlaHisThrLeuLeuAlaProProAlaSerSerGlnLysIleCysThrValGln 275
|||:
DB 1227 CTAAAGGCTGCCCCCATCTCCCGGGGCTTCGCGCCACCCACCTGTGTACCCCGGGG 1286
QY 276 LeuValGlyAsnSer-----TrpThrProGlyTyrProGlnThrGlnAlaLeuCys 293
|||:
DB 1287 CCTCGGGCTCCACACCACTCTGTACCCGGGGCTCTCGGCTCTCCACCACTCTGTACCC 1346
QY 294 ProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaAla 313
|||:
DB 1347 CCAGTTCCAGAAATGG-----GAAGCCAGGCGCCCGCCAGCGCCCGCC 1385
QY 314 ProThrLeuSerProGlnSerProAlaGlySerProAlaMetMetLeuGlnProGlyPro 333
|||:
DB 1386 GATCACTGCGGGATGCCAGACCCGCG----- 1412

QY 334 GlnLeuTyrAspValMetAspAlaValProAlaIarGArGTTrpLysGluPheValArgThr 353
Db 1413 ACCGTGTCAGCGGTGAGCGCGTCCCGCGCGCGTGGAGAGTGTGGCGCG 1472
QY 354 LeuGlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArg--PheArg 372
Db 1473 CTGGGACACTGAGGACAGACAGATCCAGCGCGCTGGAGCTGGAGAACGGGCGCACCTGCGC 1532
QY 373 AspGlnIleTyrGluMetLeuLysArgTTrpArgGlnGlnPro-----AlaGly 389
Db 1533 GAGGCGCAGTACAGCATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1592
QY 390 LeuGlyAlaValTyrAlaAlaLeuLysArgMetGlyLeuAspGlyCysValGluAspLeu 409
Db 1593 CTGGAGCTGTGGCGCGCGCTGCTCAGGAGACAGCTGGTGGCTGGAGAAACATA 1652
QY 410 ArgSerArgLeu 413
Db 1653 GAGGAGCGCGCTG 1664

RESULT 11
US-08-050-319B-24

Sequence 24, Application US/08050319B

Patent No. 5633145

GENERAL INFORMATION:

APPLICANT: M. Feldmann, P.W. Gray,

APPLICANT: M.J.C. Turner, F.M. Brennan

TITLE OF INVENTION: Modified human TNFalpha (Tumor

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Reed & Robblins

STREET: 635 Bryant Street

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/050,319B

FILING DATE: 10-May-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Robbins, Roberta L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 5150-0030

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 617-8999

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 2062 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

FEATURE:

NAME/KEY: CDS

LOCATION: 155..1519

US-08-050-319B-24

Alignment Scores:

Pred. No.: 1.36e-21

Score: 376.00

Percent Similarity: 39.09%

Best Local Similarity: 28.29%

Query Match: 16.19%

DB: 1

Length: 2062
Matches: 131
Conservative: 50
Mismatch: 182
Indels: 100
Gaps: 22

US-09-993-234-6 (1-417) x US-08-050-319B-24 (1-2062)

QY 15 LeuLeuLeuValLeuLeuGlyAlaArgAlaGlnGly----- 26
Db 197 CTCCTGGAGCTTGTGGTGAATATACCCCTCAGGGGTTATTGACGTGCTCCACCTA 256
QY 27 GlyTrpArgSerProArg-----CysAspCysAlaGlyAspPheHisLysIle 43
Db 257 GGGGACAGGAGAGAGAGATAGTGTGTGTGCTCCCAAGGAAATATATATCCCTCAAAAT 316
QY 44 GlyLeuPheCysArgGlyCysProAlaGlyHisLysIleValAlaProCysThrGlu 63
Db 317 AATTGATTTGTGTGATACCAAGTCCCAAGAACCTTGTATACAAAGACTGTCCAGGC 376
QY 64 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpLysn 83
Db 377 CCGGGGACAGATACGAGACTGCGAGGAGTGTAGACGGCTCTTCACCGCTTCAGAAAC 436
QY 84 HisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAla 103
Db 437 CACCTCAGA--CACTGCTCAGTGTCTCCAAATGCCCAAGAAATGGTCAAGGTGAG 493
QY 104 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheVal 123
Db 494 ATCTCTTCTTGACAGTGGAGCCGCGGACACCGTGTGCTGCAGAGAACACGATACCG 553
QY 124 GluCys-----GlnValSerGlnCysValSerSerSerProPheTyrCysGlnPro 140
Db 554 CATTTTGGAGGAAACCTTTCCAGTGC-----TTCAATTGACGCTC 598
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgPheThr 160
Db 599 TGCCCTCAAT--GGGACCGTGCAC-----CTCTCCTGCAGAGAAACAGAAC 643
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
Db 644 ACCGTGCACCTGCCAGTGCAGTGTCTTTTAAAGAGAAACAGTGTCTCTCTGT-- 700
QY 181 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 195
Db 701 -----AGTAAGTGAAGAAAGCCGAGAGTGCAGCAATTTGCTTACCAG 748
QY 196 -----GlyTrpArgGlnMetPheTyrValGlnValLeu 206
Db 749 ATTGAGAAATTAAAGGACAGTGCAGTGCAGACACAGTGTGCTGCTGCTGCTGCTGCT 808
QY 207 LeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrArgHis 226
Db 809 TTTCTTGGTCTTGGCTTTTATCCCTCTCTCATTTGTTAAATGATATGCTACCAACGG 868
QY 227 CysTrpProHisLys-----ProLeuValThrAlaAspGluAla 239
Db 869 ---TGAAGTCCAGCTTACTCCATGTTGTTGGGAATGCAGACCTGAAAAAGAGGG 925
QY 240 GlyMetGluAlaLeuThrProProAlaThrHisLeuSerProLeuAspSer----- 257
Db 926 GAGCTTGAAGAACTACTACTAAGCC-----CTGGCCCAACCAAGCTTCACTAGT 976
QY 258 -----AlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCys 272
Db 977 CCCACTCCAGGCTTCACCCCACTGAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1036
QY 273 ThrValGlnLeuValGlyAsnSerThrProGlyTyrProGluThrGlnGlnAlaLeu 292
Db 1037 TCC-----AGCTCACTATACCCCGGTGAC----- 1063
QY 293 CysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro----- 310
Db 1064 TGTCCCACTTTGGG-----GCTCCCGCAGAGAGGTGACACCACTAT 1108
QY 311 -----AlaAlaAlaProThrLeuSerPro--- 318
Db 1109 CAGGGGCTGACCCCATCTTGCAGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1168


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QY 293 CysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro----- 310
    |||||
Db 1064 TGTCACAACTTTGG-----GCTCCCGCAGAGAGGGGACCAACCTTAT 1108
QY 311 -----AlaAlaAlaProThrLeuSerPro-- 318
    |||||
Db 1109 CAGGGGGCTGACCCCATCTTGGACAGCCCTGCTCCGACCCCATCCCAACCCCTT 1168
QY 319 -----GluSerProAlaGlySerProAlaMetMetLeuGlnProGlyProGln--- 334
    |||||
Db 1169 CAGAAAGTGGAGAGACAGTGGCCACAAAGCCACAGACCTGATGACCCCGGAGC 1228
QY 335 LeuTrpAspValMetAspAlaValProAlaArgArgTrpGlyIupheValArgThrLeu 354
    |||||
Db 1229 CTGTACGCGCTGTGGAGAACGTGCCCCCTGCTGGAAAGAAATCGTGGCGCCCTA 1288
QY 355 GlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAsp 373
    |||||
Db 1289 GGGCTAGCAGCACCACAGATCGATCGGCTGGAGCTGACAGAACGGCGCTGCTGCGCAG 1348
QY 374 GlnGlnTrpGlnMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeu 390
    |||||
Db 1349 GCCCAATACAGCATGCTGGAGACCTGGAGCGCGGCGGCGGCGGCGGCGGCGGCGG 1408
QY 391 GlyAlaValThrAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg 410
    |||||
Db 1409 GAGCTCTGGAGCGCTGCTCGCGACATGACCTGCTGCTGGAGGACATCGAG 1468
QY 411 SerArgLeu 413
    |||||
Db 1469 GAGGCGCTT 1477

RESULT 13
US-09-106-038A-1
; Sequence 1, Application US/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFRI
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue
; CITY: Carlsbad
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 MB
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,038A
; FILING DATE: June 26, 1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Laurel Spear Bernstein
; REGISTRATION NUMBER: 37,280
; REFERENCE/DOCKET NUMBER: RTS-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (760) 931-9200
; TELEFAX: (760) 603-3820
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-106-038A-1

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Alignment Scores:

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Pred. No.: 2,12e-21 Length: 2161
Score: 374.00 Matches: 131
Percent Similarity: 38.88% Conservative: 49
Best Local Similarity: 28.29% Mismatches: 183
Query Match: 16.10% Indels: 100
DB: 3 Gaps: 22

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US-09-993-234-6 (1-417) x US-09-106-038A-1 (1-2161)

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QY 15 LeuLeuLeuValLeuLeuGluAlaArgAlaGlnGly----- 26
    |||||
Db 298 CTCCTGAGACCTGTGTGGTGGAAATATACCCCTCAGGGGTTATTGACTGCTCCCTACCTA 357
QY 27 GlyThrArgSerProArg-----CysAspCysAlaGlyAspPheHisLysLysIle 43
    |||||
Db 358 GGGAGCAGGAGAGAGAGAGATAGTGTGTGCTCCCAAGAAATAATATATACACCTCAAAAT 417
QY 44 GlyLeuPheCysCysArgGlyCysProAlaGlnHisTrpLeuValAlaProCysThrGlu 63
    |||||
Db 418 AATTGATTTGCTGTATCCAGTGCACAAAGAACCTTGTATACATGACTGTCAGGC 477
QY 64 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpIleAsn 83
    |||||
Db 478 CCGGGGAGAGATACGAGACTGCAGGAGTGTGAGACGGCTCTTACCGGCTTCAGAAAC 537
QY 84 HisHisAsnSerGluCysAlaAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAla 103
    |||||
Db 538 CACCTTCAG-----CACTGCTCAGCTGCTCCAAATCCGAAAGAAATGGTACAGTGGAG 594
QY 104 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal 123
    |||||
Db 595 ATCTCTCTTGACAGTGGAGACCGGACACCGTGTGTGCTGACGAGAAACAGTACCGG 654
QY 124 GluCys-----GlnValSerGlnCysValSerSerProPheTrpCysGlnPro 140
    |||||
Db 655 CATATTGAGTGAAGAAACCTTTTCCAGTGC-----TTCAATTGACGGCTC 699
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
    |||||
Db 700 TGCCCAT-----GGGACCGTGCAC-----CTCTCTCCAGAGAAACAGAAC 744
QY 161 AspCysGlyThrCysLeuProGlyPheTrpGlnHisGlyAspGlyCysValSerCysPro 180
    |||||
Db 745 ACCGTGTCACCTGCATGACGAGTTCTTCTTAGAGAAAGAGAGTGTCTCTG 801
QY 181 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 195
    |||||
Db 802 -----AGTAACTGTAAAGAAAGCCGTGAGTGCAGAGAGTTGTGCTACCCAG 849
QY 196 -----GlyTrpArgGlnMetPheTrpValGlnValLeu 206
    |||||
Db 850 ATTGAGATGTTAAGGAGCTAGGAGCTCAGGACAGCAACAGCGCTGTTGCCCTGTCAT 909
QY 207 LeuAlaGlyLeuValAlaProLeuLeuGluAlaThrLeuThrTrpTrpArgHis 226
    |||||
Db 910 TTTCTTGTCTTTCCTTATATCCCTCTCTCATTTGTTAATGATCTACCAACGG 969
QY 227 CysTrpProHisLys-----ProLeuValThrAlaAspGluAla 239
    |||||
Db 970 ---TGAAAGTCCAAAGCTCTACATTTGTTTGGGAAATGCACACCTGAAAAAGAGGG 1026
QY 240 GlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSer----- 257
    |||||
Db 1027 GAGCTTGAGGAAGAACTACTATAAGCC-----CTGGCCCAAAACCAACACTTCAGT 1077
QY 258 -----AlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCys 272
    |||||
Db 1078 CCACATCCAGGCTTACACCCCGGCTGAGTCCGCTGACAGTTCACACTTCAC 1137
QY 273 ThrValGlnLeuValGlyAsnSerTrpThrProGlyTrpProGlnThrGlnGluAlaLeu 292
    |||||
Db 1138 TCC-----AGCTTCACCTATATACCCCGGTGC----- 1164

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OY 293 CysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro----- 310
    |||||
Db 1165 TGTCCAACTTTTCG-----GCTCCCGCAGAGAGGTGGCACCACCTAT 1209
OY 311 -----AlaAlaAlaProThrLeuSerPro--- 318
    |||||
Db 1210 CAGGGGGCTGACCCCATCTTGGACAGCCCTCGCCACCCCATCCACCCCTT 1269
OY 319 -----GluSerProAlaGlySerProAlaMetLeuGlnProGlyPro---Gln 334
    |||||
Db 1270 CAGAACTGGAGAGACAGCCGCCCAAGCCACAGACCTACACTGATGACCCCGCAGC 1329
OY 335 LeuTrpAspValMetAspAlaValProAlaArgArgTrpLysGlnPheValArgThrLeu 354
    |||||
Db 1330 CTGTACGGCGTGTGGAGAAACGTGCCCGCTGCTGGAAGAAATTCGTGGCGGCTTA 1389
OY 355 GlyLeuArgGlnAlaGlnLeuGlnAlaValGlnValGlnLeuArg---PheArgAsp 373
    |||||
Db 1390 GGGCTGACGACACACAGATCGATCGCTGACCTGCAGAACGGCGCTGCTGCGCGAG 1449
OY 374 GlnGlnTrpGlnMetLeuLysArgTrpArgGlnGlnPro-----AlaGlyLeu 390
    |||||
Db 1450 GCGCAATFACAGCATGCTGGCGACCTGGAGCGCGCAGCGCGCGCGCAGCGCAGCTG 1509
OY 391 GlyAlaValAlaValAlaLeuGlnArgMetGlyLeuAspGlyCysValGlnAspLeuArg 410
    |||||
Db 1510 GAGCTCTGGGAGCGGTGCTCCGCGACATGACCTGTGCGCTGGAAGATCGAG 1569
OY 411 SerArgLeu 413
    |||
Db 1570 GAGCGCGCT 1578

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RESULT 14

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US-09-505-250-3
; Sequence 3, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
; APPLICANT: Rosen, Glenn
; APPLICANT: Kao, Peter
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; FILE REFERENCE: SDN-109PRV2
; CURRENT APPLICATION NUMBER: US/09/505,250A
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2161
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (256)...(1623)
US-09-505-250-3

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Alignment Scores:

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Pred. No.: 2,12e-21 Length: 2161
Score: 374.00 Matches: 131
Percent Similarity: 38.888 Conservative: 49
Best Local Similarity: 28.298 Mismatches: 183
Query Match: 16.10% Indels: 100
Gaps: 22

```

US-09-993-234-6 (1-417) x US-09-505-250-3 (1-2161)

```

OY 15 LeuLeuLeuValLeuLeuGlnAlaArgAlaGlnGly----- 26
    |||||
Db 298 CTCCTGAGATGTTGGTGGAAATATACCCCTCAGGGGTATGACTGTCCTCACAATA 357
OY 27 GlyThrAspSerProArg-----CysAspCysAlaGlnAspPheHisLysIle 43
    |||||
Db 358 GGGGACAGGAGAGAGAGACTAGTGTGTGTCCTCCCAAGAAATATATTCACCTCAAAAT 417

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OY 44 GlyLeuPheCysArgGlyCysProAlaGlyHisIleLeuLysAlaProCysThrGlu 63
    |||||
Db 418 AATTGCATTTGCTGTACCAAGTGCACAAAGAACCTACTTGTACATGACTGTCCAGGC 477
OY 64 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGlnAsn 83
    |||||
Db 478 CCGGGGCGAGTATCGGACTCGAGAGTGTGACAGCGGCTCTTCCACCGCTTCAGAAAC 537
OY 84 HisHisAsnSerGlyCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAla 103
    |||||
Db 538 CACCTTCAGA---CACTCCCTCAGCTGCTCCAAATAGCCGAAAGAAAGAGGTGACGTGAG 594
OY 104 LeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal 123
    |||||
Db 595 ATCTCTTCTTGACACAGTGGAGACCGGGACACCGTGTGTGGTGCAGAGAAACACGTACCG 654
OY 124 GluLys-----GlnValSerGlnCysValSerSerProPheTrpCysGlnPro 140
    |||||
Db 655 CATTATTGAGTGAACAACTTTTCCAGTGC-----TTCAAATTCAGACCTTC 699
OY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLysSerArgArgAspThr 160
    |||||
Db 700 TGCCTCAT---GGGACCGTGCAC-----CTCTCTCCGACGAGAAACAGAAC 744
OY 161 AspCysGlyThrCysLeuProGlyPheTrpGlnHisGlyAspGlyCysValSerCysPro 180
    |||||
Db 745 ACCGTGTGACACTGCTGCATGACGTTCTTCTTAAGAAACAGAGTGTCTCTCTG--- 801
OY 181 ThrSerThrLeuGlySerCysProGln-----ArgCysAlaAlaValCys----- 195
    |||||
Db 802 -----ACTACTGTAAAGAAACCGCTGAGTGCACAGATGTCGCTACCCAG 849
OY 196 -----GlyTrpArgGlnMetPheTrpValGlnValLeu 206
    |||||
Db 850 ATTGAGAAATGTAAGGCGACTGAGACTGAGCAGCAGCAGCTGCTGCTGCCCTGCTATT 909
OY 207 LeuAlaGlyLeuValAlaProLeuLeuGlnGlyAlaThrLeuThrTrpThrArgHis 226
    |||||
Db 910 TTCTTGTGTTGCTTGGCTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 969
OY 227 CysTrpProHisLys-----ProLeuValThrAlaAspGlnAla 239
    |||||
Db 970 ---TGAAAGTCAAGCTCTCATCTCATTTGTTGGAAATCGACACCTGAAAGAGGGG 2026
OY 240 GlyMetGlnAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSer----- 257
    |||||
Db 1027 GAGCTTGAAGCACTACTACTTAAGCCC-----CTGGCCCCCAACCAAGCTTCAGT 1077
OY 258 -----AlaHisThrLeuLeuAlaProProAspSerSerGlyLysIleCys 272
    |||||
Db 1078 CCCACTCCAGGCTTCACACCCACCCCTGGCTGACGTCCGCGCACTTCACCTTACAC 1137
OY 273 ThrValGlnLeuValGlyAsnSerTrpThrProGlyTrpProGlnThrGlnAlaLeu 292
    |||||
Db 1138 TCC-----ACCTCCACCTATACCCCGGTGAC----- 1164
OY 293 CysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro----- 310
    |||||
Db 1165 TGTCCAACTTTTCG-----GCTCCCGCAGAGAGGTGGCACCACCTAT 1209
OY 311 -----AlaAlaAlaProThrLeuSerPro--- 318
    |||||
Db 1210 CAGGGGGCTGACCCCATCTTGGACAGCCCTCGCCACCCCATCCACCCCTT 1269
OY 319 -----GluSerProAlaGlySerProAlaMetLeuGlnProGlyPro---Gln 334
    |||||
Db 1270 CAGAACTGGAGAGACAGCCGCCCAAGCCACAGACCTACACTGATGACCCCGCAGC 1329
OY 335 LeuTrpAspValMetAspAlaValProAlaArgArgTrpLysGlnPheValArgThrLeu 354
    |||||
Db 1330 CTGTACCGCGTGTGGAGAAACGTGCCCGCTGCTGGAAGAAATTCGTGGCGGCTTA 1389

```

QY 355 G1YLeuArgL1uAlaGluLeuIleGluAlaValAlaGluIleGlyArg---PheArgasp 373
 DB 1390 GGGCTGAGCGACACGACATCCATCGCGTGGAGCTGCACAGCGCGCTGCTCCGAG 1449
 QY 374 G1ngIntYrGluMetLeuIleuysArgTrpArgG1ngInglInPro-----AlaGlyLeu 390
 DB 1450 GGGCAATACAGATGTGTGGCGACTGAGCGCGCGCGCGCGCGAGGCCACGCTG 1509
 QY 391 G1YAlaValTyrAlaAlaLeuGluArgMetG1YLeuAspG1YcysValG1uAspLeuArg 410
 DB 1510 GAGCTGCTGGAGCGCGTGTCTCGCGACATGACCTGCTGCTCGTGGAGCATCGAG 1569
 QY 411 SerArgLeu 413
 DB 1570 GAGCGCGCTT 1578
 RESULT 15
 US-08-321-668-1
 ; Sequence 1, Application US/08321668
 ; Patent No. 5665859
 ; GENERAL INFORMATION:
 ; APPLICANT: WALLACH, David
 ; APPLICANT: BRAKEBUSCH, Cord
 ; APPLICANT: VARFOLOMEY, Eugene
 ; APPLICANT: BARKIN, Michael
 ; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/321,668
 ; FILING DATE: 12-OCT-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: IL 107268
 ; FILING DATE: 12-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: WALLACH-13
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2175 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 256..1620
 ; US-08-321-668-1
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 Score: 374.00 Matches: 131
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 Query Match: 16.10% Indels: 100

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 QY 104 LeuGluAsnCysSerAlaValAlaAspThrArgCysG1YcysLysProG1YTrpPheVal 123
 DB 595 ATCTCTTGTGACAGTGGACCGGACACCGTGTGTGCTGTGCTGACAGAACACAGTACCG 654
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 QY 181 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 195
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 QY 196 -----GlyTrpArgIleMetPheTrpValGlnValLeu 206
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 QY 207 LeuAlaGlyLeuValValProLeuLeuLeuGluAlaThrLeuThrTyrTrpArgHis 226
 DB 910 TTCCTTGTGCTTTCCTTTATCCCTCTCTTCATTTGGTTAATGTAATCCGTACCAACGG 969
 QY 227 CysTrpProHisLys-----ProLeuValIleAlaAspGluAla 239
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 QY 240 GlyMetGluAlaLeuThrProProAlaThrHisLeuSerProLeuAspSer----- 257
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 QY 273 ThrValGlnLeuValGlyAsnSerTrpThrProG1YTrpGluThrGlnGlnAlaLeu 292
 DB 1138 TCC-----ACTGCACCTATACCCCGGTGAC----- 1164
 QY 293 CysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro----- 310
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 QY 311 -----AlaAlaAlaProThrLeuSerPro--- 318


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QY 355 GlyLeuArgGluAlaGluLeuGluAlaValGluValGluLeuArg---PheArgAsp 373
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QY 374 GlnGlnTyrGluMetLeuLysArgTyrPargGlnGlnPro-----AlaGlyLeu 390
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QY 391 GlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg 410
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GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:35:34 ; Search time 2022.14 seconds
(without alignments)
2504.221 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=GenEmbl -OFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -MODE=LOCAL
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1038	100.0	1143	9 HSU94510	U94510 Human Lymph
2	1038	100.0	1254	6 AR119657	AR119657 Sequence
3	1038	100.0	1254	9 HSU72763	U72763 Human death
4	1038	100.0	1254	9 HSU78029	U78029 Human death
5	1038	100.0	1254	9 HSU94501	U94501 Human Lymph
6	1038	100.0	1257	9 HSU94502	U94502 Human Lymph
7	1038	100.0	1355	9 HSU94503	U94503 Human Lymph
8	1038	100.0	1634	9 HSU74611	U74611 Human Apo-3
9	1038	100.0	1662	6 AX055442	AX055442 Sequence
10	1038	100.0	1662	6 AX201344	AX201344 Sequence
11	1038	100.0	1743	6 AX331947	AX331947 Sequence
12	1038	100.0	1743	9 HSW51	Y09392 H. sapiens m
13	1038	100.0	1783	6 AR119656	AR119656 Sequence
14	1028	99.0	1528	9 HSU83597	U83597 Human death
15	1028	99.0	1557	9 HSU75380	U75380 Human apopt
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17	1002	96.5	1763	9 AF026071	AF026071 Homo sapi
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19	950	91.5	808	9 HSU75381	U75381 Human apopt
20	950	91.5	809	9 HSU94512	U94512 Human Lymph
21	950	91.5	816	6 AX335086	AX335086 Sequence
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23	938.5	90.4	1198	9 HSU94504	U94504 Human Lymph
24	937	90.3	1087	9 HSU94505	U94505 Human Lymph
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RESULT 1

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 DEFINITION spliced, complete cds.
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 VERSION U94510.1 GI:20719666
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 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1143)
 AUTHORS McMichael, A.J., Xu, X.N., Olsen, A.L., Cowper, A.E., Tan, R.,
 LARD: a new lymphoid-specific death domain containing receptor
 regulated by alternative pre-mRNA splicing
 Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
 JOURNAL 9114039
 PUBLISHED
 MEDLINE
 REFERENCES 2 (bases 1 to 1143)
 AUTHORS Screation, G.R.
 TITLE Direct Submission
 JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
 Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
 9DU, UK
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 LOCUS AR119657
 DEFINITION Sequence 3 from patent US 6153402.
 ACCESSION AR119657
 VERSION AR119657.1 GI:14102356
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 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1254)
 AUTHORS Yu, G.-L., Ni, J., Gentz, R.L. and Dillon, P.J.
 TITLE Death domain containing receptors
 JOURNAL Patent: US 6153402-A 3 28-NOV-2000;
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 Query Match: 100.00% Indels: 0
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DEFINITION Human death receptor 3 (DR3) mRNA, complete cds.
ACCESSION U72763
VERSION U72763.1 GI:1669511
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Chinnaiyan,A.M., O'Rourke,K., Yu,G.L., Lyons,R.H., Garg,M.,
1 (bases 1 to 1254)
Chinnaiyan,A.M., O'Rourke,K., Yu,G.L., Lyons,R.H., Garg,M.,
Duan,D.R., Xing,L., Gentz,R., Ni,J. and Dixit,V.M.
Signal transduction by DR3, a death domain-containing receptor
related to TNFR-1 and CD95 (1996) Nov
JOURNAL Science 274 (5289), 990-992 (1996)
MEDLINE 97081063
PUBMED 8875942
REFERENCE
2 (bases 1 to 1254)
Chinnaiyan,A.M., O'Rourke,K., Yu,G.L., Lyons,R.H., Garg,M.,
Duan,R., Xing,L., Gentz,R., Ni,J. and Dixit,V.M.
Direct Submission
Submitted (29-SEP-1996) Pathology, University of Michigan Medical
School, 1301 Catherine St., Box 0602, Ann Arbor, MI 48109, USA
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RESULT 4
LOCUS HSU78029 1254 bp mRNA linear PRI 15-JAN-1997
DEFINITION Human apoptosis inducing receptor AIR mRNA, complete cds.
ACCESSION U78029
VERSION U78029.1 GI:1778763
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Degli-Esposti,M.A., Din,W.S., Cosman,D., Smith,C.A. and
Goodwin,R.G.
1 (bases 1 to 1254)
AIR, A Novel Member of the TNF Receptor Family, Is a Strong Inducer
of Apoptosis
Unpublished
JOURNAL J Biol Chem 271 (12):7911-7916 (1996)
AUTHORS Degli-Esposti,M.A. and Goodwin,R.G.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1996) Biochemistry, Immunex Corporation, 51
University St., Seattle, WA 98101, USA
FEATURES
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1..1254
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/feature="DR3"
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Alignment Scores:

Pred. No.: 5.53e-66

Score: 1038.00

Percent Similarity: 100.008

Best Local Similarity: 100.008

Query Match: 100.008

Length: 1254

Matches: 174

Conservative: 0

Mismatches: 0

Indels: 0

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DCGTCLPGFYEHDGCVSCPTSLGSCPERCAAVGMRWVAVLLAGLVPLLLGA
TLTYTRHCHWPKPLVTADMEALTPPAPTHLSPLDSATLLAPDSSKRTTVO
VGNSTPGYPERTOALCPQVMSDOLPRSLGPAAPTLSPESPASPMAMLOPQPO
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BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN

Alignment Scores:

Pred. No.:	5.53e-66	Length:	1254
Score:	1038.00	Matches:	174
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-993-234-6_COPY_25_198 (1-174) x HS078029 (1-1254)

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QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 133 CTGTTTGTGGCAGAGCTGCGCCAGCGGACATCTGAAGGCCCTTGCACGAGACCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 193 TGGCGCAACCTCCACTGCTGTGTGTGCCAAGACACCTTTGGCTGGGAAACAC 252
QY 61 HisAsnSerGlyCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
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DB 313 GAGACAGCTTCACAGCGGCGGACACCGCTGTGGCTGTGAAGCAGGCTGTTGTGGAG 372
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DB 373 TGGCAGGTCTAGCAATGTGTGACAGATGTCCTTCTACGCCAACATGCTAGACTGC 432
QY 121 GluAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 433 GGGGCGGCTGACCGCCACACACGCTACTGTTCGCCGAGATACTGCTGGGAGCC 492
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 493 TGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 552
QY 161 GlySerCysProGlnArgCysAlaAlaValCysGlyTyrPheArg 174
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RESULT 5
HS094501 1254 bp mRNA linear PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 1a mRNA, complete
DEFINITION cds.
ACCESSION U94501
VERSION U94501.1 GI:2071948
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
Screation, G.R., Xu, X.N., Olsen, A.L., Cowper, A.E., Tan, R.,
McMichael, A.J. and Bell, J.I.

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
97272273
9114039
2 (bases 1 to 1254)
Screation, G.R.
Direct Submission
Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

FEATURES

source
location/Qualifiers
1. 1254
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1. 1254
/function="mediates apoptosis"
/note="LARD-1a: membrane protein: similar to Fas and
TNF-R1; contains a death domain"
/codon_start=1
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/db_xref="GI:2071949"

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DB 133 CTGTTTGTGGCAGAGCTGCGCCAGCGGACATCTGAAGGCCCTTGCACGAGACCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 193 TGGCGCAACCTCCACTGCTGTGTGTGCCAAGACACCTTTGGCTGGGAAACAC 252
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DB 253 CATATTTCTGAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
DB 313 GAGACAGCTTCACAGCGGCGGACACCGCTGTGGCTGTGAAGCAGGCTGTTGTGGAG 372
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 373 TGGCAGGTCTAGCAATGTGTGACAGATGTCCTTCTACGCCAACATGCTAGACTGC 432
QY 121 GluAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
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Alignment Scores:

Pred. No.:	5.53e-66	Length:	1254
Score:	1038.00	Matches:	174
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

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Db 493 TGCTGCTGCTCTATGAACATGCGATGCTGCTGCCACGACGACCCCTG 552
QY 161 GlySerCysProgluarGyCysAlaAlaValCysGlyTTParg 174
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Db 553 GGGAGCTGTCAGAGCGCTGCGCTGTGTGTGGTGAGG 594

RESULT 6
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LOCUS Human lymphocyte associated receptor of death 1b mRNA,
DEFINITION alternatively spliced, complete cds.
ACCESSION U94502
VERSION U94502.1 GI:2071950
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Sreeton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
1 (bases 1 to 1257)
Michael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1257)
Sreeton,G.R.
AUTHORS Direct Submission
TITLE Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
JOURNAL Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

FEATURES
source location/Qualifiers
1.1257
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/db_xref="taxon:9606"
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/note="LARD-1b; membrane protein; similar to Fas and
TNF-R1; contains a death domain"
/codon_start=1
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TLITYYRRCRHKRPVLTADAEAGMEALTPPRNHLSPDSARTLLAPDSSEICTVQ
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Accession Number U94501, probably represents alternative
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BASE COUNT 202 a 421 c 408 g 226 t
ORIGIN

Alignment Scores:
Pred. No.: 5.54e-66 Length: 1257
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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Db 133 CTGTTTGTTCACAGAGCTGCCAGCGGGCAGACACGGAAGGCCCTTGCACGAGGCC 192
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Db 193 TCGGCACTCCACCTGCTGTGTGTGTGTCACAGACACTTCTTGCGCTGGAGAACAC 252
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Db 433 GGGGCGCTGCAGCCGACACACAGGCTACTGTGTCGCCAGAGATAGATGATGGAGCC 492
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Db 493 TGCTGCTGCTCTATGAACATGCGATGCTGCTGCCACGACGACCCCTG 552
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Db 553 GGGAGCTGTCAGAGCGCTGCGCTGTGTGTGGTGAGG 594

RESULT 7
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LOCUS Human lymphocyte associated receptor of death 2 mRNA, alternatively
DEFINITION spliced, complete cds.
ACCESSION U94503
VERSION U94503.1 GI:2071952
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Sreeton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
1 (bases 1 to 1355)
Michael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1355)
Sreeton,G.R.
AUTHORS Direct Submission
TITLE Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
JOURNAL Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

FEATURES
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1.1355
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1.1355
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AX055442
LOCUS AX055442 1662 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 72 from Patent W0073452.
ACCESSION AX055442
VERSION AX055442.1 GI:12228713
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1662)
AUTHORS Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,
Gurney,A.L., Heberle,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,
Tunas,D., Watanabe,C.K. and Wood,W.I.
TITLE Compositions and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 0073452-A 72 07-DEC-2000;
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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Alignment Scores:
Pred. No.: 7.31e-66 Length: 1662
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Db 295 TCCGGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTCTGTGGCTGGAGAAACCAC 354
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Oy 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrrpPheValGlu 100
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Oy 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
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Db 535 GGGGCCCCGACCGCCACACAGCGCTACTCTGTCCCGAGAGATACGTGTGGACC 594
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Db 595 TGCCTGCCGCGGCTTCTATTAACATGGCGATGGCTGCGTCTCTGCCCCACGACACCTCG 654
Oy 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 174
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RESULT 10
AX201344
LOCUS AX201344 1662 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 23 from Patent W00153486.
ACCESSION AX201344
VERSION AX201344.1 GI:15391165
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1662)
AUTHORS Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
Hillan,K.J., Masters,S.A., Pan,D., Pitti,R.M., Roy,M.A., Smith,V.,
Stone,D.M., Watanabe,C.K. and Wood,W.I.
TITLE Compositions and methods for the treatment of tumour
JOURNAL Patent: WO 0153486-A 23 26-JUL-2001;
FEATURES
source Location/Qualifiers
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BASE COUNT 302 a 540 c 531 g 289 t
ORIGIN
Alignment Scores:
Pred. No.: 7.31e-66 Length: 1662
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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US-09-993-234-6_COPY_25_198 (1-174) x AX201344 (1-1662)
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Db 175 CAGGGCGGACCTGTAAGCCCCAGGTGTGACTGTGCCGCTGACTCCACAAAGAAATTTGGT 234
Oy 21 LeupheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 235 CTTGTTTGTGTGAGAGGCTGCCACAGGGGCACTACCTGAAGGCCCTTTGACAGGAGCCC 294
Oy 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrrpLubnHis 60
Db 295 TCCGGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTCTGTGGCTGGAGAAACCAC 354
Oy 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 355 CATTAATTCGAAATGTGCCGCTGCCAGGCTGTGTATGAGCAGGCTCCCAAGGTGGCGCTG 414
Oy 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrrpPheValGlu 100
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Oy 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 475 TCCCAAGCTCAGCCAAATGTGTGACAGCTTACCCCTTCTACTGCCAACAATGCTTACAGTC 534
Oy 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 535 GGGGCCCCGACCGCCACACAGCGCTACTCTGTCCCGAGAGATACGTGTGGACC 594
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QY 141 CysleuProglIyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrleu 160
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RESULT 11
AX331947 1743 bp DNA linear PAT 09-JAN-2002
LOCUS
DEFINITION Sequence 2456 from Patent WO0194629.
ACCESSION AX331947
VERSION AX331947.1 GI:18122581
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horligan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 2456 13-DEC-2001;
FEATURES
source
1. .1743
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/db_xref="taxon:9606"
Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 7.66e-66 Length: 1743
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x AX331947 (1-1743)
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Db 201 CTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGTAAGGCCCTTGCAGGAGGCC 260
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
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Db 321 CATAAATTCGAATGTGCTCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTGGCGCTG 380
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrrPheValGlu 100
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Db 381 GAGAACTGTTCACAGCTAGGCGCGACACCGCTGTGCTGTGAGCGAGGCTGTGTGAG 440
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QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
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Db 501 GGGGCGCTCAGCCAGCAGCAGCGCTACTGTTCGCCGAGAAATAGTACTGTGGAGCC 560
QY 141 CysLeuProglIyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrleu 160
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Db 561 TGCTGCTGCTCTCTATGAACAGGCGCGTGGCTGCTCCCGCCAGAGCACCCTG 620
QY 161 GlySerCysProgluArgCysAlaAlaValCysGlyTrrParg 174
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Db 621 GGAAGCTGTCCAGAGCGCTGTGCTGTCTGTGTGCTGAGG 662
RESULT 12
HSM5L1
LOCUS
DEFINITION H.sapiens mRNA for WSL-1R, WSL-S1 and WSL-S2 proteins.
ACCESSION Y09392.1
VERSION Y09392.1 GI:1669690
KEYWORDS WSL-1 gene; WSL-1R protein; WSL-S1 protein; WSL-S2 protein.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Kitson, J., Raven, T., Jiang, Y.P., Goeddel, D.V., Giles, K.M.,
Pun, K.T., Grinham, C.J., Brown, R. and Farrow, S.N.
TITLE A death-domain-containing receptor that mediates apoptosis
JOURNAL Nature 384 (6607), 372-375 (1996)
MEDLINE 97088617
PUBMED 8934525
REFERENCE
AUTHORS Kitson, J.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1996) J. Kitson, GLAXO-Wellcome, Medicines
Research Centre, Gunnels Wood Road, Stevenage, SG1 2NT, UK
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ORGANISM    Unknown.
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Unclassified.
REFERENCE    1 (bases 1 to 1783)
AUTHORS      Yu,G.-L., Gentz,R.L. and Dillon,P.J.
TITLE        Death domain containing receptors
JOURNAL      Patent: US 6153402-A 1 28-NOV-2000;
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DEFINITION Human death domain receptor 3 (DDR3) mRNA, partial cds.
ACCESSION  U83597
VERSION     U83597.1  GI:1800292
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REFERENCE    1 (bases 1 to 1528)
AUTHORS      Chaudhary,P.M. and Hood,L.E.
TITLE        Direct Submission
JOURNAL      Submitted (03-JAN-1997) Molecular Biotechnology, University of
Washington, 1705 NE Pacific Street, HSB-K360, Seattle, WA 98195,
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Bodmer, J.L., Burns, K., Schneider, P., Hofmann, K., Steiner, V.,
Thome, M., Borman, T., Hahne, M., Schroter, M., Wilson, A.,
French, L.E., Browning, J.L., Hahne, M., MacDonald, R. and Tschopp, J.
TRAMP, a novel apoptosis-mediating receptor with sequence homology
to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95)
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JOURNAL MEDLINE
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Direct Submission
Submitted (18-OCT-1996) Institute of Biochemistry, University of
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Db 124 CTGTTTGTGCAGAGCGTCCGACGGGGGCGACTACTGTAAGGCCCTTGACAGGAGCCC 183
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40	203	19.6	2161	21	AAZ48475	Human tumor necro
41	203	19.6	2161	24	ABK13194	Human tumor necro
42	203	19.6	2175	16	AAQ90513	p55 TNF-R gene. H
43	203	19.6	6889	17	AAT15931	DHFR/Intcon (WTras
44	203	19.6	6926	18	AAV04431	Vector pCDNA3-19G1
45	202	19.5	2170	14	AAQ50870	p55 Tumor necrosi

ALIGNMENTS

RESULT 1	
AAT89427	
AAT89427	standard; CDNA: 1254 BP.
AAT89427:	
02-MAR-1998	(first entry)
DT	
XX	Death domain containing receptor DR3 CDNA.
XX	
DE	Death domain containing receptor DR3 CDNA.
XX	
KW	Death domain containing receptor; DR3; human; apoptosis;
XX	
OS	Inflammation; NF-kappaB; ds.
XX	
XX	Homo sapiens.
XX	
FT	key
FT	sig_peptide
FT	Location/Qualifiers
FT	1..72
FT	/*tag- a

FT mat_peptide 73..1251
 FT //tag- b
 XX MO9733904-A1.
 XX 18-SEP-1997.
 XX
 XX
 XX
 XX 17-OCT-1996; 96WO-US16849.
 XX
 XX 12-MAR-1996; 96US-0013285.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (UNMI) UNIV MICHIGAN.
 XX
 XX Dillion PJ, Dixit VM, Gentz RL, Ni J, Yu G;
 XX WPI; 1997-470812/43.
 XX P-PSDB; AAW31517.
 XX
 XX Death domain containing receptor polypeptide(s) DR3 and DR3-V1
 XX for activation of apoptosis and NF-kappaB, antagonists can be used
 XX to treat inflammatory diseases
 XX
 XX Claim 6; Page 75-77; 108bp; English.
 XX
 XX This cDNA clone codes for human death domain containing receptor
 XX DR3 (see AAW31517), a novel member of the tumour necrosis factor
 XX receptor family. It was isolated from a HUVRC cDNA library.
 XX Related death domain containing receptor DR3-V1 cDNA (see AAT89426)
 XX was isolated from a human testis tumour cDNA library. The genes
 XX have also been identified in cDNA libraries of foetal liver,
 XX foetal brain, tonsil and leukocyte. Nucleic acids encoding full-
 XX length or mature DR3, or the extracellular, transmembrane,
 XX intracellular or especially the death domain of DR3, can be used to
 XX produce recombinant polypeptides in transformed host cells. These
 XX polypeptides can be used to treat diseases and disorders associated
 XX with the inhibition of apoptosis. Antagonists can be used to treat
 XX diseases and disorders associated with increased apoptosis and for
 XX treating inflammatory diseases and disorders.
 XX
 XX Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;
 XX
 XX Alignment Scores:
 XX Pred. No.: 7.96e-72 Length: 1254
 XX Score: 1038.00 Matches: 174
 XX Percent Similarity: 100.00% Conservative: 0
 XX Best Local Similarity: 100.00% Mismatches: 0
 XX Query Match: 100.00% Indels: 0
 XX DB: 18 Gaps: 0
 XX
 XX US-09-993-234-6_COPY_25_198 (1-174) x AAT89427 (1-1254)
 XX
 XX 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisIstysIleGly 20
 XX |||||||
 XX 73 CAGGGGGGCACTGCTGAGCCCAAGGTGTGACTGTGCGGAGACTTCCACAAGAAGATTGGT 132
 XX |||||||
 XX 21 LeuPheCysCysArgGlyCysProAlaGlyHisIstysIleGlyAlaProCysThrGluPro 40
 XX |||||||
 XX 133 CTTGTTGTGTCAGAGAGCTGCCAGCGGGGCACTTAAAGCCCTTGCAGGAGGCC 192
 XX |||||||
 XX 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
 XX |||||||
 XX 193 TCGGGCACTCCACCGCTTGTGTGTGCCCAAGACACTTTTGGCTGGGAGAACAC 252
 XX |||||||
 XX 61 HisAsnSerGlyCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
 XX |||||||
 XX 233 CATTAATTCGAATGTGCCCGCTGCCAGGCTGTGATGACAGAGCCCTCCAGGTGGGCTG 312
 XX |||||||
 XX 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysIysProGlyTrpPheValGlu 100
 XX |||||||
 XX 313 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGAACCCAGGCGCTTGTGGAG 372
 XX |||||||
 XX 101 CysGlnValSerGlnCysValSerSerSerProPheIstysGlnProCysLeuAspCys 120

DB 373 TGCCAGGTCCACCAATGTGTCAGCAGTTCACCTTACTTCCCAACACTGCTAGACTGC 432
 |||||||
 QY 121 GlyAlaLeuHisArgHisIsthrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
 |||||||
 DB 433 GGGGCGCTGCACCGCCACACACAGGCTACTCTGTGCCGACAGATACTGATGTGGGCC 492
 |||||||
 QY 141 CysLeuProGlyPheIsthrGlyHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
 |||||||
 DB 493 TGCCGTGCTGCTTCTTATGAACATGGCAGATGGCTGCTGCTGCTGCTGCTGCTGCTG 552
 |||||||
 QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
 |||||||
 DB 553 GGAGAGCTGCCAGAGCGCTGTGCTGTGTGTGGTGGAG 594
 |||||||
 RESULT 2
 ID AAX00925 standard; cDNA; 1254 BP.
 XX AAX00925;
 AC AAX00925;
 XX
 XX 25-MAR-1999 (first entry)
 DE Death domain containing receptor polypeptide (DR3) encoding cDNA.
 XX
 XX Death domain; receptor; DR3-V1; DR3; recombinant; ds.
 KW
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH CDS 1..1254
 FT //tag- a
 FT sig_peptide 1..72
 FT //product- "Death domain containing receptor DR3"
 FT mat_peptide 73..1251
 FT //tag- b
 FT //tag- c
 XX JP11000170-A.
 XX
 XX 06-JAN-1999.
 PD
 XX
 XX 12-MAR-1997; 97JP-0057503.
 PF
 XX 06-FEB-1997; 97US-0037341.
 PR 12-MAR-1996; 96US-0013285.
 PR 17-OCT-1996; 96US-0028711.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (UNMI) UNIV MICHIGAN.
 XX
 XX WPI; 1999-124390/11.
 DR P-PSDB; AAW95538.
 DR
 XX
 XX New death domain containing receptor and recombinant vector -
 PT optionally comprising leader sequence
 XX
 XX Claim 6; Fig 3; 50pp; Japanese.
 XX
 XX The invention provides nucleotide sequences encoding death domain
 XX containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
 XX is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
 XX contained in ATCC deposition No. 97757. Recombinant vectors comprising
 XX the nucleic acid sequences and optionally the leader sequences are
 XX used for the recombinant production of the proteins. The present
 XX sequence represents a cDNA encoding the death domain containing
 XX receptor polypeptide (DR3).
 XX
 XX Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;
 XX
 XX Alignment Scores:
 XX Pred. No.: 7.96e-72 Length: 1254
 XX Score: 1038.00 Matches: 174

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x AAX00925 (1-1254)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 73 CAGGCGGCACTCCAGTCCAGGAGTGTACTGTGCGGTGACTTCCACAGAGAGATTGGT 132
QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 133 CTGTTTGTTCAGAGGCTGCCACAGCGGCGCACTGAGAGGCCCTTGGACAGGAGCC 192
QY 41 CysGlnAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 193 TGGCGCACTCCAGTCCAGTGTGTCGCCACAGACACTTCTTGCGCTGGAGAGACAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 253 CATATTCTGAAATGTGCGGCTGCCAGGCTGTGATGAGAGGCGCTCCAGAGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
DB 313 GAGAACTGTTCAGAGGCTGCCAGACCCGCTGTGCTTAAGCCAGCGCTGTGTGTGGAG 372
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 373 TGGCAGGTCACCAATGTGTAGCAGATTCACCTTCTTACCTCCACAGACCTGACACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 433 GGGGCGCTGCACCGCCACACAGCGCTACTCTGTCCGACAGATAGTACTGTGGAGCC 492
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspArgLysValSerCysProThrSerThrLeu 160
DB 493 TGCCTGCTGCTCTTAAGAACATGCGCATGCGCTGCTGCTGCCCGCCACAGACCTGC 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrArg 174
DB 553 GGGAGCTGTCCAGAGCGCTGTGCGGCTGTCTGTGGCTGGAGG 594

RESULT 3

AAC68777 standard; cDNA; 1254 BP.

AC AAC68777:

XX 20-FEB-2001 (first entry)

DE Human death domain containing receptor DR3 coding sequence.

KW Human: death domain containing receptor; DR3; cancer;

KW autoimmune disorder; inflammation; cardiovascular disorder; infection;

KW neurodegenerative disease; angiogenesis; ss.

XX Homo sapiens.

OS WO200064465-A1.

PN 02-NOV-2000.

XX 21-APR-2000; 2000MO-US10741.

XX 22-APR-1999; 99US-0130488.

XX 28-MAY-1999; 99US-0136741.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (UNMI) UNIV MICHIGAN.

PA (YUGG/) YU G.

PA (NIJ/) NI J.

PA (GENTZ) GENTZ R L.

PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;
XX WPI: 2000-687263/67.
XX P-PSDB; AAB36265.

Example 2B; Fig 2; 273pp; English.
The present invention provides the protein and coding sequences for two death domain containing receptors, designated DR3 and DR3-V1. These receptors are involved in apoptosis, and the sequences given can be used in the treatment of cancers, infections, cardiovascular disorders such as arhythmias, ischemia, aneurysms, arterial occlusive diseases, embolisms and congenital heart defects, neurodegenerative diseases including Alzheimer's and Parkinson's diseases, autoimmune diseases such as multiple sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis, and to promote angiogenesis and wound healing.

Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:

Pred. No.:	7,96e-72	Length:	1254
Score:	1038.00	Matches:	174
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-993-234-6_COPY_25_198 (1-174) x AAC68777 (1-1254)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 73 CAGGCGGCACTCCAGTCCAGGAGTGTACTGTGCGGTGACTTCCACAGAGAGATTGGT 132
QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 133 CTGTTTGTTCAGAGGCTGCCAGCGGCGCACTGAGAGGCCCTTGGACAGGAGCC 192
QY 41 CysGlnAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 193 TGGCAGGTCACCAATGTGTAGCAGATTCACCTTCTTACCTCCACAGACCTGACACTGC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 253 CATATTCTGAAATGTGCGGCTGCCAGGCTGTGATGAGAGGCGCTCCAGAGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
DB 313 GAGAACTGTTCAGAGGCTGCCAGACCCGCTGTGCTTAAGCCAGCGCTGTGTGTGGAG 372
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 373 TGGCAGGTCACCAATGTGTAGCAGATTCACCTTCTTACCTCCACAGACCTGACACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 433 GGGGCGCTGCACCGCCACACAGCGCTACTGTGTCCGACAGATAGTACTGTGGAGCC 492
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspArgLysValSerCysProThrSerThrLeu 160
DB 493 TGCCTGCTGCTCTTAAGAACATGCGCATGCGCTGCTGCTGCCCGCCACAGACCTGC 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrArg 174
DB 553 GGGAGCTGTCCAGAGCGCTGTGCGGCTGTCTGTGGCTGGAGG 594

RESULT 4

AA91180
ID AA91180 standard; cDNA: 1634 BP.
AC AA91180;
DT 14-APR-1998 (first entry)
XX Human apoptosis protein Apo-3 cDNA clone FH20.57.
DE Apo-3; apoptosis; human; therapy; drug screening; ss.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 89..1342
FT sig_peptide /tag= a
FT 89..160 /tag= b
FT /note= "determined by hydropathy analysis"
FT mat_peptide 161..1339
FT /tag= c
PN WO9737020-A1.
XX 09-OCT-1997.
XX 31-MAR-1997; 97WO-US05230.
XX 23-SEP-1996; 96US-0710802.
XX 01-APR-1996; 96US-0625328.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ;
XX WPI: 1997-503105/46.
DR Polyptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis
PT in mammalian cells
XX Example 1; Page 45-46; 70pp; English.
XX CDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see
CC W26709), designated Apo-3, that stimulates or induces apoptotic
CC activity in mammalian cells. It was isolated from a human foetal
CC heat cDNA library by screening with probes (see T91183-84) based
CC on an EST sequence (Genbank locus W71984) that showed homology to
CC the intracellular domain of human TNFRI and CD95. Amino acid
CC residues 1-181 of Apo-3 are identical to another novel apoptosis
CC polypeptide, Apo-2LI (see W26708). Nucleic acids encoding Apo-3
CC can be used diagnostically for tissue-specific typing and to
CC produce recombinant Apo-3 polypeptides, especially the
CC extracellular domain (amino acids 1-198) or death domain (amino
CC acids 338-417). Apo-3 can be used to induce apoptosis or
CC NF-kappa-B or JNK-mediated gene expression for therapeutic
CC purposes. Non-human transgenic animals containing cells that
CC express Apo-3 nucleic acid, and knockout animals containing
CC cells that have an altered Apo-3 gene, can be used in drug
CC screening and development.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;
Alignment Scores:
Pred. No.: 1,08e-71 Length: 1634
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x AA91180 (1-1634)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20

|||||
Db 161 CAGGCGCGACCTGCTACCCCGAGGTGTGACTGTCCGGTACTCCACAGAAAGATTGCT 220
QY 21 LeuPheCysArsgLYcysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 221 CTGTTTGTTCAGAGAGCTGCGCAGCGGGCAGTACTGAAAGGCCCTTCACGAGACCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTyrGluAsnHis 60
Db 281 TGGCGCAACTCCACCTGCTGTGTGTGCCAAGACACCTTCTGGCTGGAGAACACC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 341 CATAAATCTGAATGTGCCCTGCGCAGGCTGTGATGACAGAGCCCTCCAGGTGGCCTG 400
QY 81 GluAsnSerSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
Db 401 GAGAACTGTTCAGCAGTGGCGCAGACCCGCTGTGGCTGTAAAGCCAGGCTGTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 461 TGCAGGTCAGCCAAATGTGTACAGAGTTCACCTTCTACTGCCAACCATCTAGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyTyr 140
Db 521 GGGGCCCTGCACGCCACACACAGGCTACTGTCTCCGAGAGATACTGACTGTGGAGCC 580
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 581 TGCCTGCTGCTGCTTCTATGAAACATGGCAGATGGCTGTGCTGTGCCCCAGACGACCCCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrArg 174
Db 641 GGGAGCTGTCCAGAGCGCTGTGCCGTGTCTGTGGCTGGAGG 682
RESULT 5
AAH27782
ID AAH27782 standard; DNA: 1634 BP.
XX
AC AAH27782;
XX
DT 15-NOV-2001 (first entry)
XX
DE Human genomic DNA encoding a rheumatoid arthritis associated protein.
XX
KW Rheumatoid arthritis; transmembrane protein; human; ds.
XX
OS Homo sapiens.
FH
FT Key Location/Qualifiers
FT CDS 89..1342 /tag= a
FT /product= "Rheumatoid arthritis associated protein"
PN WO200132921-A2.
XX
PD 10-MAY-2001.
XX
PF 01-NOV-2000; 2000WO-JP07690.
XX
PR 01-NOV-1999; 99JP-0310805.
XX
PA (SHIO/) SHIOZAWA S.
XX
PI Shiozawa S, Konishi Y;
XX
XX WPI: 2001-308750/32.
XX P-PSDB: AAB97370.
XX
XX Diagnosing rheumatoid arthritis by probing digested human genomic DNA
PT or comparing expression of mRNA or polypeptide of a region of
PT transmembrane protein
XX

PS Claim 1; Page 14-18; 21pp; Japanese.

CC This invention relates to a method of diagnosing chronic rheumatoid
CC arthritis by digesting human genomic DNA with EcoRI and hybridizing it
CC with a probe containing a fragment of the present sequence which
CC represents DNA encoding a transmembrane protein. The method is used for
CC the diagnosis of chronic rheumatoid arthritis, and for developing new
CC treatments.

XX Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:

Pred. No.:	1.08e-71	Length:	1634
Score:	1038.00	Matches:	174
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-993-234-6_COPY_25_198 (1-174) x AAH27782 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 161 CAGGGCGGCACTCTAGCCGCCAGGTGACTGTGCCGGTGACTTCCACAGACATTGGT 220
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 221 CTGTTTGTTCAGAGAGGCTGCCAGCGGGGACACTGAGAGGCCCTTGACAGCGAGCC 280
QY 41 CysGlnValSerGlnCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 281 TGCGCAACCTCCACCTGCTGTGTGCCCAAGACACCTTGGCTGGGAGAACCCAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 341 CATAAATCTGAATGTGCCCGCTGCCAGGCTGTGATGACAGCGCTCCAGAGTGGCCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 401 GAGAACTGTTCAAGAGTGGCCGACACCCGCTGTGGCTGAAGCAGAGGTGGTTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 461 TGCAGGTGACCAATGTGTGAGCATGTCACCTCTTACTGCCCAACCATGTGACTGAC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgAspThrAspCysGlyThr 140
DB 521 GGGGCGGCGACCGCCACACACCGGCTACTGTGTCCCGACAGATAGTACTGTGGAGCC 580
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 581 TGCGTGGCTGCTTGAATGAAATGAGGCGATGGCGGTGCTGCGCCACAGCACCCCTG 640
QY 161 GlySerCysProGlyArgCysAlaValCysGlyTrpArg 174
DB 641 GGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGCTGGAGG 682

RESULT 6

AAI47186 ID AAI47186 standard; cDNA; 1634 BP.

AAI47186;

22-AUG-2002 (first entry)

Human rheumatoid arthritis associated DR3 gene related cDNA #1.

Human: DR3; Rheumatoid arthritis; antirheumatic; antiarthritic;

gene therapy; gene; ss.

Homo sapiens.

Location/Qualifiers

FT CDS 89..1342
FT /*tag= a
FT /product= "AAI017879"

W0200234912-A1.

02-MAY-2002.

24-OCT-2001; 2001WO-JP09313.

24-OCT-2000; 2000JP-0324296.

27-MAR-2001; 2001JP-0090546.

30-MAR-2001; 2001JP-0099990.

(NEMI-) NEM IND RES ORG.

(SHIO/) SHIOZAWA S.

Shiozawa S, Konishi Y;

WPI; 2002-417132/44.

P-PSDB; AAI017879.

Genomes, particularly DR3 genomic DNA, participating in rheumatoid

arthritis via mutation, useful in evaluating disease onset and its

possibility and providing therapy and remedies -

Example 1; Page 66-69; 84pp; Japanese.

The present invention relates to the human DR3 gene, which is associated

with rheumatoid arthritis. Certain mutations in the gene can be linked to

the disease. The sequences can be used to evaluate disease onset and its

possibility and to provide therapy and remedies. The present sequence is

a coding sequence described in the exemplification of the invention.

SO Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:

Pred. No.:	1.08e-71	Length:	1634
Score:	1038.00	Matches:	174
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-993-234-6_COPY_25_198 (1-174) x AAI47186 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 161 CAGGGCGGCACTCTAGCCGCCAGGTGACTGTGCCGGTGACTTCCACAGACATTGGT 220
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 221 CTGTTTGTTCAGAGAGGCTGCCAGCGGGGACACTGAGAGGCCCTTGACAGCGAGCC 280
QY 41 CysGlnValSerGlnCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 281 TGCGCAACCTCCACCTGCTGTGTGCCCAAGACACCTTGGCTGGGAGAACCCAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 341 CATAAATCTGAATGTGCCCGCTGCCAGGCTGTGATGACAGCGCTCCAGAGTGGCCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 401 GAGAACTGTTCAAGAGTGGCCGACACCGGCTACTGTGTCCCGACAGATAGTACTGTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 461 TGCAGGTGACCAATGTGTGAGCATGTCACCTCTTACTGCCCAACCATGTGACTGAC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgAspThrAspCysGlyThr 140
DB 521 GGGGCGGCGACCGCCACACACCGGCTACTGTGTCCCGACAGATAGTACTGTGGAGCC 580

QY 141 CysleuProGlyIleuGluHisGlyAspGlyCysValSerCysProThrSerThrIleu 160
XX |||||||
DB 581 TGCGTGGCTGCTTCTATGACATGGCGATGGCTGCTGCTGCCACAGACACCTTG 640
QY 161 GlySerCysProGlyIleuGluHisGlyAspGlyCysValSerCysProThrSerThrIleu 174
XX |||||||
DB 641 GGGAGCTGTCAGAGCGCTGTGCGCTGTCTGTGCTGAGG 682
RESULT 7
AAC91477
ID AAC91477 standard; cDNA; 1662 bp.
XX
AC AAC91477;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO779 cDNA.
XX
KW Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW antihematitic; cardiant; antianaemic; immunosuppressive; antihypoid;
KW antidiabetic; nontropic; neuroprotective; hepatotropic; virucide;
KW anti-allergic; antiasthmatic; immune related disorder;
KW hepatobiliary disease; autoimmune disease; allergy; ss.
OS Homo sapiens.
XX
XX MO200073452-A2.
XX
PD 07-DEC-2000.
XX
PE 02-JUN-2000; 2000MO-US15264.
XX
XX 02-JUN-1999; 99MO-US12252.
XX 20-JUL-1999; 99US-0144732.
XX 20-JUL-1999; 99US-0144758.
XX 28-JUL-1999; 99US-0146222.
XX 01-SEP-1999; 99MO-US20111.
XX 15-SEP-1999; 99MO-US21090.
XX 29-OCT-1999; 99MO-US21547.
XX 30-NOV-1999; 99US-0162506.
XX 01-DEC-1999; 99MO-US28313.
XX 09-DEC-1999; 99US-0170262.
XX 20-DEC-1999; 99MO-US30911.
XX 05-JAN-2000; 2000MO-US00219.
XX 06-JAN-2000; 2000MO-US00376.
XX 11-FEB-2000; 2000MO-US00365.
XX 18-FEB-2000; 2000MO-US04341.
XX 22-FEB-2000; 2000MO-US04414.
XX 24-FEB-2000; 2000MO-US04914.
XX 15-MAR-2000; 2000MO-US06884.
XX 20-MAR-2000; 2000MO-US07377.
XX 21-MAR-2000; 2000MO-US07532.
XX 30-MAR-2000; 2000MO-US08439.
XX 17-MAY-2000; 2000MO-US13705.
XX 22-MAY-2000; 2000MO-US14042.
XX
XX (GENE) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;
PI Wood W;
XX
DR WPI: 2001-025253/03.
XX P-PSDB; AAB50918.
XX
PI Thirty three nucleic acids encoding PRO polypeptides which are useful
PI in the diagnosis and treatment of immune related disorders, e.g.
PI systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
PI thyroiditis and diabetes mellitus -
XX

PS Claim 48; Fig 33; 218pp; English.
XX
CC The present sequence is one of thirty three nucleic acids encoding PRO
CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
CC antagonists are useful for treating and diagnosing immune related
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases
CC (such as infectious, autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC disease, autoimmune or immune-mediated skin diseases (such as bullous
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC food hypersensitivity and urticaria), immunological diseases of the
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
CC and hypersensitivity pneumonitis), transplantation associated diseases
CC including graft rejection and graft-versus-host diseases.
XX
SQ Sequence 1662 bp; 302 A; 540 C; 531 G; 289 T; 0 other;
Alignment Scores:
Pred. No.: 1.1e-71 Length: 1662
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x AAC91477 (1-1662)
QY 1 GlnGlyIleuThrArgSerProArgCysAspGlyAlaGlyAspPheHisLysLysIleGly 20
DB 175 CAGGGGGGACACTGATGCCGCCAGAGTGTGCTGCGGAGACTCCACAGAGAGATGGT 234
QY 21 LeuPheCysCysArgGlyCysProAlaGluHisLysLysAlaProCysThrGluPro 40
DB 235 CTTTGTGTTGGCAGAGGCTGCCAGGGGGGACCTACCTGAAGGCCCTTGACGGAGGCC 294
QY 41 CysGlyAsnSerThrCysleuValCysProGlnAspThrPheLeuAlaTrpLeuAsnHis 60
DB 295 TCGGGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCGCTGGGAGAACAC 354
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 355 CATTAATTGTGATGTGCGCGCTGCCAGGCTGTGATGACAGAGCTCCAGGTGGCGCTG 414
QY 81 GluAsnSerSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 415 GAGAACTGTTCAGAGTGGCCGACACCGCTGTGCTGTAACCCAGGCTGGTTGTGGAG 474
QY 101 CysGlnValSerGlnCysValSerSerProPheTrpCysGlnProCysLeuAspCys 120
DB 475 TGCCAGGTCAGCCAAATGTGTGACAGCTTACCTTCTACTGCAACCAATGCTTACACTGC 534
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 535 GGGGCCCTGCACCGCCACACAGGCTACTGTGTTCCCGCAAGATACGATGTGGAGCC 594
QY 141 CysleuProGlyIleuGluHisGlyAspGlyCysValSerCysProThrSerThrIleu 160
DB 595 TGCGTGGCTGCTTCTATGACATGGCGATGGCTGCTGCTGCCACAGACACCTTG 654
QY 161 GlySerCysProGlyIleuGluHisGlyAspGlyCysValSerCysProThrSerThrIleu 174
DB 655 GGGAGCTGTCAGAGCGCTGTGCGCTGTCTGTGCTGAGG 696

RESULT 8
ABK40265
ID ABR40265 standard; cDNA; 1662 BP.
XX AC ABR40265;
XX 15-JUL-2002 (first entry)
XX cDNA encoding human PRO779 polypeptide.
XX
XX Human: PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukemia; neuronal disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder;
KW gene therapy; cytosolic; neuroprotective; gene; ss.
XX
XX Homo sapiens.
XX MO200153486-A1.
XX 26-JUL-2001.
XX
XX 11-FEB-2000; 2000MO-US03565.
XX
XX 08-MAR-1999; 99MO-US05028.
XX 11-MAR-1999; 99US-123972P.
XX 11-MAY-1999; 99US-133459P.
XX 02-JUN-1999; 99MO-US12252.
XX 22-JUN-1999; 99US-140650P.
XX 22-JUN-1999; 99US-140653P.
XX 20-JUL-1999; 99US-144758P.
XX 26-JUL-1999; 99US-146989P.
XX 28-JUL-1999; 99US-146222P.
XX 17-AUG-1999; 99US-149395P.
XX 31-AUG-1999; 99US-151689P.
XX 01-SEP-1999; 99MO-US20111.
XX 15-SEP-1999; 99MO-US21090.
XX 30-NOV-1999; 99MO-US28313.
XX 01-DEC-1999; 99MO-US28301.
XX 01-DEC-1999; 99MO-US28634.
XX 05-JAN-2000; 2000MO-US00219.
XX
XX (GENTH) GENENTECH INC.
XX
XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pitli RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX WPI: 2002-205567/26.
XX P-PSDB; AA086139.
XX
XX Thirty five nucleic acids encoding PRO polypeptides, useful for
PT treating benign or malignant tumours, leukemias and lymphoid
PT malignancies, inflammatory, angiogenic and immunologic disorders -
XX
XX Claim 50; Fig 23; 302pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The
CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
CC useful for treating benign or malignant tumours (e.g. renal, kidney,
CC bladder, breast, etc), leukemias and lymphoid malignancies, other
CC disorders such as neuronal, glial, astrocytic, hypothalamic, glandular,
CC macrophagal, stromal and blastocoele disorders, inflammatory, immune
CC and angiogenic disorders. The polynucleotide sequences are also
CC useful in gene therapy. ABR40254-ABR40288 encode for the human PRO
CC polypeptides of the invention.
XX
XX Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;
SQ
Alignment Scores: 1, 1e-71 Length: 1662
Pred. No.: 1038.00 Matches: 174
Score: 100.00
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x ABR40265 (1-1662)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 175 CAGGCGGCGACTCGAGCCCGCAGGTGTGACTGTGCGGTGATCTCCACAAAGATGGT 234
QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrIleuLysAlaProCysThrLuro 40
DB 235 CTGTTTGTGAGAGGTGCGCCAGCGGAGCACTACCTGAAGCCCTTGGACGAGGCC 294
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpDluAsnHis 60
DB 295 TCGCGCAACTCCACCTGCTGTGTGTGTCCCAAGACACTTCTTGCTGGAGAACAC 354
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnGlnAlaSerGlnValAlaLeu 80
DB 355 CATATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGACAGGCTCCAGGTGGCGGTG 414
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
DB 415 GAGAACTGTTCAGCAGTGGCCGACACCGCTGTGCTGTATGACCAAGCTGTGTGGAG 474
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 475 TGCCAGGTGAGCCAAATGTGTGAGCACTTCTTCTGCAACCAATGCTTACAGCTGC 534
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 535 GGGGCGCTGCACCGCCACACAGGCTACTGCTTCCCGAGAGATACAGACTGTGGAGC 594
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 595 TGCCGCTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 654
QY 161 GlySerCysProGluArgCysAlaValCysGlyTTPArg 174
DB 655 GGGAGCTGTCCAGACGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 696
RESULT 9
ABL64119
ID ABL64119 standard; DNA; 1743 BP.
XX
XX ABL64119;
XX
XX 15-MAY-2002 (first entry)
XX
XX Breast cancer related gene sequence SEQ ID NO:2456.
XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytosolic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
KW gene; ds.
XX
XX Homo sapiens.
XX
XX WO200194629-A2.
XX 13-DEC-2001.
XX
XX 30-MAY-2001; 2001MO-US10838.
XX
XX 05-JUN-2000; 2000US-209473P.
XX 05-JUN-2000; 2000US-209531P.
XX 18-SEP-2000; 2000US-233133P.
XX 18-SEP-2000; 2000US-233617P.
XX 20-SEP-2000; 2000US-234009P.
XX 20-SEP-2000; 2000US-234034P.
XX 20-SEP-2000; 2000US-234052P.
XX 22-SEP-2000; 2000US-234509P.

PR 22-SEP-2000; 2000US-234567P.
 PR 25-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 03-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.

(AVAL-) AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Edner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX WPI; 2002-188264/24.

XX Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set -
 XX
 PS Claim 1; SEQ ID 2456; 44pp; English.

XX The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I1) of a signature gene set, where (I1)
 CC comprises a sequence (S) selected from 8447 sequences (given in AB161664
 CC to AB170110), or is at least 95% identical to (S), where (I1) has
 CC expression is indicative of anti-neoplastic activity. (I1) has cytosolic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms' tumour.

XX Sequence 1743 BP; 347 A; 543 C; 549 G; 304 T; 0 other;

Alignment Scores:

Score: 1.17e-71 Length: 1743
 Percent Similarity: 1038.00 Matches: 174
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0
 US-09-993-234-6_COPY_25_198 (1-174) x AB164119 (1-1743)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
 DB 141 CAGGCGGCACTCGTAGCCCGAGGTGACTGTCGGGTACTTCCACAGAGATTGGT 200
 QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysTrpGluPro 40
 DB 201 CTGTTTGTTGCAGAGGCTGCCAGCGGGCAGTACTGAAGGCCCTTCACAGGAGCC 260
 QY 41 CysGlyAsnSerThrCysLeuValCysProGluAspThrPheLeuAlaTrpGluAsnHis 60
 DB 261 TGGCGCACTCCACTCTCTGTGTGTCGCCAAGACACTTCTTGGCTGGAGAACAC 320
 QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluAlaSerGluValAlaLeu 80
 DB 321 CATATCTGATGTGCGCTGCCAGGCTGTGTATGACGAGGCTCCAGGTGGCGCTG 380
 QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
 DB 381 GAGAACTGTCACAGAGCGGACACCCGCTGTGCTGTGAAGCCAGGCTGTGTGGAG 440
 QY 101 CysGluValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
 DB 441 TGGCAGGTCCAGCCAACTGTGCACAGTTCACCTTTCTACTGCCAACCACTAGCACTGC 500
 QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgTrpAspCysGlyTrp 140
 DB 501 GGGGCCCTGCACGCCACACACGCGTACTGTGTCCCGCAGATGACTGCTGGAGAC 560
 QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
 DB 561 TGCCCTGCTGCTTCTTATGACATGCGGATGCTGCTGCTGCCGCCAGACACCTGC 620
 QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
 DB 621 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGCTGTGGAGG 662

RESULT 10

ID AAT89426 standard; CDNA; 1783 BP.

XX AAT89426;

DT 02-MAR-1998 (first entry)

XX Death domain containing receptor DR3-V1 cDNA.

XX Death domain containing receptor; DR3-V1; human; apoptosis;
 KW Inflammation; NF-kappaB; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 198..1484

FT sig_peptide 198..302

FT mat_peptide 304..1481

PN WO9733904-A1.

PD 18-SEP-1997.

PF 17-OCT-1996; 96WO-US16849.

PR 12-MAR-1996; 96US-0013285.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (UNMI) UNIV MICHIGAN.
 XX
 PI Dillon PJ, Dixit VM, Gentz RL, M J, Yu G;
 XX
 DR WPI: 1997-470812/43.
 XX P-PSDB: AAW31516.
 XX
 PT Death domain containing receptor polypeptide(s) DR3 and DR3-VI -
 PT for activation of apoptosis and NF-kappaB, antagonists can be used
 PT to treat inflammatory diseases
 XX
 PS Claim 2: Page 71-73; 108pp; English.
 XX
 CC This cDNA clone, deposited as ATCC 97456, codes for human death
 CC domain containing receptor DR3-VI (see AAW31516), a novel member of
 CC the tumor necrosis factor receptor family. It was isolated from a
 CC cDNA library derived from cells of a human testis tumour. Related
 CC death domain containing receptor DR3 cDNA (see AAT89427) was isolated
 CC from a HVEC cDNA library. The genes have also been identified in
 CC cDNA libraries of foetal liver, foetal brain, tonsil and leukocyte.
 CC Nucleic acids encoding full-length or mature DR3-VI can be used to
 CC produce recombinant polypeptides in transformed host cells. These
 CC polypeptides can be used to treat diseases and disorders associated
 CC with the inhibition of apoptosis. Antagonists, such as antibodies
 CC raised against DR3-VI, can be used to treat diseases and disorders
 CC associated with increased apoptosis and for treating inflammatory
 CC diseases and disorders.
 CC
 XX
 SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 1.2e-71 Length: 1783
 Score: 1038.00 Matches: 174
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0
 18
 US-09-993-234-6_COPY_25_198 (1-174) x AAT89426 (1-1783)
 QY 1 Glnclgltgthrrarsserproargcysaspccysalaglasphehslslysllegly 20
 DB 303 CAGGGCGGCACTCTAGACCCAGGTGTGACGTGCCGGTGTCTCCACAAAGATTGGT 362
 QY 21 Leuphecyscysaraglycysproalaglyhlsfyrleuysalaprocysthglupro 40
 DB 363 CTGTTTGTGTCAGAGCGTGGCCAGCGGGGACATACCTGAAGGGCCCTGACAGGAGCC 422
 QY 41 Cysgllysnserthrhcysleuvalcysproglinsprrhphelualatrpqlasnhis 60
 DB 423 TGGCGCAACTCCACCTCCCTGTGTGTGCCCAAGACACCTTCTGGCTGGAGAACCCAC 482
 QY 61 Hisanserglucysalargcysglinalacysaspgluglnalaserglinalaleu 80
 DB 483 CATATATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCGGCTCCAGAGTGGCGCTG 542
 QY 81 Gluasnrcysseralavalalaasprthrargcysglcyslyspgolytrprrhphvalglu 100
 DB 543 GAGAAAGCTTCAGCAGTGGCGGACACCCCGCTGTGCTGAAGCCAGGTGTTTGTGAG 602
 QY 101 CysglvalserglncysvalserSerSerPropheryrcysglinsprrhphvalaleu 120
 DB 603 TGGCAGGTTCAGCCAAATGTGTGACAGTGTTCACCTTCTACTCCCAACCATGCTAGACTGC 662
 QY 121 Glvalaleuhsarghlsrthrargleuancysserargaraprrhphaspcysgllythr 140
 DB 663 GGGGCGCTGCACCGCCACACACGGCTACTCTGTTCGCCGAGAGTACTGATGTGGAGCC 722
 QY 141 Cysleubprogllythryrglulhslglsaspolycysvalsercysprothrserthrleu 160
 DB 723 TGCCTGGCTGGCTTCATGAACATGGGAGATGGGTGGCGTGGCTCCACAGAGACCCCTG 782
 QY 161 Glysercysprogluargcysalaleuvalcysgllytrprrg 174

DB 783 GGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGTGGAGG 824
 RESULT 11
 AAX00924
 ID AAX00924 standard; cDNA: 1783 BP.
 XX
 AC AAX00924;
 XX
 DT 25-MAR-1999 (first entry)
 XX
 DE Death domain containing receptor polypeptide (DR3-VI) encoding cDNA.
 XX
 KW Death domain; receptor; DR3-VI; DR3; recombinant; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 198..1484
 FT /*tag= a
 FT /product= "Death domain containing receptor DR3-VI"
 FT sig_peptide 198..300
 FT /*tag= b
 FT mat_peptide 301..1481
 FT /*tag= c
 XX
 PN JP11000170-A.
 XX
 PD 06-JAN-1999.
 XX
 PF 12-MAR-1997; 97JP-0057503.
 XX
 PR 06-FEB-1997; 97US-0037341.
 PR 12-MAR-1996; 96US-0013285.
 PR 17-OCT-1996; 96US-0028711.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (UNMI) UNIV MICHIGAN.
 XX
 DR WPI: 1999-124390/11.
 DR P-PSDB: AAW95537.
 XX
 DT New death domain containing receptor and recombinant vector -
 PT optionally comprising leader sequence
 XX
 PS Claim 2: Fig 1, 2; 50pp; Japanese.
 XX
 CC The invention provides nucleotide sequences encoding death domain
 CC containing receptor polypeptides DR3-VI and DR3. The DR3-VI cDNA clone
 CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
 CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
 CC the nucleic acid sequences and optionally the leader sequences are
 CC used for the recombinant production of the proteins. The present
 CC sequence represents a cDNA encoding the death domain containing
 CC receptor polypeptide (DR3-VI).
 XX
 SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 1.2e-71 Length: 1783
 Score: 1038.00 Matches: 174
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0
 US-09-993-234-6_COPY_25_198 (1-174) x AAX00924 (1-1783)
 QY 1 Glnclgltgthrrarsserproargcysaspccysalaglasphehslslysllegly 20
 DB 303 CAGGGCGGCACTCTAGACCCAGGTGTGACGTGCCGGTGTCTCCACAAAGATTGGT 362
 QY 21 Leuphecyscysaraglycysproalaglyhlsfyrleuysalaprocysthglupro 40

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Db 363 CTGTTTGTTCACAGAGGCTGCCACCGGGGCACTACCGAAGGCCCTTCGACGAGGCC 422
QY 41 CysGlnValSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 423 TGGCGCAACTCCACCTGCTGTGTGTGCCCAACAGACACCTTCTTGCTGGAGAACAC 482
QY 61 HisAsnSerGluCysAlaValCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 483 CATAAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGTGGCGCTG 542
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysProGlyTyrPheValGlu 100
Db 543 GAGAACTGTTCAGCAGTGGCCGACACCGGCTGTGCTGAAGCCAGGCTGGTTGTGAG 602
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 603 TGCAGGTTCAGCCAAATGTGTGACAGATTCACCTTACCTCCAAACATGCTTACACTGC 662
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 663 GGGGCGCTGCACCGCCACACAGCGCTACTCTGTCCCGCAGAGATGACTGTGGAGCC 722
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 723 TGCGTGGCTGGCTTCTATGAACATGGCGATGCTGCTGCTGCTGCCACAGACACCTG 782
QY 161 GlySerCysProGluArgCysAlaValCysGlyTyrParg 174
Db 783 GGGAGCTGTCCAGAGCGCTGTCGCGCTGTGTGGGTGGAGG 824

RESULT 12
AAC68776
ID AAC68776 standard; cDNA: 1783 BP.
AC AAC68776;
DX 20-FEB-2001 (first entry)
DE Human death domain containing receptor DR3-VI coding sequence.
XX
KW Human: death domain containing receptor; DR3-VI; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis; ss.
OS Homo sapiens.
XX
PN WO200064465-A1.
XX
PD 02-NOV-2000.
XX
PF 21-APR-2000; 2000WO-US10741.
XX
PR 22-APR-1999; 99US-0130488.
PR 28-MAY-1999; 99US-0136741.
XX
PA (HDMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
PA (YUGG/) YU G.
PA (NLIJ/) NI J.
PA (GENTZ) GENTZ R L.
PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX
PI Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;
XX
DR WPI: 2000-687263/67.
DR P-PSDB; AAB36264.
XX
PT Treating graft-versus-host disease, cancer, immunodeficiency or an
XX autoimmune disease comprising administering an antibody to Death Domain
XX Containing Receptor proteins and a second therapeutic agent -

```

```

PS Example 1; Fig 1; 273pp; English.
XX
CC The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-VI. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune diseases such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.
XX
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Alignment Scores:
Pred. No.: 1,2e-71 Length: 1783
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x AAC68776 (1-1783)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisIstLysIleGly 20
Db 303 CAGGGGGGCACTGTGTAGCCGCCAGTGTGACTGTGCCGTTACTTCCACAGAAATGGT 362
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 363 CTGTTTGTGTGACAGAGCGTCCCGCAGCGGGGCACTACCTGAAGGCCCTTGCACGAGGCC 422
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 423 TGGCGCAACTCCACCTGCTGTGTGTGCCCAACAGACACCTTCTTGCTGGAGAACAC 482
QY 61 HisAsnSerGluCysAlaValCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 483 CATAAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGTGGCGCTG 542
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysValSerArgArgAspThrAspCysGlyThr 100
Db 543 GAGAACTGTTCAGCAGTGGCCGACACCGGCTGTGCTGAAGCCAGGCTGGTTGTGAG 602
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 603 TGCAGGTTCAGCCAAATGTGTGACAGATTCACCTTACCTCCAAACATGCTTACACTGC 662
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 663 GGGGCGCTGCACCGCCACACAGCGCTACTCTGTCCCGCAGAGATGACTGTGGAGCC 722
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 723 TGCGTGGCTGGCTTCTATGAACATGGCGATGCTGCTGCTGCTGCCACAGACACCTG 782
QY 161 GlySerCysProGluArgCysAlaValCysGlyTyrParg 174
Db 783 GGGAGCTGTCCAGAGCGCTGTCGCGCTGTGTGGGTGGAGG 824

RESULT 13
AAV28700
ID AAV28700 standard; cDNA: 1847 BP.
AC AAV28700;
DX 20-AUG-1998 (first entry)
DE Human apoptosis inducing receptor coding sequence.
XX
KW Apoptosis inducing receptor; AIR protein; human; cell death regulator;
KW Type I transmembrane protein; tumour cell death; autoimmune disease;
KW therapy; ss.

```



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XX OS Homo sapiens.
XX Key Location/Qualifiers
XX CDS 236..1489
XX FT /*tag= a
XX FT /product= AIR
XX PN MO814565-A1.
XX PD 09-APR-1998.
XX PF 03-OCT-1997; 97WO-US17876.
XX PR 04-OCT-1996; 96US-0044456.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Perkins PA;
XX PS Claim 2; Page 28-30; 45pp; English.
XX PT DNA encoding apoptosis inducing receptor - which is Type I
XX P-PSDB; AAW57045.
XX PS Claim 2; Page 28-30; 45pp; English.
XX CC This sequence encodes the human apoptosis inducing receptor (AIR) of the
XX CC invention. AIR is a type I transmembrane protein, soluble forms of which
XX CC can be used to regulate cell death in a therapeutic setting. Soluble AIR
XX CC can also be used in vitro to block apoptosis or AIR-expressing cells, or
XX CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain
XX CC of AIR can be used to develop assays for inhibitors of AIR-induced cell
XX CC death, which is useful to regulate cell death in a therapeutic setting as
XX CC well as in vitro. Agonists of AIR activity can be used to kill tumour
XX CC cells that express AIR, or T cells expressing AIR in autoimmune diseases.
XX SQ Sequence 1847 BP; 316 A; 605 C; 579 G; 347 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 1.25e-71 Length: 1847
XX Score: 1038.00 Matches: 174
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 19 Gaps: 0
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XX US-09-993-234-6_COPY_25_198 (1-174) x AAW28700 (1-1847)
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XX 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
XX |||||||
XX DB 308 CAGGCGGCGCACTGACCCAGAGTGTGACGTGCGGTGACCTTCCACAGAAAGATTGGT 367
XX |||||||
XX 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
XX |||||||
XX DB 368 CTGTTTGTGTCAGACAGCTGCCAGCGGACACTGACCTGAAGGCCCTTGCACGAGGCC 427
XX |||||||
XX 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
XX |||||||
XX DB 428 TGGCGCAACTCCCTGCTGTGTGTGTCGCCAAGACACCTTCTGGCTGGGAACACCC 487
XX |||||||
XX 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnGlnAlaSerGlnValAlaLeu 80
XX |||||||
XX DB 488 CATAAATTCTGAATGTGCCCGGTGCCAGGCCCTGTGATGAGCGAGGCTCCAGAGTGGCGTG 547
XX |||||||
XX 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
XX |||||||
XX DB 548 GAGAACTGTTCAAGCAGTGGCGACACCCGCTGTGCTAAGCAGAGGTGCTTTGTGGAG 607
XX |||||||
XX 101 CysGlnValSerGlnCysValSerSerSerProGlyTyrCysGlnProCysLeuAspCys 120
XX |||||||
XX DB 608 TGCAGAGTCAAGCAATGTGTGAGCAATGTTCAACCTTTACTGCAACCATGCTGAGACTGC 667
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XX 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
XX |||||||
XX DB 668 GGGGCGCCGCGACCCGACACAGCGCTACTCTGTCCGCCAAGATACTGACTGTGGAGCC 727
XX |||||||
XX 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
XX |||||||
XX DB 728 TGCCTGCGCTGCTTATGACATGCGATGGCTGCGTCTGCTGCCACAGCACCCCTG 787
XX |||||||
XX 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 174
XX |||||||
XX DB 788 GGGAGCTGTCCAGAGCGCTGTGCGCTGTGTGCTGAGG 829
XX |||||||
XX RESULT 14
XX ID AAF83770 standard; DNA; 1250 BP.
XX AC AAF83770;
XX XX 06-AUG-2001 (first entry)
XX DE Nucleotide sequence of human TR3 gene.
XX XX
XX KW TR3; cell proliferation; leukemia; immunosuppressive; cytostatic;
XX KW dermatological; antidiabetic; neuroprotective; cardiant;
XX KW antithyroid; antiinflammatory; antiallergic; T-cell-inhibitor; ds.
XX XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1250
XX FT /*tag= a
XX FT /transl_except= "(pos:481..482, aa:Asp)"
XX FT /note= "this codon has an apparent 1 nucleotide
XX FT deletion which alters the reading frame"
XX FT /transl_except= "(pos:558..559, aa:Cys)"
XX FT /note= "this codon has an apparent 1 nucleotide
XX FT deletion which alters the reading frame"
XX FT /transl_except= "(pos:638..639, aa:Leu)"
XX FT /note= "this codon has an apparent 1 nucleotide
XX FT deletion which alters the reading frame"
XX FT /transl_except= "(pos:718..719, aa:Met)"
XX FT /note= "this codon has an apparent 1 nucleotide
XX FT deletion which alters the reading frame"
XX FT sig_peptide 1..72
XX FT /*tag= b
XX FT mat_peptide 73..1247
XX FT /*tag= c
XX
XX W0200135995-A2.
XX PD 25-MAY-2001.
XX PF 17-NOV-2000; 2000WO-US31692.
XX PR 19-NOV-1999; 99US-0166583.
XX XX
XX PA (TTT/) TITTL T V.
XX PA (WEGM/) WEGMANN K W.
XX PI Tittle TV, Wegmann KW;
XX XX
XX DR WPI: 2001-343711/36.
XX DR P-PSDB; AAB84941.
XX
XX Composition for treatment of T-cell mediated disease e.g. arthritis,
XX PT cancer comprises a biologically active TR3-specific binding agent
XX PT especially a monoclonal antibody -
XX PS
XX PS Disclosure; Page 72: 77pp; English.
XX CC The invention relates to a composition comprising a biologically active
XX CC TR3-specific binding agent (i) that binds to TR3 and inhibits the
```


CC expression is indicative of anti-neoplastic activity. (1) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophagal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms' tumour.

XX
SQ Sequence 816 BP: 149 A: 235 C: 264 G: 168 T: 0 other:

Alignment Scores:

Pred. No.:	3.37e-65	Length:	816
Score:	950.00	Matches:	163
Percent Similarity:	93.68%	Conservative:	0
Best Local Similarity:	93.68%	Mismatches:	3
Query Match:	91.52%	Indels:	8
DB:	24	Gaps:	1

US-09-993-234-6_COPY_25_198 (1-174) x ABL67258 (1-816)

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QY      1  GlnGlyGlyThrArgSerProArgCysAlaGlyAspPheHisLysIleGly  20
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DB     57  CAGGCGCGACCTGCTACCCCGAGGTGACGTCCGGTACTTCACAGACATTGGT  116

QY     21  LeuPheCysCysArgGlyCysProAlaGlyHisThrLeuLysAlaProCysThrGluPro  40
      |||
DB    117  CTGTTTGTTCACAGGCTGCCCGAGGGGACACTACTGAAAGGCCCTTGACAGGAGCCC  176

QY     41  CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis  60
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DB    177  TGCAGCAACTCCACTGCTGTGTGCCCAAGACACCTTCTGGCCTGGAGACAC  236

QY     61  HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu  80
      |||
DB    237  CATAAATTCGTGAATGTGCCCGCTGCAGGCCGTGATGAGCGCCCTCCAGGTGGCGCTG  296

QY     81  GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu  100
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DB    297  GAGAACTGTTCAGCAGTGGCGGACACCCGCTGTGCTGTAAAGCCAGGCTGTTGTGGAG  356

QY    101  CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys  120
      |||
DB    357  TGCAGGCTCAGCCCAATGTGTACAGCATTCACCTTACTGCCAACCATGCTAGACTGC  416

QY    121  GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr  140
      |||
DB    417  GGGGCCCTGCACCCGACACAGCGCTACTCTGTTCGCCGACAGATACACTGTGGGACC  476

QY    141  CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu  160
      |||
DB    477  TGCTTGCCTGGCTTCTATGAACATGCGAGTGGCTGCGGTCTGCCCCACGTAATTCCTA  536

QY    161  GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg  174
      |||
DB    537  -----GCTGTGCTGGGATGGAGG  554
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Search completed: April 6, 2003, 16:52:37
Job time : 169.014 secs

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GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 21:08:18 ; Search time 66.2544 Seconds
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2303.655 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_198

Perfect score: 1038
Sequence: 1 OGCTSPRCDCAGDFHKKIG.....CPTSTLGSCPERCAAVCGMR 174

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Searched: 593429 segs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published.Applications.NA -QEXT=fastcap SUFFIX=rnpb MINMATCH=0.1
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-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published.Applications.NA:*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1038	100.0	1254	10	US-09-333-966-3
2	1038	100.0	1634	9	US-10-081-280-9
3	1038	100.0	1634	9	US-10-112-793-9
4	1038	100.0	1634	9	US-10-112-193-11

5	1038	100.0	1634	10	US-09-993-234-9	Sequence 9, Appl1
6	1038	100.0 <td>1743</td> <td>9</td> <td>US-09-954-531-1389</td> <td>Sequence 1389, Ap</td>	1743	9	US-09-954-531-1389	Sequence 1389, Ap
7	1038	100.0 <td>1763</td> <td>9</td> <td>US-09-333-966-1</td> <td>Sequence 1, Appl1</td>	1763	9	US-09-333-966-1	Sequence 1, Appl1
8	950	91.5	1438	10	US-09-964-824A-292	Sequence 292, App
9	950	91.5	1438	9	US-10-081-280-5	Sequence 5, Appl1
10	950	91.5	1438	9	US-10-112-793-5	Sequence 5, Appl1
11	950	91.5	1438	9	US-10-112-793-5	Sequence 5, Appl1
12	950	91.5	1438	10	US-09-884-733-5	Sequence 5, Appl1
13	950	91.5	1438	10	US-09-993-234-5	Sequence 5, Appl1
14	738	71.1	10797	9	US-10-092-154-1577	Sequence 1577, Ap
15	738	71.1	10797	10	US-09-764-847-1577	Sequence 1577, Ap
16	666	64.2	433	9	US-10-081-280-2	Sequence 2, Appl1
17	666	64.2	433	9	US-10-112-793-2	Sequence 2, Appl1
18	666	64.2	433	9	US-10-112-793-2	Sequence 2, Appl1
19	666	64.2	433	10	US-09-884-733-2	Sequence 2, Appl1
20	666	64.2	433	10	US-09-993-234-2	Sequence 2, Appl1
21	214	20.6	2130	10	US-09-917-800A-1601	Sequence 1601, Ap
22	212.5	20.5	1049	10	US-09-756-186-1	Sequence 1601, Ap
23	211	20.3	5870	10	US-09-838-718A-8	Sequence 8, Appl1
24	205.5	19.8	1301	10	US-09-756-186-7	Sequence 7, Appl1
25	205	19.7	1674	9	US-09-359-595-12	Sequence 12, Appl1
26	203.5	19.6	1202	10	US-09-756-186-3	Sequence 3, Appl1
27	203	19.6	519	9	US-09-899-429A-15	Sequence 15, Appl1
28	203	19.6	549	9	US-09-899-429A-9	Sequence 9, Appl1
29	203	19.6	603	9	US-09-899-429A-13	Sequence 13, Appl1
30	203	19.6	633	9	US-09-899-429A-7	Sequence 7, Appl1
31	203	19.6	1334	9	US-09-898-234-11	Sequence 11, Appl1
32	203	19.6	1334	9	US-09-792-356-11	Sequence 11, Appl1
33	203	19.6	1334	10	US-09-899-422-11	Sequence 11, Appl1
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36	203	19.6	1368	9	US-09-792-356-1	Sequence 1, Appl1
37	203	19.6	1368	10	US-09-899-422-1	Sequence 1, Appl1
38	203	19.6	2111	10	US-09-880-107-2360	Sequence 2360, Ap
39	203	19.6	2141	9	US-09-898-234-16	Sequence 16, Appl1
40	203	19.6	2141	9	US-09-899-429A-26	Sequence 26, Appl1
41	203	19.6	2141	9	US-09-792-356-16	Sequence 16, Appl1
42	203	19.6	2141	10	US-09-899-422-16	Sequence 16, Appl1
43	203	19.6	2175	12	US-10-120-397-1	Sequence 12, Appl1
44	202	19.5	1334	9	US-09-899-429A-21	Sequence 21, Appl1
45	201	19.4	1147	10	US-09-756-186-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-09-333-966-3
Sequence 3, Application US/09333966
Patent No. US2002009773A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
FILING DATE: 06-FEB-1997
APPLICATION NUMBER: No. US20020009773A1 yet Assigned
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488, 0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-09-333-966-3

Alignment Scores:
Pred. No.: 7.16e-99 Length: 1254
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-09-333-966-3 (1-1254)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
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QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisLysIleValAlaProCysThrGluPro 40
DB 133 CTGTTTGTGGAGAGCGTCCAGCGGGGACCTTGAAGGCCCTTGCACGGAGGCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 193 TCCGGGACCTCCAGCTGTGTGTGTCGCCCAAGACACTTCTGGCGTGGAGAACAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 253 CATATTCTGATGTGCGCCGCTGCCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyThrPheValGlu 100
DB 313 GAGACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGAAGCCAGGCTGTGTGGAG 372
QY 101 CysGlnValSerGlnCysValSerSerProPheThrCysGlnProCysLeuAspCys 120
DB 373 TCCAGGGTCAGCAATGTGTGTCAGCTTACCCCTTCTACTGCCAACCAATGCTGACCTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuLeuSerAlaGlyAspThrAspCysGlyThr 140
DB 433 GGGGGCCCTGACACCCGACACACGGCTACTGTGTGTCGCCCAAGATACGACTGTGGAGCC 492
QY 141 CysLeuProGlyPheThrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 493 TGCCTGCTGCTGCTGTATGACATGGCGATGGCTGCGTCTGCTGCCACGACGACCTCG 552
QY 161 GlySerCysProGluArgCysAlaValAlaCysGlyThrArg 174

DB 553 GGGAGCTGTCCAGACGGTGTGCGCGCTGTGTGCTGAGG 594

RESULT 2
US-10-081-280-9
Sequence 9, Application US/10081280
Patent No. US20020165157A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEFAX: 415/952-5416
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
TOPOLOGY: Linear
STRANDEDNESS: Single
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-081-280-9

Alignment Scores:
Pred. No.: 9.85e-99 Length: 1634
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-10-081-280-9 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 161 CAGGGGGGACCTGTCGAGCCCGAGGTGTGACTGTGCGGTGACTTCCACAAGAGATTGGT 220
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisLysIleValAlaProCysThrGluPro 40
DB 221 CTGTTTGTGGAGAGCGTCCAGCGGGGACCTTGAAGGCCCTTGCACGGAGGCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 281 TCCGGGACCTCCAGCTGTGTGTGTCGCCCAAGACACTTCTTGGCGTGGAGAACAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 341 CATATTCTGATGTGCGCCGCTGCCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 400

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-112-193-11

Alignment Scores:
Pred. No.: 9,85e-99 Length: 1634
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-10-112-193-11 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 161 CAGGGCGGACCTGCTAGCCCGAGCTGTGACCTGCCGCTACCTCCACAGAGATTGGT 220
QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 221 CTGTTTGTGGCAGAGGCTGCCCGGGGACACTGAAAGCCCTTCACAGGAGCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 281 TGGGGCAACCTCCACTCTGTGTGTGCTCCCAAGACACTTCTTGGCTGGAGAACAC 340
QY 61 HisAsnSerGlyCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 80
DB 341 CATATTCTGAATGTGCTGCTGCCAGGCTGTGATGAGACAGGCTCCCAAGGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
DB 401 GAAACCTGTTACACAGTGGCCGACACCGCTGTGCTGTAAAGCAGGCTGTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 461 TGGCAGGTGACCAATGTGTGACAGTTCACCTTACTGCGCAACCATGCTAGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 521 GGGGCCCCGACCGCCACACAGCTACTCTGTCCCGCAGAGATGACTGCTGGAGCC 580
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 581 TGGCTGCTGGGCTCTATATACATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 174
DB 641 GGAAGCTGTCCAGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 682

RESULT 5
US-09-993-234-9
Sequence 9, Application US/09993234
Patent No. US20020146768A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/993,234
FILING DATE: 19-No. US20020146768A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,683
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-993-234-9

Alignment Scores:
Pred. No.: 9,85e-99 Length: 1634
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-09-993-234-9 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 161 CAGGGCGGACCTGCTAGCCCGAGCTGTGACCTGCCGCTACCTCCACAGAGATTGGT 220
QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 221 CTGTTTGTGGCAGAGGCTGCCCGGGGACACTGAAAGCCCTTCACAGGAGCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 281 TGGGGCAACCTCCACTCTGTGTGTGCTCCCAAGACACTTCTTGGCTGGAGAACAC 340
QY 61 HisAsnSerGlyCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 80
DB 341 CATATTCTGAATGTGCTGCTGCCAGGCTGTGATGAGACAGGCTCCCAAGGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
DB 401 GAAACCTGTTACAGAGTGGCCGACACCGCTGTGCTGTAAAGCAGGCTGTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 461 TGGCAGGTGACCAATGTGTGACAGTTCACCTTACTGCGCAACCATGCTAGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 521 GGGGCCCCGACCGCCACACAGCTACTCTGTCCCGCAGAGATGACTGCTGGAGCC 580
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 581 TGGCTGCTGGGCTCTATATACATGCGGATGCTGCTGCTGCTGCTGCTGCTGCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 174

Db 641 GGGAGCTGTCCAGAGCGCTGTGCGCTGTCTGTGCTGAGG 682

RESULT 6
US-09-954-531-1389
: Sequence 1389, Application US/09954531
: Patent No. US20020165180A1
: GENERAL INFORMATION:
: APPLICANT: Weaver, Zoe
: TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
: FILE REFERENCE: 689290-77
: CURRENT APPLICATION NUMBER: US/09/954,531
: PRIOR APPLICATION NUMBER: US/60/233,133
: PRIOR FILING DATE: 2000-09-18
: PRIOR APPLICATION NUMBER: US/60/234,009
: PRIOR FILING DATE: 2000-09-20
: PRIOR APPLICATION NUMBER: US/60/234,034
: PRIOR FILING DATE: 2000-09-20
: PRIOR APPLICATION NUMBER: US/60/234,509
: PRIOR FILING DATE: 2000-09-22
: PRIOR APPLICATION NUMBER: US/60/234,567
: NUMBER OF SEQ ID NOS: 1392
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1389
: LENGTH: 1743
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-954-531-1389

Alignment Scores:
Pred. No.: 1.06e-98 Length: 1743
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-09-954-531-1389 (1-1743)

Qy 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 141 CAGGCGCGGACTCGTAGCGCCAGGCTGACGTGCGGCTGACTCCACAAAGATTGTGT 200
Qy 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 201 CTGTTTTCAGAGAGGTGCGCCAGCGGGGCACTACCTGAAGGCCCTTGCAAGAGCC 260
Qy 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 261 TGGCGCACTCCACCTGCTGTGTGTCGCCAAGACACCTTCTGGCTGGAGAACAC 320
Qy 61 HisAsnSerGlyCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 321 CATATTCTGATGTGCGCGCTGCGAGCGCTGTGATGAGCGCCCTCCAGAGTGTGCGCTG 380
Qy 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
Db 381 GAGAACTTTACAGAGTGTGCGCGGACACCGCTGTGCTTAAGCCAGGCTGTTTGTGAG 440
Qy 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 441 TGGCAGGTGACCAATGTGTGAGCAGTTCACCTTCTACGCAACCAATGCTAGACTGC 500
Qy 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerAlaGlyAspThrAspCysGlyThr 140
Db 501 GGGCGCCGTGACCGCGCACACAGGCTACTGTGTTCCCGCAGAGATACAGATGTGCGACC 560
Qy 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 561 TGCTGCTGCTGTCTATGAACATGGCGATGGCTGTGCTGTGCTGCGCCACAGACACCTG 620

Qy 161 GlySerCysProGlnArgCysAlaAlaValCysGlyTrpArg 174
Db 621 GGGAGCTGTCCAGAGCGCTGTGCGCTGTCTGTGCTGAGG 662

RESULT 7
US-09-333-966-1
: Sequence 1, Application US/09333966
: Patent No. US20020009773A1
: GENERAL INFORMATION:
: APPLICANT: Yu, Guo-Liang
: APPLICANT: Ni, Jian
: APPLICANT: Dixit, Vishva
: APPLICANT: Gentz, Reiner L.
: APPLICANT: Dillon, Patrick J.
: TITLE OF INVENTION: Death Domain Containing Receptors
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
: STREET: 1100 New York Ave., NW, Suite 600
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/333,966
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/815,469
: FILING DATE:
: APPLICATION NUMBER: NO. US20020009773A1 yet Assigned
: FILING DATE: 06-FEB-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/028,711
: FILING DATE: 17-OCT-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/013,285
: FILING DATE: 12-MAR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Steffe, Eric K.
: REGISTRATION NUMBER: 36,688
: REFERENCE/DOCKET NUMBER: 1488, 0310003/EKS/KRM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1783 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: both
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 198..1481
US-09-333-966-1

Alignment Scores:
Pred. No.: 1.09e-98 Length: 1783
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-09-333-966-1 (1-1783)

Qy 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20

Db 303 CAGGGGGGCACTGTAGCCCGGAGGTGTGCTGCGGTACTTCCACGAAGATTGGT 362
Qy 21 LeupheCysArgrglYcysProAlaGlyHstYrLeuYsaLaProCysThrGluPro 40
Db 363 CTGTTTGTTCGAGAGGCTGCCAGGGGGGCACTACTGAAGGCCCTTTCAGAGAGCCC 422
Qy 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 423 TGGGGCAACCCACCTGCTGTGTGTGCCCAAGACACCTTCTTGGCTGGGAGAACCC 482
Qy 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAsnValAlaLeu 80
Db 483 CATTAATTCGAATGTGCCCCCTGCCAGGCTGTGATGAGAGGCGCTCCAGGTGGCGCTG 542
Qy 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 543 GAAACTGTTCAACAGTGGCGGACACCCGCTGTGGCTGTAGCCAGGCTGTTTGTGGAG 602
Qy 101 CysGlnValSerGlnCysValSerSerProPheTrpCysGlnProCysLeuAspCys 120
Db 603 TGCACAGTCAAGCAATGTGCACAGTACCTTCTACTGCCAACCATGCTAGACTGC 662
Qy 121 GlyAlaLeuHisArgHstHrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 663 GGGGCGCTGCACCGCACACACGCTACTCTGTCCCGGAGATACTGACTGTGGAGCC 722
Qy 141 CysLeuProGlyPheTrpGluHstGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 723 TGGCTGCTGCTTCTATGAACATGGCGAGGTGCGTGTCTGCTGCCCGACAGACCCCTG 782
Qy 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 783 GGGAGCTGTCCAGAGCGCTGTGCTGTCTGTGGCTGGAGG 824

RESULT 8
US-09-964-824A-292
Sequence 292, Application US/09964824A
Patent No. US20020102531A1
GENERAL INFORMATION:
APPLICANT: Horitzan, Stephen
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE REFERENCE: 689290-73
CURRENT APPLICATION NUMBER: US/09/964,824A
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
SOFTWARE: PatentIn version 3.0
SEQ ID NO 292
LENGTH: 816
TYPE: DNA
ORGANISM: Homo sapiens
US-09-964-824A-292

Alignment Scores:
Pred. No.: 5,76e-90 Length: 816
Score: 950.00 Matches: 163
Percent Similarity: 93.68% Conservative: 0
Best Local Similarity: 93.68% Mismatches: 3
Query Match: 91.52% Indels: 8
DB: 10 Gaps: 1

US-09-993-234-6_COPY_25_198 (1-174) x US-09-964-824A-292 (1-816)

Qy 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 57 CAGGGCGGCACTGTAGCCCGGAGGTGTGCTGCGGTACTTCCACGAAGATTGGT 116

Qy 21 LeupheCysArgrglYcysProAlaGlyHstYrLeuYsaLaProCysThrGluPro 40
Db 117 CTGTTTGTTCGAGAGGCTGCCAGGGGGGCACTACTGAAGGCCCTTTCAGAGAGCCC 176
Qy 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 177 TGGGGCAACCCACCTGCTGTGTGTGCCCAAGACACCTTCTTGGCTGGGAGAACCC 236
Qy 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAsnValAlaLeu 80
Db 237 CATTAATTCGAATGTGCCCCCTGCCAGGCTGTGATGAGAGGCGCTCCAGGTGGCGCTG 296
Qy 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 297 GAAACTGTTCAACAGTGGCGGACACCCGCTGTGGCTGTAGCCAGGCTGTTTGTGGAG 356
Qy 101 CysGlnValSerGlnCysValSerSerProPheTrpCysGlnProCysLeuAspCys 120
Db 357 TGCACAGTCAAGCAATGTGCACAGTACCTTCTACTGCCAACCATGCTAGACTGC 416
Qy 121 GlyAlaLeuHisArgHstHrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 417 GGGGCGCTGCACCGCACACACGCTACTCTGTCCCGGAGATACTGACTGTGGAGCC 476
Qy 141 CysLeuProGlyPheTrpGluHstGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 477 TGGCTGCTGCTTCTATGAACATGGCGAGGTGCGTGTCTGCTGCCCGACAGTAACTCTTA 536
Qy 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 537 -----GCTGTGCTGGAGATGGAGG 554

RESULT 9
US-10-081-280-5
Sequence 5, Application US/10081280
Patent No. US20020165157A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single

TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5
US-10-081-280-5

Alignment Scores:
Pred. No.: 1,14e-89 Length: 1438
Score: 950.00 Matches: 163
Percent Similarity: 93.68% Conservative: 0
Best Local Similarity: 93.68% Mismatches: 3
Query Match: 91.52% Indels: 8
DB: 9 Gaps: 1

US-09-993-234-6_COPY_25_198 (1-174) x US-10-081-280-5 (1-1438)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 449 CAGGGCGGACCTCGTAGCCCGGAGGTGACGTGGCGGTGACTTCCACAGAAAGATTGGT 508
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisIleLysAlaProCysThrGluPro 40
DB 509 CTGTTTGTTCAGACAGGTGCCCGGAGGCGGACCTGAAAGGCCCTTGCACGGAGGCC 568
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 569 TGGGGAACCTCCACCTGCTGTGTGTGTCCAGAGACCTTCTTGCCGGAGAACAC 628
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 629 CATAAATTCGTAATGTGCCCGCTGCCAGGCGCTGTATGACAGAGCGCTCCAGAGTGGCGTG 688
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 689 GAGAACTGTTCCAGAGGTGCCCGGAGGCGGACCTGTGCTTGAAGCAGGCTGTTGTGGAG 748
QY 101 CysGlnValSerGlnCysValSerSerProPheTrpCysGlnProCysLeuAspLys 120
DB 749 TGCAGAGGACCAATGTGTGAGCAGTTCACCTTCTACTCCACCAATGCTTACACTGC 808
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgAspThrAspCysGlyThr 140
DB 809 GGGGCGCTGCACCGCCACACAGCGCTACTCTGTCCCGCAAGAACTGACTGTGGAGCC 868
QY 141 CysLeuProGlyPheTrpGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 869 TGCCGTGCTGCTTCTAATGAAACATGGCGATGGCTGCTGCTGCCCGCAGCTAATTCCTA 928
QY 161 GlySerCysProGluArgCysAlaValCysGlyTrpArg 174
DB 929 -----GCTGTGCTGGAGTGAGG 946

RESULT 10
US-10-112-793-5
Sequence 5, Application US/10112793
Publication No. US20020192729A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-793-5

Alignment Scores:
Pred. No.: 1,14e-89 Length: 1438
Score: 950.00 Matches: 163
Percent Similarity: 93.68% Conservative: 0
Best Local Similarity: 93.68% Mismatches: 3
Query Match: 91.52% Indels: 8
DB: 9 Gaps: 1

US-09-993-234-6_COPY_25_198 (1-174) x US-10-112-793-5 (1-1438)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 449 CAGGGCGGACCTCGTAGCCCGGAGGTGACGTGGCGGTGACTTCCACAGAAAGATTGGT 508
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisIleLysAlaProCysThrGluPro 40
DB 509 CTGTTTGTTCAGAGGTGCCCGGAGGCGGACCTGTGATGACAGAGCGCTCCAGAGTGGCGTG 568
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 569 TGGGGAACCTCCACCTGCTGTGTGTGTCCAGAGACCTTCTTGCCGGAGAACAC 628
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 629 CATAAATTCGTAATGTGCCCGCTGCCAGGCGCTGTGATGACAGAGCGCTCCAGAGTGGCGTG 688
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 809 GGGGCGCTGCACCGCCACACAGCGCTACTCTGTCCCGCAAGAACTGACTGTGGAGCC 868
QY 141 CysLeuProGlyPheTrpGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 869 TGCCGTGCTGCTTCTAATGAAACATGGCGATGGCTGCTGCTGCCCGCAGCTAATTCCTA 928
QY 161 GlySerCysProGluArgCysAlaValCysGlyTrpArg 174
DB 929 -----GCTGTGCTGGAGTGAGG 946

RESULT 11
US-10-112-193-5
Sequence 5, Application US/10112193

Publication No. US20030004313A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,193
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,069
FILING DATE: 11-Sep-1997
APPLICATION NUMBER: 60/026943
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-193-5
Alignment Scores:
Pred. No.: 1.14e-89 Length: 1438
Score: 950.00 Matches: 163
Percent Similarity: 93.68% Conservative: 0
Best Local Similarity: 93.68% Mismatches: 3
Query Match: 91.52% Indels: 8
DB: Gaps: 1
US-09-993-234-6_COPY_25_198 (1-174) x US-10-112-193-5 (1-1438)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 449 CAGGGGGGCGACTGTAGCCCGCAGAGGTGTACTGTGGTACTTCCACAAGAGATTGGT 508
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisLysLysAlaPheCysThrGluPhe 40
Db 509 CTGTCTTTGTGCAGAGGCTGCCAGGGGGCACTTACTTAAGGCCCTTGCACGGAGCC 568
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspPheLeuAlaTrpGlnAsnHis 60
Db 569 TCGGGGACCTCCACCTGCTGTGTGTCCCAAGACCTCTTGGCTGGGAGAGAACAC 628
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnGlnAlaSerGlnValAlaLeu 80
Db 629 CATTAATTCGAAATGTCCCGCTGCCAGGCTGTGATGACAGAGCCCTCCAGGTGGCGCTG 688
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 689 GAGAACTGTTCAGCAGTGGCGACACCGCCTGTGCTGTAAACCAAGCGCTTTGTGGAG 748
QY 101 CysGlnValSerGlnCysValSerSerProPheTrpCysGlnProCysLeuAspCys 120

Db 749 TCCAGGTACGCATGTGTAGCAGTTCACCTTCTACTCCCAACCATGCTAGACTGC 808
QY 121 GlyAlaLeuHisArgHisThrArgLeuPheCysSerArgAspPheAspCysGlyThr 140
Db 809 GGGGGCTGTGACCGGCACACAGGCTACTGTGTCCGCAAGATGACTGTGGAGCC 868
QY 141 CysLeuProGlyPheTrpGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 869 TGCCTGCTGCTGTGTGAAACATGGGATGGCTGCTGCTGCCACCTAATTCCTA 928
QY 161 GlySerCysProGluArgCysAlaValCysGlyTrpArg 174
Db 929 -----GCTGTCTGGGATGGAGG 946
RESULT 12
US-09-884-733-5
Sequence 5, Application US/09884733
Patent No. US20020123116A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 Ligand Inhibitor
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/884,733
FILING DATE: 19-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/304,003
FILING DATE: 14-JUNE-2000
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-884-733-5
Alignment Scores:
Pred. No.: 1.14e-89 Length: 1438
Score: 950.00 Matches: 163
Percent Similarity: 93.68% Conservative: 0
Best Local Similarity: 93.68% Mismatches: 3
Query Match: 91.52% Indels: 8
DB: Gaps: 1
US-09-993-234-6_COPY_25_198 (1-174) x US-09-884-733-5 (1-1438)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 449 CAGGGGGGCGACTGTAGCCCGCAGAGGTGTACTGTGGTACTTCCACAAGAGATTGGT 508

QY 21 LeuphcyScyArGgLyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
 DB 509 CTGTTTGTTCAGACAGCGCCGACCGGGGACATACCTGAAGGCCCTTTCACACGAGCC
 QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGlnAsnHis 60
 DB 569 TGGCGCAACTCCACTGCTGTGTGTGCCAAGACACCTTCTGGCTGGGAGAAACAC
 QY 61 HisAsnSerGlyCysAlaArgCysGlnAlaCysAspGlnGlnAlaSerGlnValAlaLeu 80
 DB 629 CATAAATCTGAATGTGCCCGCTGCCAGGCCCTGTATGACGAGGCCCTCCACAGTGGCGT
 QY 81 GluAsnSerSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
 DB 689 GAGAACTGTTCAGACAGCGCCGACACCCGCTGTGTATGACGAGCGCTGTTCGTGAG
 QY 101 CysGlnAlaSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
 DB 749 TGGCAGGTCAACCAATGTGTACAGATTCACCTTCTACTCCCAACCATGCTGACTGC
 QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgAspThrAspCysGlyThr 140
 DB 809 GGGGCCCTGCACCGCCACACACGCGCTACTCTGTCCCGACAGATGACTGTGGACCC
 QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
 DB 869 TGCCTGCGCTGCTCTATGAACATGCGCATGCGTGCCTGCCACCACTAATTCCTA 928
 QY 161 GlySerCysProGluArgCysAlaValCysGlyTyrPheValGlu 174
 DB 929 -----GCTGCTCGTGGATGAGG 946

RESULT 13
 US-09-993-234-5
 : Sequence 5, Application US/09993234
 : Patent No. US20020146768A1

GENERAL INFORMATION:
 : APPLICANT: Ashkenazi, Avi J.
 : TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
 : NUMBER OF SEQUENCES: 11
 : CORRESPONDENCE ADDRESS:

: ADDRESSEE: Genentech, Inc.
 : STREET: 460 Point San Bruno Blvd
 : CITY: South San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94080

: COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: WinPatIn (Genentech)
 : CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/993,234
 : FILING DATE: 19-NO. US20020146768A1-2001
 : CLASSIFICATION: <Unknown>
 : PRIOR APPLICATION DATA:

: APPLICATION NUMBER: 08/828,683
 : FILING DATE: <Unknown>
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Marschang, Diane L.
 : REGISTRATION NUMBER: 35,600
 : REFERENCE/DOCKET NUMBER: P1007P1
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 415/225-5416
 : TELEFAX: 415/952-9881
 : TELEX: 910/371-7168

: INFORMATION FOR SEQ ID NO: 5:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1438 base pairs
 : TYPE: Nucleic Acid
 : STRANDEDNESS: Single
 : TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-993-234-5

Alignment Scores:
 Pred. No.: 1,14e-89 Length: 1438
 Score: 930.00 Matches: 163
 Percent Similarity: 93.68% Conserved: 0
 Best Local Similarity: 93.68% Mismatches: 3
 Query Match: 91.52% Indels: 8
 DB: 10 Gaps: 1

US-09-993-234-6_COPY_25_198 (1-174) x US-09-993-234-5 (1-1438)

QY 1 GlnGlyLysThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
 DB 449 CAGGCGGCACTCCAGGCCAGGTGACCTGTGCCGTGACTTCCACAGACAGTTGCT 508
 QY 21 LeuphcyScyArGgLyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
 DB 509 CTGTTTGTTCAGACAGCGCCGACCGGGGACATACCTGAAGGCCCTTTCACACGAGCC 568
 QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGlnAsnHis 60
 DB 569 TGGCGCAACTCCACTGCTGTGTGTGCCAAGACACCTTCTGGCTGGGAGAAACAC 628
 QY 61 HisAsnSerGlyCysAlaArgCysGlnAlaCysAspGlnGlnAlaSerGlnValAlaLeu 80
 DB 629 CATAAATCTGAATGTGCCCGCTGCCAGGCCCTGTATGACGAGGCCCTCCACAGTGGCGT 688
 QY 81 GluAsnSerSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
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 QY 101 CysGlnAlaSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
 DB 749 TGGCAGGTCAACCAATGTGTACAGATTCACCTTCTACTCCCAACCATGCTGACTGC 808
 QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgAspThrAspCysGlyThr 140
 DB 809 GGGGCCCTGCACCGCCACACACGCGCTACTCTGTCCCGACAGATGACTGTGGACCC 868
 QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
 DB 869 TGCCTGCGCTGCTCTATGAACATGCGCATGCGTGCCTGCCACCACTAATTCCTA 928
 QY 161 GlySerCysProGluArgCysAlaValCysGlyTyrPheValGlu 174
 DB 929 -----GCTGCTCGTGGATGAGG 946

RESULT 14
 US-10-092-154-1577
 : Sequence 1577, Application US/10092154
 : Publication No. US20030054375A1

GENERAL INFORMATION:

: APPLICANT: Rosen et al.
 : TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 : FILE REFERENCE: PC00931

: CURRENT APPLICATION NUMBER: US/10/092,154
 : CURRENT FILING DATE: 2002-03-07

: NUMBER OF SEQ ID NOS: 2003
 : Prior Application removed - See file Wrapper or Palm
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 1577

: LENGTH: 10797
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-10-092-154-1577

Alignment Scores:
 Pred. No.: 1,29e-66 Length: 10797
 Score: 738.00 Matches: 161
 Percent Similarity: 39.95% Conserved: 0
 Best Local Similarity: 39.95% Mismatches: 5

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			Gaps:	4
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Db	5268 CAGGGGGGACGTCGAGGCCAGGGGTGACGTCTCCGGTACCTTCCAGAAAGATTGGT			5322
0Y	21 LeuPheCysAlaGlyCysProAla-----			29
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0Y	29 -----			29
Db	5388 GCAGGCAGGGCTGGAGAGGTGGCGGCGAGGCCGGGAGGTAAAGAGAGGCTGGCAGGGGA			5447
0Y	29 -----			29
Db	5448 GGTAGGGGTAGGCTGCACAGAGATAGGAGAGCTGGAGAGAAAGAGGAGAGGCGAGGG			5507
0Y	29 -----			29
Db	5508 TGGAAAGCAGGCTCGGGGGGTGCTGGGAGGCCCTTGCTGCTGCACCCCTGGCTGTTC			5567
0Y	30 ----GlyHisIyIleuIysAlaProCysThrGluProCysGlyAsnSerThrCysIeuVa			48
Db	5568 CACAGGGGACTACCTGAAAGGCCCTTGACAGAGACCCTGGGGCAACTCCACTGGCTGT			5627
0Y	48 ICysProGlnAspThrPheIeuAlaTTPGluAsnHisIAsnSerGluCysAlaArgCy			68
Db	5628 GTGTCCCAACACACCTTTGGCTGGGAGAACCAACATAATTGTGATGTGCCCGCG			5687
0Y	68 sGlnIlaCysAspGlu-----			73
Db	5688 CCAGGCTGTGATAGCAGGGGTGAGGGCTTTCACAGTCTTGCGCAGGAGTTCTTAAGA			5747
0Y	73 -----			73
Db	5748 CAGGCTTTTGAAAGAAAGTGGCTGGCTGGGGCCAAACTTGGGGTGTAGAGGTCTTGA			5807
0Y	73 -----			73
Db	5808 CCCACCTTGCAGAACCTTCACACCTGATCTCTTTCAGAGGTGCCCTTGCCCTTCTCT			5867
0Y	73 -----			73
Db	5868 CTTCCTGGTGACCTTCCCACTCTCCATGTGCTTGCCCTTGCTGGTGGCCCTTAATCTCG			5927
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Db	5928 AGCTTCTCTCTTTTATAGGGTAGCCCTGTACCTGTCTGTCTTTCGGCTATTCTGTCTCC			5987
0Y	73 -----			73
Db	5988 ATTATCTTGGGATATAGCTCTGTGCTCTCCATGGAGACCTTGGCCCTGACTAATCTCC			6047
0Y	74 -----GlnIlaSerGlnValAlaIleuGluAsnCysSerAl			85
Db	6048 ACTGCCCATCTCCCTGCAGCCGCCACCAAGCC-TCACAGGTGGCGCTGGAGAACTGTCTAGC			6106
0Y	85 aValAlaAspThrArgCysGlyCysLysProGlyTTPheValGluCysGlnValSerG1			105
Db	6107 AGTGGCCGAGACCCGGTGTGGCTGTAAAGCCAGAGCTGGTGTGGAGTGCAGAGTACGCA			6166
0Y	105 nCysValSerSerSerProPheIyIyCysGlnProCysIleuAspCysGlyAlaIleuHisAr			125
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0Y	125 gHisThrArgLeuIleuCysSer-----			132
Db	6227 CCACACACGGCTACTCTGTGA-CTACCCCCACCAAGGGCTCTTACTCTCCAGAACCCCTTT			6285

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Patent No. US20020132767A1			
GENERAL INFORMATION:			
APPLICANT: Rosen et al.			
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies			
FILE REFERENCE: PC009			
CURRENT APPLICATION NUMBER: US/09/764,847			
Prior application data removed - consult PALM or file wrapper			
NUMBER OF SEQ ID NOS: 2003			
SOFTWARE: Patentia Ver. 2.0			
SEQ ID NO 1577			
LENGTH: 10797			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-09-764-847-1577			
Alignment Scores:			
Pred. No.: 1,29e-66			
Score: 738.00			
Length: 10797			
Matches: 161			
Conservative: 0			
Mismatches: 5			
Indels: 239			
Gaps: 4			
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QY	1	GlnlgllylthrrarSerProArgCysaspCysalaGlyaspPheHnlsLysIleGly	20
Db	5268	CAGGGCGGCACTGTACCCCCAGAGTGTGACTGTGCGGTGACTTCACAAAGATGTGT	5327
QY	21	LeupheCysysArtrGlyCysProAla-----	29
Db	5338	CTGTTTGTTCAGAGGCTGCGCCAGGGGTAAAGTGACACAGGGGTGGAGAGCATGGG	5387
QY	29	-----	29
Db	5388	GCAAGCAGGGCTGAGAGAGTGGCGGCGAGCCCGGAGGTAAAGAGAGAGGCTGGCAGGGGA	5447
QY	29	-----	29
Db	5448	GGTAGGGGTAGCTGACAGAGAAAGTAAAGAGCTGGAGAGAAAGAGGAGGAGCAAGG	5507
QY	29	-----	29
Db	5508	TGGAAAGCAGGTGGGGGTTTCTGGGCGAGCCCTTGCCTGCTGACCCCTGCTGTTTC	5567
QY	30	---GlyHnlsTyrlleuLysalaProCysThrGluProCysglYasnSerThrCysLeuA	48
Db	5568	CACAGGGCACTACTGTAAGGCCCTTGGCAGCGAGGCCCTGGCGCAACTCTGCTTGT	5627
QY	48	lCysProGluAspThrPheLeuAlaTrpGluAsnHnlsHsAsnSerGlyCysalaArgCy	68
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QY 68 sGlnAlaCysAspLys----- 73
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Db 5688 CCAGGCTGTGATGAGCAGGGGTGAGGGCTTCAGTGCCTTGCGAGGAGTTCTTAAGA 5747
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Db 5808 CCCACCTTGCGAGAACCTCCACCTGATTCCTTCAGGGTGCCTTGCCCTTCTCT 5867
QY 73 ----- 73
Db 5868 CTTCCTGTGACCTTCCCATCTCTCATGTCCTTGCGCTGTGGGCTTAATCTCTG 5927
QY 73 ----- 73
Db 5928 AGCTTCTCTTTTAAAGGTAGCCCTGTACCTGTCTGTCTTCGCTATTCTGTCTCC 5987
QY 73 ----- 73
Db 5988 ATTATCTGGATATAGCTCTGTGCTCTCCATGGAGCCTTGGCCCTGACTAATCTCC 6047
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QY 85 aValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGluCysGlnValSerG1 105
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Db 6107 AGTGGCCGACACCCGCTGTGCGCTGTAAAGCAGCGCTGTGTGGAGTGCAGGTACAGCA 6166
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Db 6167 ATGTGTACAGCAGTTCACCTTCTACTGCAACATGCTAGACTGCGGGGCCCTGCACCG 6226
QY 125 gHisThrArgLeuLeuCysSer----- 132
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Db 6227 CCACACACGGGTACTGTGTGA-GTACCCCAACCCAGGGCTCTCTAATCCAGACCCCTT 6285
QY 132 ----- 132
Db 6286 CTCCCTGCTGACCCACTCTCTGCCAATGATGACGCAATGCCCTTCCTGGAATTGCAGGTTTC 6345
QY 133 -ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCy 152
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Run on: April 6, 2003, 16:19:54 ; Search time 1088.39 seconds

(without alignments)

2589.161 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_198

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Scoring table: BIOSUM62

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
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2	1019	98.2	632 9	AW268610
3	1014	97.7	688 9	AI242936
4	1009	97.2	698 9	AI807913
5	979	94.3	562 9	AI140043
6	950	91.5	552 14	BM783972
7	950	91.5	585 10	AW517358
8	941	90.7	565 14	BM744307
9	937	90.3	514 14	BM756372
10	937	90.3	514 14	BM783979
11	932	89.8	492 14	BM741016
12	916	88.2	508 9	AI203624
13	893	86.0	488 14	BM770798
14	862	83.0	1010 14	BC068309
15	798.5	76.9	478 10	AM002222
16	781	75.2	427 12	BE696572
17	680	65.5	422 9	AI700459
18	666	64.2	433 14	HA1522
19	639	61.6	572 10	BE668836
20	591	56.9	432 14	N71143
21	580.5	55.9	434 14	BM826048
22	517	49.8	345 9	AA934992
23	516.5	49.8	443 14	HA6211
24	470.5	45.3	755 13	BI655045
25	461	44.4	468 14	HA6374
26	443	42.7	673 13	BM251737
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31	395.5	38.1	639 10	BB636341
32	389.5	37.5	393 14	HA1851
33	360.5	34.7	418 14	HA6662
34	323	31.1	397 14	HA6378
35	296	28.5	246 14	HA46424
36	292	28.1	246 14	HA19739
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43	209.5	20.2	775 13	BI555040
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION 603065172F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214568 5',
ACCESSION BI909448
VERSION BI909448.1 GI:16172666
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 767)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMN at:
http://image.llnl.gov
Plate: LAM1538 row: o column: 17
High quality sequence stop: 754.
Location/Qualifiers
1. 767
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5214568"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: PCMV-SPORE6; Site-1: NotI; Site-2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

BASE COUNT 122 a 243 c 241 g 161 t
ORIGIN

Alignment Scores:

Score: 1,11e-88 length: 767
Percent Similarity: 1025.00 Matches: 174
Best Local Similarity: 99.43% Conservative: 0
Query Match: 98.75% Mismatches: 0
Indels: 1
Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x B1909448 (1-767)

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OY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisTyrIleGly 20
Db 109 CAGGGGGGCGACTGTGAGCCCGAGGTGACTGTGCGGGGACTTCCACAAGAGATTGG 168
OY 21 LeuPheCysAspArgGlyCysProAla-GlyHisTyrLeuLysAlaProCysThrGlu 40
Db 169 CTGTTTGTGTCAGAGGCTGCGCAGCTGAGGCGACTGAAAGCCCTTCGACGAGCC 228
OY 40 OCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGlnAsn 60
Db 229 CTGGCGCACTCCACTGCTGTGTGTCGCCAAGACACTTCTTGCTGGAGAACCA 288
OY 60 SHAsnSerGlyCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLe 80
Db 289 CCAATATTGTGATGTGCGCGCTGCGCAGGCTGTGTGAGCAGGCTCCAGGTGGCGCT 348
OY 80 uGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheVal 100
Db 349 GGAGAACTTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAAGCCAGGCTGTTGTGA 408
OY 100 uCysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAsp 120
Db 409 GTGGCAGGTCACAGTGTGTCAGCAGTTCACCCCTTACTCCCAACATGCTTGA 468
OY 120 sGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgAspThrAspCysGly 140
Db 469 CGGGGCGCTGCACCGCACACAGGCTACTGTGTCCGCGAGATTAAGTGTGGGAC 528
OY 140 rCysLeuProGlyPheTyrGlyHisGlyAspGlyCysValSerCysProThrSer 160
Db 529 CTGGCTGCTGCTTCTTATGAACATGCGAGTGGCTGTGCTGCTGCCACGAGACCT 588
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OY 160 uGlySerCysProGlnArgCysAlaValAlaCysGlyTyrParg 174
Db 589 GGGAGCTGTCCAGAGCGCTGTGCTGTGCTGTGCTGAGG 631

RESULT 2
AM268610
LOCUS
DEFINITION
AM268610 632 bp mRNA linear EST 03-JAN-2000
xv41b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2815679.3 similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PREDICOROR ; mRNA sequence.
ACCESSION
AM268610
VERSION
AM268610.1 GI:6655640
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
This clone is available royalty-free through LMN; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -400P from gibco
High quality sequence stop: 455.
Location/Qualifiers
1. 632
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2815679"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pTZ19-Pac (Pharmacia) with
a modified polylinker; Site-1: Not I; Site-2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19, testis NHT, and B-cell
NCL-CGAP-GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo.

FEATURES

BASE COUNT 102 a 194 c 192 g 143 t 1 others
ORIGIN

Alignment Scores:

Score: 3.16e-88 length: 632
Percent Similarity: 1019.00 Matches: 172
Best Local Similarity: 98.85% Conservative: 0
Query Match: 98.85% Mismatches: 2
Indels: 0
Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x AM268610 (1-632)

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OY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisTyrIleGly 20
Db 27 CAGGGGCGCACTGTGAGCCCGAGGTGACTGTGCGGTGCTTCCACAAGAGATTGG 86
OY 21 LeuPheCysAspArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGlu 40
Db 87 CTGTTTGTGTCAGAGGCTGCGCAGCGGGGCACTAAGGAGGCGCTTGCACGAGACC 146
OY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGlnAsn 60
```

D	b	147	TGCGGCAACGTGCAGCTGGCTTGTGTGTGCCAAGACACTTTTGCCCTGGGAGAACAC	206
O	y	61	HISANSERGLUCYGAATATGCGSGLNALACYSAAPGLUGINALLASERGINVALALEU	80
D	b	207	CATAATTTCGTAATGATGCCCCGTGCCAGGCTGTGTATGAGAGGCCCTCCAGATGGCCTG	266
O	y	81	GIUANCYSSERLALAVALLASPRTARCYSGLYSCYSPROGLYTIRPHEVALGU	100
D	b	267	GAGAACITTTACAGCAGTGGCCGACACCCTGCTGTGGCTTAAGCCAGCTGGTTGTGAG	326
O	y	101	CysglnValSerGlnCysValSerSerProPheTYrGlnProCysLeuAspCys	120
D	b	327	TGCCAGGTCCAGCCAAATGTGTGACAGTTCCACCTTCCTACTGCCAACCATGCTGACATGC	386
O	y	121	GLYALAIEUNHISARGHSHTHRArgleueuencysSerArgArgAspTHRAspCysglythr	140
D	b	387	GGGGCCCTGCACCGCACACAGGCTACTGTGTCCGCAAGATACTGACTGTGGACC	446
O	y	141	CysLeuProGlyPheTYrGlnHisglYaspGlyCysValSerCysProThrSerThreu	160
D	b	447	TGCCGTGCCTGGCTTGTANGAACATGGCATGGATGGATGTGTCTCTGGCCACAGACACNCTG	506
O	y	161	GlySerCysProGluArgCysAlaAlaValCysglYTPRag	174
D	b	507	GGGACCTGTGCAGACCGCTGTGCCGCTGTCTGTGCTGTGAGG	548
R	E	S	RESULT 3	
L	O	A1424936	LOCUS	
D	E	A1424936	DEFINITION	688 bp mRNA linear EST 30-MAR-1999
A	C	A1424936	VERSION	tq19db08.x1 NCI_CGAP_CL11 Homo sapiens CDNA clone IMAGE:2109207 3'
K	E	A1424936	KEYWORDS	Similar to TR:000276 000276 LYMPHOCTYTE ASSOCIATED RECEPTOR OF DEATH
S	O	A1424936	EST.	2. /, mRNA sequence.
O	R	human.	ORGANISM	
E	A	Homo sapiens	REFERENCE	
A	T	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	AUTHORS	
T	I	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	TITLE	
J	O	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	JOURNAL	
C	O	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	COMMENT	
M	E	Tumor Gene Index		
E	N	Unpublished (1997)		
N	O	Contact: Robert Strausberg, Ph.D.		
T	I	Email: cgaaps-remail.nih.gov		
E	N	Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,		
N	O	M.D., Louis M. Staudt, M.D., Ph.D.		
T	I	CDNA Library Preparation: M. Bento Soares, Ph.D.		
E	N	CDNA Library Arrayed by: Greg Lennon, Ph.D.		
N	O	DNA sequencing by: Washington University Genome Sequencing Center		
T	I	Clone distribution: NCI-CGAP clone distribution Information can be		
E	N	found through the I.M.A.G.E. Consortium/LIML at:		
N	O	www-bio.llnl.gov/dbrrp/image/image.html		
T	I	Insert length: 2028 Std Error: 0.00		
E	N	Seq primer: -40UP from Glbpco		
N	O	High quality sequence stop: 445.		
T	I	Location/Qualifiers		
E	N	1..688		

BASE COUNT	113 a	208 c	229 g	138 t
ORIGIN	Scores and M. Fatima Bernaldo.			
Alignment Scores:				
Pred. No.:	1,09e-87	Length:	688	
Score:	1014.00	Matches:	171	
Percent Similarity:	98.85%	Conservative:	1	
Best Local Similarity:	98.28%	Mismatches:	2	
Query Match:	97.69%	Indels:	0	
DB:	9	Gaps:	0	
US-09-993-234-6_COPY_25_198 (1-174) x A1424936 (1-688)				
OY	1	g1ng1gyltYthArGSeTProArGcYsaRcYsaLaG1aYsaRPhn1aLys1l1eG1y	20	
Db	65	CGGGCGGGACACTCGTACGCCCCAGTGTGACTGTGCGGGTACTTCCACAGAAATTTGGT	124	
OY	21	LeuPhicYcYsaArG1yCySaPrOlaAG1yH1sYtTLeuYsaLaRProCYsThG1uPro	40	
Db	125	CTGTTTGTGTGGAGAGGGTCCCGACGGGGGCACTCCATGAAGGCCCTTGGACGGAGGCC	184	
OY	41	CYsG1YAsnSerThCYsLeuValCYsProG1nAsPrtPhLeuAlATrG1uAsnH1s	60	
Db	185	TCCGGCACTCCACCTGCTTGTGTGTCGCCACAGACACTTCTTGCTGGGAGAACAC	244	
OY	61	H1sAsnSerG1uCYsaLaArGcYsG1n1aCYaSPR1uG1n1aSerG1nValaLaLeu	80	
Db	245	CATATTTCTGATGTGCGCGGTGCCAGGGCTGTGATGAGCAGGCTCCAGGTGGCGCTG	304	
OY	81	GlUaSnCYsSerAlaValAlaSPHrArGcYsG1yCYsLysPRoG1YTTPheVal1u	100	
Db	305	GAGAACTGTTCAGCAGTGGCCGACACCGGCTGTGCTGTAA6CCAGGCTGTGTGGAG	364	
OY	101	CYsG1nValSerG1aCYsaLaserSerSerProPhetYrCYsG1nPRoCYsLeuAsPCys	120	
Db	365	TCCAGAGTCCAGCAATGTGTCTGACGAGTTCACCTTCTTACTGCCAACCACTTGCCTAGACTGC	424	
OY	121	g1YalAlaLeuH1sArG1H1sThrArGLeuLeuCYsSerArGArGAsPrtPhrAsPCysG1Ythr	140	
Db	425	GGGGCCCTTGCACCGGCACACAGGGCTACTGTGTCCCGAGAGTACTGAGTGGAGCC	484	
OY	141	CysLeuPRoG1YPhetYrG1nH1sG1yAsrG1yCYsValSerCYsPRoThSerThLeu	160	
Db	485	TCCCGTCCGTGTGTATGAACTATGCGCATGGCTCAGTGTCTGTGCCACGAGCACCCTG	544	
OY	161	GlYSerCYsPRoG1uArGcYsaLaLaValaCYsG1YTTParG	174	
Db	545	GGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGGCTTGAGG	586	
RESULT 4				
LOCUS	A1807913	698 bp	mRNA	linear
DEFINITION	v5f2c03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone			
VERSION	IMAGE:235204.3, similar to SW:WSLI_HUMAN Q93038 WSL-1 PROTEIN			
KEYWORDS	PRECURSOR ; mRNA sequence.			
ACCESSION	A1807913			
VERSION	A1807913.1			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
TITLE	NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap.			
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
COMMENT	Tumor Gene Index			
	Unpublished (1997)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cga@bcrfemail.nih.gov			
	This clone is available royalty-free through LNL ; contact the			
	IMAGE Consortium (info@image.lnl.gov) for further information.			
	Insert Length: 1568 Std Error: 0.00			


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|||||
Db 305 GAGAACTGTTGACGAGTGGCCGACACCCGCTGTGCTGTAAAGCCAGGGTGTGTGGAG 364
Qy 101 CysGlnValSerGlnCysValSerSerProPheTYrCysGlnProCysLeuAspCys 120
Db 365 TGGCAGGTGACGCAATGTGTGACAGATTACACCTTTCTACTCCAAACATGGCTGAGACG 424
Qy 121 GtAlaLeuHisArgHisArgLeuLeuCysSerArgArgAspPheAspCysGlyThr 140
Db 425 GGGGCCCCGACCCGACACACAGCGCTACTGTCTCCGACAGATAGTACTGTGGACC 484
Qy 141 CysLeuProGlyPheTYrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 485 TGGCTGGCTGGCTCTGTATGAACATGGCGATGGCTGCTGCTCCGACAGACCCCTG 544
Qy 161 GlySerCysProGluArg 166
Db 545 NGAGAGCTGTCCAGAGCCG 562

RESULT 6
BM783972 / BM783972 552 bp mRNA linear EST 05-MAR-2002
LOCUS R-EST0062019 S6SNU620 Homo sapiens cDNA clone S6SNU620-31-H06 5',
DEFINITION mRNA sequence.
ACCESSION BM783972
VERSION BM783972.1 GI:19132204
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 552)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
CONTACT: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsungemail.kr@kb.re.kr
Plate: 31 row: H column: 06
High quality sequence stop: 552.
Location/Qualifiers
1..552
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-31-H06"
/clone_1id="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/lab_host="SNU-620"
/notes="Organ: Stomach; Vector: pCNS; Site:1: EcoRI;
Site:2: NotI. The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP). The decapped
with tabacco acid pyrophosphatase (TAP). The decapped
Intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10f by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
```

```
BASE COUNT 92 a 172 c 173 g 115 t
ORIGIN
Alignment Scores:
Pred. No.: 1,15e-81 Length: 552
Score: 950.00 Matches: 163
Percent Similarity: 93.688 Conservative: 0
Best Local Similarity: 93.688 Mismatches: 3
Query Match: 91.528 Indels: 8
DB: 14 Gaps: 1

US-09-993-234-6_COPY_25_198 (1-174) x BM783972 (1-552)
Qy 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 38 CAGGCGGACACTCGTAGGCCGCCAGGTGTGACTGTGCCGGGTGACTTCACAAAGATGTGT 97
Qy 21 LeuPheCysArgGlyCysProAlaGlyHisTYrLeuLysAlaProCysThrGluPro 40
Db 98 CTGTTTGTTCAGAGCGCTGCCACGCGGCGCACTACCTGAAGGCCCTTTCACGAGGCC 157
Qy 41 CysGlnAsnSerThrCysLeuValCysProGlnAspPheLeuAlaTropGluAsnHis 60
Db 158 TGGCGCAACTCCACCTGCTGTGTGTGTCTCCCAAGACACTTCTTGCTGGAGAACAC 217
Qy 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 218 CATATTCGTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTGGCGCTG 277
Qy 81 GluAsnCysSerAlaValAlaAspPheArgCysGlyCysLysProGlyTYrPheValGlu 100
Db 278 GAGAACTGTCAGACGTGGCCGACACCCGCTGTGCTGTAAACCCAGCTGTGTGTGGAG 337
Qy 101 CysGlnValSerGlnCysValSerSerProPheTYrCysGlnProCysLeuAspCys 120
Db 338 TGGCAGGTGACGCAATGTGTGACAGAGTTCACCTTCTTACTGCCAACATGCTTACACTGC 397
Qy 121 GtAlaLeuHisArgHisArgLeuLeuCysSerArgArgAspPheAspCysGlyThr 140
Db 398 GGGGCCCCGACCCGACACAGCGGTACTGCTTCCCGACAGATAGTACTGTGGAGCC 457
Qy 141 CysLeuProGlyPheTYrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 458 TGGCTGGCTGGCTCTGTATGAACATGGCGATGGCTGCTCCGACAGATTAATTCCTA 517
Qy 161 GlySerCysProGluArgCysAlaValCysGlyTYrParg 174
Db 518 -----GCTGTCTGTGGATGGAGG 535

RESULT 7
AW517358 585 bp mRNA linear EST 03-MAR-2000
LOCUS x093g02.x1 Soares_NHCE_cervix Homo sapiens cDNA clone IMAGE:2747954
DEFINITION 3, similar to TR:000276 000276 LYMPHOCTYE ASSOCIATED RECEPTOR OF
DEATH 2. ;, mRNA sequence.
ACCESSION AW517358
VERSION AW517358.1 GI:7155440
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 585)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyA not found
```

Accession	Definition	LOCUS	Result
U00001	1 glnGlu1, 17th trpSerProAlaGlyAspCysAlaGlyAspHisLeu1ys1Leu1	1	1
U00002	65 CAGGGGGGACGTGTAGAGCCACAGGTGTGACTGTGGCGGTACTTCCACAGAAATTGGT	65	20
U00003	21 leuPhcCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro	21	40
U00004	125 CTTTGTGTGTGCAGAGGCTGCCAGGGGGGCACTACTTGAAGGCCCTTGCACGGAGGCC	125	184
U00005	41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis	41	60
U00006	185 TCGCGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTTCTTGGCTGTGGGAACAC	185	244
U00007	61 HisAsnSerGlnCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu	61	80
U00008	245 CATTAATTCGAATGTGCCGCTGCCAGGCTGTGAAGACAGAGCTTCCAGTGGCGCTG	245	304
U00009	81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu	81	100
U00010	305 GAGAACTGTTCAGAGGTGCCAGACACCCCTGTGGCTGTGAAGCAGAGCTGTGTGGAG	305	364
U00011	101 CysGlnValSerGlnCysValSerSerSerProPheTrpCysGlnProCysLeuAspCys	101	120
U00012	365 TCCCAAGGTCAGGCATGTCTCAGAGTTTCAACCTTCTACTGCCAACCAAGCTACAGTGC	365	424
U00013	121 GluAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyTrp	121	140
U00014	425 GGGGGCCCTACACGCCACACAGGCTACTCTGTTCGCCGAGAGATCTACTGTGGAGCC	425	484
U00015	141 CysLeuProGlyPheTrpGluHisGlyAspGlyCysValSerCysProThrSerThrLeu	141	160
U00016	485 TGGCGGCTGGCTGTATCAACATGAGCGCATGGCTGGTCTCTGCCGCCACGTAATTCTTA	485	544
U00017	161 GlySerCysProGlnArgCysAlaAlaValCysGlyTrpArg	161	174
U00018	545 -----GCTGTGCGGATGGAGG	545	562
U00019	BM744307	565 bp	linear
U00020	BM744307	565 bp	linear
U00021	K-EST001782 S65NMU620 Homo sapiens cDNA clone S65NMU620-17-C06 5'	EST 01-MAR-2007	
U00022	BM744307	565 bp	linear

QY 1 GInGlyGLYThrARSerProARCYAspCysAlaGLYAspPheHisLysLysLILeLY 20
|||
Db 38 CAGTGGGCACCTGTAAGCCCAAGGTGTGACTGTCCGGTGACTTCCACAAGAAGATTGGT 97

QY 21 LeuPheCYsAArgLYCYAsProAlaGLYHisTyrLeuLysAlaProCysThrILuPro 40
|||
Db 98 CTGTGTTTGTGGAGAGCGTGGCCAGCGGGGCGACTACTCTAAGGCCCTTTGCCACGGAGGCC 157

QY 41 CysGLYAsnSerThrCYsLeuValCYsProGLInAsPThrPheLeuAlaTrpGLYAsnHis 60
|||
Db 158 TGGGGCAACTCCACTGCGCTTGTGTGTGCCAAGACACTTTGTGGCGCTGGGAGAACAC 217

Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 32 row: A column: 05
High quality sequence stop: 514.

FEATURES

Location/Qualifiers
1. 514
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="S6SNU620-32-A05"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pcNS; Site: 1: EcoRI; Site: 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT
ORIGIN

86 a 166 c 153 g 109 t

Alignment Scores:

Pred. No.: 1.85e-80 Length: 514
Score: 937.00 Matches: 157
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.27% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x BM783979 (1-514)

OY 1 GINGLGLYThrArgSerProArgCysAspCysAlaGlyAspPheHisIstysIleGly 20
DB 38 CAGGGGGGCACTGTAAGCCCAAGGTGTGACTGTGCGGTGACTTCCACAAGAGATTGGT 97
OY 21 LeuPheCysAspArgIstysCysProAlaGlyHisIstysIleuIstysAlaProCysThrGluPro 40
DB 98 CTGTTTGTGGAGAGCGCGCCAGGGGGCACTACTGTAAGCCCTTGCACGGAGGCC 157
OY 41 CysGlyAspSerThrCysIleuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 158 TCGGGCAATCCACCTCTGTGTGTCCCAAGACACCTTCTGCGTGGGAGAACAC 217
OY 61 HisAspSerGlnCysAlaArgCysGlnAlaCysAspGlnAlaSerIleuValAlaIleu 80
DB 218 CATTAATTCGATGTGCGCGCTGCGCCAGGCTGTGATGACAGGCTCCAGGTGGCGCTG 277
OY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysIstysProGlyTrpPheValGlu 100
DB 278 GAGAACTGTTACAGAGTGGCCGACACCCGCTGTGGCTGTAAACCGAGCGTGTGGAG 337
OY 101 CysGlnValSerGlnCysAlaSerSerProPheTrpCysGlnProCysLeuAspCys 120
DB 338 TCCAGGCTCAGCAATGTGTGACAGTTCCACCTTCTACTGCCAACCATGCTTACAGCTGC 397
OY 121 GlyAlaLeuHisArgHisThrArgLeuIstysCysSerArgArgAspThrAspCysGlyThr 140
DB 398 GGGGGCCCTGACACCGCACACAGGCTACTCTGTCCCGAGAGATACGTACTGTGGAGCC 457
OY 141 CysIleuProGlyPheTrpGluHisIstysAlaGlyCysValSerCysProThr 157

DB 458 TGCCCTGCTGCTCTTCTATGAAACATGCGATGCTGCTGTCTGCCACG 508

RESULT 11
LOCUS
DEFINITION

BM741016 492 bp mRNA linear EST 01-MAR-2002
K-EST0013376 S6SNU620 Homo sapiens cDNA clone S6SNU620-2-C03 5',
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BM741016
BM741016.1 GI:19062345
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 492)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS

COMMENT

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 2 row: C column: 03
High quality sequence stop: 492.
Location/Qualifiers

FEATURES
source

1. 492
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-2-C03"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNR-620"
/lab_host="Top10F"

/note="Organ: Stomach; Vector: pcNS; Site: 1: EcoRI; Site: 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 85 a 157 c 146 g 104 t

ORIGIN

Alignment Scores:

Pred. No.: 5.26e-80 Length: 492
Score: 932.00 Matches: 156
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 89.79% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x BM741016 (1-492)

OY 2 GINGLGLYThrArgSerProArgCysAspCysAlaGlyAspPheHisIstysIleGlyIleu 21
DB 19 GCGGCACTGTAAGCCCAAGGTGTGACTGTGCGGTGACTTCCACAAGAGATTGGTCTG 78

QY 22 PhecycysatrggIyCysProAlaGlyHstTyrLeuLysAlaProCysThGluProCys 41
|||||
Db 79 TTTGTTGCAAGAGGCTGCCAGCGGGGACATGAAAGCCCTTGCACGAGCCCTGC 138
QY 42 GlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 61
|||||
Db 139 GGCATCTCCACTGCTTGTGTGTCCCAAGACCTTCTTGGCTGGGAAACACCAT 198
QY 62 AsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 81
|||||
Db 199 AATTCTGAATGTGCCCTGCGAGGCTGTGATAGCAGGCTCCAGAGTGGCTGGAG 258
QY 82 AsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGluCys 101
Db 259 AACTGTCAGAGTGGCGACACCGCTGTGCTGTAGCAGAGCTGTTGTGGAGTGC 318
QY 102 GlnValSerGlnCysValSerSerProPheThrCysGlnProCysLeuAspCysGly 121
Db 319 CAGGTCAAGCCAAATGTTCAGAGTTCACCCCTTCTACTGCAACCATGCTGAGCTGCGGG 378
QY 122 AlaLeuHisArgHisThrArgLeuLeuLeuCysSerArgArgAspThrAspCysGlyThrCys 141
Db 379 GCCCTGCACCGCCACACAGCGCTACTGTTCCCGCAGAGTACTGACTGTGGACCTGC 438
QY 142 LeuProGlyPheThrGluHisGlyAspGlyCysValSerCysProThr 157
Db 439 CTGCTGCTCTATGAACATGAGGATGGCTGCTGCTGCCCGCAGC 486
RESULT 12
AI203624 508 bp mRNA linear EST 29-OCT-1998
LOCUS AI203624
DEFINITION g675f02.x1 Soares-fetal_lung_NbH19w Homo sapiens cDNA clone
IMAGE:174827 3' similar to SW:MSL1_HUMAN 093038 MSL-1 PROTEIN
PRECURSOR ; mRNA sequence.
ACCESSION AI203624
VERSION AI203624.1 GI:3756230
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 508)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1699 Std Error: 0.00
Seq primer: -400P from Glbco
High quality sequence stop: 442.
FEATURES
Source Location/Qualifiers
1. 508
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:174827"
/clone_lib="Soares-fetal_lung_NbH19w"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: pT73D (Pharmacia) with a
modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTCAATGAGGAGCGCCGCAATTTTCTTTTCTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares

BASE COUNT 82 a 161 c 159 g 106 t
ORIGIN
Alignment Scores:
Pred. NO.: 1.92e-78 Length: 508
Score: 916.00 Matches: 154
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.25% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_copy_25_198 (1-174) x AI203624 (1-508)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlnAlaAspPheHisLysLysIleGly 20
Db 47 CAGGGGGGACTCGTACGCCCAAGGTGTACGTGTGCGGTGACTTCCACAGAAAGTTTGGT 106
QY 21 LeuPheCysArgGlyCysProAlaGlyHstTyrLeuLysAlaProCysThrGluPro 40
Db 107 CTGTTTGTTCAGAGGCTGCCAGCGGGGCACTACTGAAGGCCCTTGCACGAGGCC 166
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 167 TCGGCAACTCCACTGCTTGTGTGTCCCAAGACACCTTCTGCGCTGGAGAACAC 226
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 227 CATATTCTGAATGTGCCCTGCGAGGCTGTGATGAGCAGGCTCCAGAGTGGCGCTG 286
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 287 GAGAACTGTTCAGCAGTGGCGACACCGCTGTGCTGTAGCCAGGCTGTTGTGGAG 346
QY 101 CysGlnValSerGlnCysValSerSerProPheThrCysGlnProCysLeuAspCys 120
Db 347 TCGCAGGTCCAAATGTTCAGAGTTCACCCCTTCTACTGCAACCATGCTGAGACTGC 406
QY 121 GlnAlaLeuHisArgHisThrArgLeuLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 407 GGGGCGCTGCACCGCCACACAGCGCTACTGTTCCCGCAGAGTACTGACTGTGGAGCC 466
QY 141 CysLeuProGlyPheThrGluHisGlyAspGlyCysValSer 154
Db 467 TGCTGTGCTCTATGAACATGAGGATGGCTGCTGCTGCCCGCAGC 508
RESULT 13
BM770798 488 bp mRNA linear EST 04-MAR-2002
LOCUS BM770798
DEFINITION K-EST0054419 S6SNU620s1 Homo sapiens cDNA clone S6SNU620s1-21-D12
5', mRNA sequence.
ACCESSION BM770798
VERSION BM770798.1 GI:19100413
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 488)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsungemail.kr@kribb.re.kr
Plate: 21 row: D column: 12
High quality sequence stop: 488.

FEATURES
SOURCE

Location/Qualifiers
1. 488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU62081-21-D12"
/clone_id="S6SNU62081"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/lab_host="Top10P"
/note="Organ: Stomach; Vector: pcns; Site: 1; EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
with tobacco acid pyrophosphatase (TAP). The deapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10P by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and
sequencing about 2,000 - 3,000 colonies in original cDNA
library, the abundant cDNAs were selected and amplified by
PCR reaction using vector region primer including T7
promotor as 5' primer and N(dR)14 as 3' primer. The PCR
products were used as template for synthesis of
biotinylated single stranded RNA by in vitro transcription
reaction. The synthesized RNA probes were hybridized with
antisense single stranded cDNAs prepared from original
library and incubated with avidin-gel. After removing
DNA-RNA hybrids by centrifuge, the substracted cDNA
libraries were constructed by transformation of the
remaining DNA into competent cells E. coli Top10P with
electroporation method."

BASE COUNT 83 a 156 c 147 g 102 t
ORIGIN

Alignment Scores:

Pred. No.: 2.98e-76 Length: 488
Score: 893.00 Matches: 150
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 86.03% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x BW707998 (1-488)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 38 CAGGGCGGACATCGTACCCAGAGGTGACTGTCGGGAGCTCCACAGAAGATTGGT 97
QY 21 LeuPheCysCysArgGlyLysProAlaGlyHisLysLysAlaProCysThrGluPro 40
DB 98 CTGTTTGTGGAGAGCGGCCAGCGGCGCACTACTCAAGCCCTTCAGCAGGAGCC 157
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 158 TCGGGGAATCCACCGCTTGTGTGTCCCAAGACACCTTGTGGCGTGGGAGAACCC 217
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 218 CATTAATTCGATGTGCGCGTCCAGGCGCTGTGATGAGCAGGCGCCAGAGTGGCGT 277
QY 81 GlyAsnGlySerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
DB 278 GAGAACTGTTCAGCAGTGGCGACACCGCTGTGCTGTAAACCGAGGCTGTGTGTGGAG 337

FEATURES
SOURCE

QY 101 CysGlnValSerGlnCysValSerSerProPheThrCysGlnProCysLeuAspCys 120
DB 338 TGCACAGGTGACACCAATGTGTACGACATTCACCTTCTACTGCAACCATGCTAGACTGC 397
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 398 GGGGCGCTGCACCGCCACACAGCGCTACTCTGTCCCGCAGAGATGACTGTGGAGCC 457
QY 141 CysLeuProGlyPheThrGluHisGlyAsp 150
DB 458 TGCCTGCTGCTGCTTCTATGAAACATGGGAT 487
RESULT 14
BQ068309
LOCUS
DEFINITION
BQ068309 1010 bp mRNA linear EST 02-APR-2002
AGENCOUNT_6794093 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5770562
5', mRNA sequence.
ACCESSION
BQ068309
VERSION
BQ068309.1 GI:19897355
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1010)
AUTHORS
NIH-MGC <http://mgc.ncl.nih.gov/>
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
<http://image.llnl.gov>
Plate: L1AM12833 row: n column: 03
High quality sequence stop: 689.

Location/Qualifiers

1. 1010
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5770562"
/clone_id="NIH_MGC_121"
/lab_host="DH10B"

/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1; NotI;
Site: 2; EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb. Insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH-MGC Library."

BASE COUNT 179 a 353 c 287 g 191 t
ORIGIN

Alignment Scores:

Pred. No.: 8.46e-73 Length: 1010
Score: 862.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.04% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x BQ068309 (1-1010)

QY 30 GlyHisLysLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCys 49
DB 50 GGGCACTACCTGAGAGGCCCTTGCAGCGAGCGCTGCGCAACTCCACCTGCTGTGTGT 109

11

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GenCore version 5.1.4.p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:28:24 ; Search time 66.3429 Seconds

(without alignments)
1816.682 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_417

Perfect score: 2209
Sequence: 1 QGCTSPRCDCAGDFHKKIG.....ERMGLDGCVEIDLRSRLQRCG 393

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 segs, 15333831 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL-frame+ p2n.model -DEV-xlh
-O/cgn2.1/USPTO.spool/US09993234/rnatc_27032003_115457_15378/app_query.fasta_1.2346
-DB-issued_Patents_NA -OFMT-fastp -SOFITX-tri -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-biosun62 -TRANS-human40.cdl
-LIST=45 -DOCALLION=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR-US09993234.@cgn1.1.116.@rnatc_27032003_115457_15378 -NCPU=6 -ICPU=3
-NO_XLPEXY -NO_MMAP -LARGEIOERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMECUT=120
-WARN_TIMECUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database :

- 1: /cgn2.6/prodata/1/lna/5A_COMB.seq.*
2: /cgn2.6/prodata/1/lna/5B_COMB.seq.*
3: /cgn2.6/prodata/1/lna/5A_COMB.seq.*
4: /cgn2.6/prodata/1/lna/5B_COMB.seq.*
5: /cgn2.6/prodata/1/lna/PCPUS_COMB.seq.*
6: /cgn2.6/prodata/1/lna/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2209	100.0	1254	3	US-08-815-469-3
2	2209	100.0	1634	4	US-08-928-069-11
3	2209	100.0	1634	4	US-08-828-683A-9
4	2209	100.0	1783	3	US-08-815-469-1
5	952	43.1	1438	4	US-08-928-069-5
6	952	43.1	1438	4	US-08-828-683A-5
7	666	30.1	433	4	US-08-928-069-2
8	393.5	17.8	1956	2	US-08-828-683A-2
9	393.5	17.8	1956	2	US-08-762-308-10
10	383.5	17.4	2440	4	US-09-513-007-1
11	371	16.8	2062	1	US-08-050-319B-24
12	371	16.8	2062	2	US-08-465-982-24

13	369	16.7	2161	3	US-09-106-038A-1	Sequence 1, Appl1
14	369	16.7	2161	4	US-09-505-250-3	Sequence 3, Appl1
15	369	16.7	2175	1	US-08-321-668-1	Sequence 1, Appl1
16	369	16.7	2175	1	US-08-837-941-1	Sequence 1, Appl1
17	369	16.7	2175	1	US-08-126-016-1	Sequence 1, Appl1
18	369	16.7	2175	4	US-08-054-970-1	Sequence 1, Appl1
19	227.5	10.3	1724	5	PCT-US96-12374-1	Sequence 1, Appl1
20	226.5	10.3	1724	4	US-08-509-024-1	Sequence 1, Appl1
21	226.5	10.3	1724	4	US-09-333-279-1	Sequence 1, Appl1
22	214	9.7	1202	4	US-08-804-166-3	Sequence 3, Appl1
23	214	9.7	1202	4	US-08-910-991-3	Sequence 3, Appl1
24	213.5	9.7	6889	1	US-08-286-740-2	Sequence 2, Appl1
25	213.5	9.7	6889	5	PCT-US95-09576-2	Sequence 2, Appl1
26	213	9.6	1049	4	US-08-804-166-1	Sequence 1, Appl1
27	213	9.6	1049	4	US-08-910-991-1	Sequence 1, Appl1
28	212.5	9.6	1929	4	US-09-146-950-1	Sequence 1, Appl1
29	212	9.6	1301	4	US-08-804-166-7	Sequence 7, Appl1
30	212	9.6	1301	4	US-08-910-991-7	Sequence 7, Appl1
31	205	9.3	600	1	US-08-050-319B-47	Sequence 47, Appl1
32	205	9.3	600	2	US-08-465-982-47	Sequence 47, Appl1
33	205	9.3	6896	2	US-08-627-151A-6	Sequence 6, Appl1
34	203.5	9.2	1323	3	US-08-883-036A-1	Sequence 1, Appl1
35	201	9.1	1147	4	US-08-804-166-5	Sequence 5, Appl1
36	201	9.1	1147	4	US-08-910-991-5	Sequence 5, Appl1
37	200.5	9.1	483	4	US-09-326-394-1	Sequence 1, Appl1
38	200.5	9.1	1478	4	US-09-149-922-6	Sequence 6, Appl1
39	199.5	9.0	1167	5	PCT-US95-17083-1	Sequence 1, Appl1
40	199.5	9.0	2534	2	US-08-219-237B-1	Sequence 1, Appl1
41	199.5	9.0	2534	4	US-08-468-560C-1	Sequence 1, Appl1
42	199.5	9.0	2534	4	US-09-180-100-16	Sequence 16, Appl1
43	193.5	8.8	1596	4	US-09-290-640-1	Sequence 1, Appl1
44	193.5	8.8	1596	4	US-09-146-950-17	Sequence 17, Appl1
45	192.5	8.7	1480	4	US-09-290-640-65	Sequence 65, Appl1

ALIGNMENTS

RESULT 1
US-08-815-469-3
Sequence 3, Appl1
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HERWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285

LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-928-069-11

Alignment Scores:
Pred. No.: 1,75e-174 Length: 1634
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 4

US-09-993-234-6_COPY_25_417 (1-393) x US-08-928-069-11 (1-1634)

QY 1 GlnGlyThrArgSerProAlaArgCysAlaGlyAspPheHisGlyTyrGly 20
DB 161 CAGGCGGCGACTGAGCCAGGCTGACGTCCGGTGACTCCACAGAAAGATTGGT 220
QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuAlaProCysThrGluPro 40
DB 221 CTGTTTGTTCAGAGGCTGCCAGCGGGGCACTACAGAGGCCCTTGACGAGGCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGlnAsnHis 60
DB 281 TGGCGCAACTCCACTGCTGTGTCTCCCAAGACACTTCTTGCGCGAGAACAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 341 CATATTTCTGATGTGCCCTGCTGAGGCTGTGATGAGCAGGCTCCAGAGTGGCGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 401 GAGAACTGTCAGAGAGGCGGACACCGCTGTGGCTGTAAGCAGGCTGTTGTGAG 460
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 461 TGCAGAGTCAACCATGTGTGAGCAGTTTCACTTCTTCACTTCACTTCACTTCACTT 520
QY 121 GlnValLeuHisArgHisThrArgLeuLeuCysSerArgAspThrAspCysGlyThr 140
DB 521 GGGGCGCTGCAACCGCCACACGCGCTGCTGTCTCCGCAAGATACGACTGTGGGCC 580
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspLysCysValSerCysProThrSerThrLeu 160
DB 581 TGCCTGCTGCTCTATGAACATGGGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 640
QY 161 GlySerCysProGluArgCysAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
DB 641 GGGAGCTGTCCAGAGCCCTGTGCGCTGTGTGCTGAGGAGATGTCTGGGATCCAG 700
QY 181 ValLeuLeuAlaGlyLeuValAlaProLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
DB 701 GTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 760
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGlnAlaLeu 220
DB 761 CGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 820
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
DB 821 ACCCCACCGCCGCGCCACCTGTCAACCTTGGACACCGCCACCTTCTTGACACT 880
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
DB 881 CTTGACAGCATGAGAGATGTGCACCTCCAGTTGGTGGGTAAACAGTGGACCCCTTGGC 940
QY 261 TyrProGluThrGlnGlnAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
DB 941 TACCCCGAGACCCAGAGAGGCTGCTGCGCCGAGGATGATGCTCTGGAGCAGATTGCC 1000
QY 281 SerArgAlaLeuGlyProAlaAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300

DB 1001 AGCAGAGCTTGGCCCGCTGCTGCGCCACACTCTCCAGAGTCCCGACGCGGCTGC 1060
QY 301 ProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
DB 1061 CCAGCATGATGTGCACCGCGCGCCGACGCTTACAGAGTGAAGAGCGGCTCCACGC 1120
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
DB 1121 CGGCGCTGGAAGAGATTGTGTCGCGACGCTGGGGCGTCCGCGAGGACAGATGAAACCTG 1180
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
DB 1181 GAGGTGAGATCGCGCGCTTCCGAGACACAGACAGTACGAGATGCTCAAGCGCTGCGCCAG 1240
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
DB 1241 CAGCAGCCCGCGCGCTGCGAGCCGTTTACGCGCGCTTGGAGCGCATGCGGCTGGACGCG 1300
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
DB 1301 TGGTGGAAAGACTTGGCGCGCGCTGCGAGCGCGCGCGCG 1339

RESULT 3

US-08-828-683A-9
Sequence 9, Application US/08828683A
Patent No. 6469144

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatlin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/828,683A

FILING DATE: 31-Mar-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/625328

FILING DATE: 1-Apr-1996

APPLICATION NUMBER: 08/710802

FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1007P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 1634 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Alignment Scores:
Pred. No.: 1,75e-174 Length: 1634
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Accession	Gene	Length (bp)
AY1301	Pro1AmelkethleusInproci1pro1InenthyrpsalMetkspalavalPro1a	320
1061	CGACCATATCTCTGCAGCCGACCCGAGCTCTACACATCTGATGGACGCGGCTCCAGG	1120
321	ATGATGTp1yglu1puevalArghr1pueul1puear1g1u1a1u1leg1u1a1a1	340
1121	CGCGCTGGAGAGAGTCTGGCACGCTGGGGCTGTCGCGAGGCTAATGATCTTAACTCTCT	1100

Alignment Scores:	
Prep. No.:	1,996-174
Score:	2209.00
Percent Similarity:	100.00%
Percent Local Similarity:	100.00%
Length:	1783
Matches:	393
Conservative:	0
Mismatches:	0

Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-09-993-234-6_COPY_25_417 (1-393) x US-08-815-469-1 (1-1783)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 303 CAGGGGGGCACTGAGTGGCCCAAGGTGTGACTGTGCGGTACTTCCCAAGAAAGATTGGT 362
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 363 CTGTTTGTGTCAGAGGCTCCACGGGGGCGACTACTGAAGGCCCTTTCAGAGAACCC 422
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 423 TGGCGCAACACCACTGCTGTGTGTGTCACCAAGACACCTTCTGGCTGGAGAACAC 482
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnLysSerGlnValAlaLeu 80
DB 483 CATTAATTCATATGATGCTCCCTGCGAGGCTGTGATGAGCAGGCGCTCCAGTGGCGCTG 542
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
DB 543 GAGAACTGTCACAGTGGCGGACACCCGCTGTGGCTGTAAAGCAGGCTGTGTGGAG 602
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 603 TGCAGAGTCAGCAATGTGTGACAGTTCACCTTCTACTGCAACACCATCTAGACTGC 662
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrArgCysGlyThr 140
DB 663 GGGGGCCCTGACCGCCACACAGCGCTACTGTGTCCGCGAAGATACTGACTGGGAGCC 722
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 723 TGGCTGCTGCTGCTTATGAAATGGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 782
QY 161 GlySerCysProGlyLysArgCysAlaAlaValCysGlyTyrArgGlnMetPheTrpValGln 180
DB 783 GGGAGCTGTCCAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 842
QY 181 ValLeuLeuAlaGlyLeuValAlaProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
DB 843 GTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 902
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGlnAlaGlyMetGlnAlaLeu 220
DB 903 CGGCACTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 962
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
DB 963 ACCCCACACCGGCGCACCCATCTGTCTACCCCTGGACAGCGCCACACCCCTTACGACCT 1022
QY 241 ProAspSerSerGlyLysIleCysThrValGlnLeuValGlnLysSerTrpThrProGly 260
DB 1023 CCGTACAGCAGTGAAGATCTCACCGCTCACTGTGGTGAACACCTGACCCCTGGG 1082
QY 261 TyrProGlnThrGlnGlnAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
DB 1083 TACCCGAGACCCAGAGAGGGCTCTGCGCCAGTGAATGGTCTCTGGAGCCAGTTGCC 1142
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
DB 1143 AGCAGAGACTCTTGGCCCGCTGCTGCGCCACACTCTCGCCAGAGTCCACAGCGGCTGC 1202
QY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspAlaMetAspAlaValProAla 320
DB 1203 CAGGCACTGATGTGAGCGGGGCGCGACCTTACGACCTGTATGAGCGGGGCTCCACGC 1262
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlyLysAlaGlnIleGlnAlaVal 340
DB 1263 CGGCGCTGGAAGAGATTCTGTGCGCACCGCTGCGGCTGCGGAGGACAGATCGAAGCCGTG 1322

QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
DB 1323 GAGGTGAGATCGGCGCTTCCGAGACACAGTACGATGTCTCAAGCCCTGGCGCCAG 1382
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
DB 1383 CAGAGCCCGCGGGCGCTGGAGCGCTTACGGGCGCTGGAGCGCATGGGGCTGGAGCGC 1442
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
DB 1443 TGGGTGGAACACTTGGCAGCCGCTGCTGACCGCGCGCCG 1481

RESULT 5

US-08-928-069-5

Sequence 5, Application US/08928069

Patent No. 6462176

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-3 POLYPEPTIDE

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/928,069

FILING DATE: 11-Sep-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/026943

FILING DATE: 09/23/1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1052R1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ. ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1438 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

US-08-928-069-5

Alignment Scores:

Pred. No.: 4.25e-70

Score: 952.00

Percent Similarity: 93.71%

Best local Similarity: 93.14%

Query Match: 43.10%

DB: 4

Gaps: 1

US-09-993-234-6_COPY_25_417 (1-393) x US-08-928-069-5 (1-1438)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 449 CAGGGGGGCACTGAGTGGCCCAAGGTGTGACTGTGCGGTACTTCCCAAGAAAGATTGGT 508
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 509 CTGTTTGTGTCAGAGGCTCCACGGGGGCGACTACTGAAGGCCCTTTCAGAGAACCC 568
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60

Db 569 TCGGGAACCTGACCTGCTTGTGTGTCTCCCAAGACACCTTGTGCTGGGAGAACAC 628
QY 61 HISAANSERGLUCYALAAARGCYSGINAAACYSAPGLUGINAAISERGLVAVALLAEU 80
Db 629 CATTAATTCGAAATGTCGCCGCTGACAGGCTGTGATGACAGACGCTCCAGGTGGCGCTG 688
QY 81 GLUASNCYSERLAVALLAASPHNRARGCYSGLYCYSYSPROGLYTRPHEVALGLU 100
Db 669 GAGAACTGTTCAGACGTGCGCCGACACCGCTGTGCTGTAAAGCAGGCTGTGGAG 748
QY 101 CYSGLINVALSERGLNCYVALSERSESRPROPHETRYCYSGINPROCYLSLEUASPYS 120
Db 749 TGCCAGGTACGACATGTGTACAGCATTCACCTTTCTACTCCAAACCAATGCTAGACTGC 808
QY 121 GLVALALEUHSARGHISTHARGLEULEUCYSSEARARGASPTHRASPCCYSGLYTHR 140
Db 809 GGGGCCCTGCACCGCCACACACGCTACTCTGTCCGACAGATGACTGTGGACAC 868
QY 141 CYSLEUPROGLYPHETRYGLUHSGLYASPGLYCYSVALSERCYSPROTHRSETRHLEU 160
Db 869 TGCTGCTGCTCTTATGAAACATGGGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 928
QY 161 GLYSERCYSPROGLUARGCYSLAVALAVALCYSGLYTRPARGLN 175
Db 929 -----GCTGTGCTGGGATGAGGAG 949

RESULT 6
US-08-828-683A-5
; Sequence 5, Application US/08828683A
; Patent No. 6468144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-828-683A-5

Alignment Scores:

Pred. No.:	4,25e-70	Length:	1438
Score:	952.00	Matches:	163
Percent Similarity:	93.71%	Conservative:	1
Best Local Similarity:	93.14%	Mismatches:	3
Query Match:	43.10%	Indels:	8
DB:	4	Gaps:	1

US-09-993-234-6_COPY_25_417 (1-393) x US-08-828-683A-5 (1-1438)

QY 1 GLNGLYGLYTHRARASERPROARGYASPCYSLAAGLYASPHENHSLSYSLIEGLY 20
Db 449 CAGGCGGACCTGCTGACCCAGCTGTGACTGTGCGGTACTTCCACAGAAATTCGT 508
QY 21 LEUPHESCYSARGGLYCYSPROAAGLYNISTYRLEULYSALAPROCYSYTRIGUPRO 40
Db 509 CTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGTAAGGCCCTTGACAGGAGCC 568
QY 41 CYSGLYASNSERHRCYSLEUVALCYSPROGLINASPTHRPHEVALATRPGLUASNHS 60
Db 569 TCGGGAACCTGACCTGCTTGTGTGTCTCCCAAGACACCTTCTGTGCTGGAGAACAC 628
QY 61 HISAANSERGLUCYSLAARGCYSGINAAACYSAPGLUGINAAISERGLVAVALLAEU 80
Db 629 CATTAATTCGAAATGTCGCCGCTGACAGGCTGTGATGACAGGCTCCAGGTGGCGCTG 688
QY 81 GLUASNCYSERLAVALLAASPHNRARGCYSGLYCYSYSPROGLYTRPHEVALGLU 100
Db 689 GAGAACTGTTCAGACGTGCGCCGACACCGCTGTGCTGTAAAGCAGGCTGTGGAG 748
QY 101 CYSGLINVALSERGLNCYVALSERSESRPROPHETRYCYSGINPROCYLSLEUASPYS 120
Db 749 TGCCAGGTACGACATGTGTACAGCATTCACCTTTCTACTCCAAACCAATGCTAGACTGC 808
QY 121 GLVALALEUHSARGHISTHARGLEULEUCYSSEARARGASPTHRASPCCYSGLYTHR 140
Db 809 GGGGCCCTGCACCGCCACACACGCTACTCTGTCCGACAGATGACTGTGGACAC 868
QY 141 CYSLEUPROGLYPHETRYGLUHSGLYASPGLYCYSVALSERCYSPROTHRSETRHLEU 160
Db 869 TGCTGCTGCTCTTATGAAACATGGGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 928
QY 161 GLYSERCYSPROGLUARGCYSLAVALAVALCYSGLYTRPARGLN 175
Db 929 -----GCTGTGCTGGGATGAGGAG 949

RESULT 7
US-08-928-069-2
; Sequence 2, Application US/08928069
; Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-928-069-2

Alignment Scores:
Pred. No.: 4.25e-47 Length: 433
Score: 666.00 Matches: 127
Percent Similarity: 93.48% Conservative: 2
Best Local Similarity: 92.03% Mismatches: 5
Query Match: 30.15% Indels: 5
DB: Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x US-08-928-069-2 (1-433)

QY 2 GlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGlyLeu 21
DB 22 GGGCGACCTGAGTCCAGAGTGTGACTGTGCGGTGACTCCACAGAGATTGCTGTG 81
QY 22 PheCysArgGlyCysProAla-GlyHisTyrLeuAlaProCysThrGluProCys 41
DB 82 TTTGTGTGACAGGCTGCCAGCGGGCACTACTGAAAGGCCCTTGCGCGAGAGCCTG 141
QY 41 sGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 61
DB 142 CGC-AACCTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCGGAGAACCA 200
QY 61 sAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 81
DB 201 TAAATTCGAATGTGCTCCGCTGCGCTGTGATGACAGCGCTCCACAGGTGGCTGGA 260
QY 81 uAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 101
DB 261 GAACCTGTTCAGACAGTGGCCGACACCCCTGTGTGCTGTGAAGCAGGCTGTGCTG 320
QY 101 sGln-ValSerGlnCysValSerSer-SerProPheTyrCysGlnProCysLeuAspCys 120
DB 321 CCAGGCTCAGCAATGTGTGACAGATTTCACCTTTAATGCCAACAATGCTAGACTGC 380
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCys-SerArgArgasp 135
DB 381 GGGGCCCTGCACACGCAACACAGCGCTAATNTGTTCCCGCAGAGAT 426

RESULT 8
US-08-828-683A-2
Sequence 2, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-828-683A-2

Alignment Scores:
Pred. No.: 4.25e-47 Length: 433
Score: 666.00 Matches: 127
Percent Similarity: 93.48% Conservative: 2
Best Local Similarity: 92.03% Mismatches: 5
Query Match: 30.15% Indels: 5
DB: Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x US-08-828-683A-2 (1-433)

QY 2 GlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGlyLeu 21
DB 22 GGGCGACCTGAGTCCAGAGTGTGACTGTGCGGTGACTCCACAGAGATTGCTGTG 81
QY 22 PheCysArgGlyCysProAla-GlyHisTyrLeuAlaProCysThrGluProCys 41
DB 82 TTTGTGTGACAGGCTGCCAGCGGGCACTACTGAAAGGCCCTTGCGCGAGAGCCTG 141
QY 41 sGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 61
DB 142 CGC-AACCTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCGGAGAACCA 200
QY 61 sAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 81
DB 201 TAAATTCGAATGTGCTCCGCTGCGCTGTGATGACAGCGCTCCACAGGTGGCTGGA 260
QY 81 uAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 101
DB 261 GAACCTGTTCAGACAGTGGCCGACACCCCTGTGTGCTGTGAAGCAGGCTGTGCTG 320
QY 101 sGln-ValSerGlnCysValSerSer-SerProPheTyrCysGlnProCysLeuAspCys 120
DB 321 CCAGGCTCAGCAATGTGTGACAGATTTCACCTTTAATGCCAACAATGCTAGACTGC 380
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCys-SerArgArgasp 135
DB 381 GGGGCCCTGCACACGCAACACAGCGCTAATNTGTTCCCGCAGAGAT 426

RESULT 9
US-08-762-308-10
Sequence 10, Application US/08762308
Patent No. 5925548
GENERAL INFORMATION:
APPLICANT: Beutler, Bruce A.
TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY
TITLE OF INVENTION: SIGNAL
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:


```

1      FILLING DATE:  June 26, 1998
2
3      CLASSIFICATION:  514
4
5      ATTORNEY/AGENT INFORMATION:
6
7      NAME:  Laurel Spear Bernstein
8      REGISTRATION NUMBER:  37,280
9      REFERENCE/DOCKET NUMBER:  RTS-0004
10
11     TELECOMMUNICATION INFORMATION:
12
13     TELEPHONE:  (760) 931-9200
14
15     TELEFAX:  (760) 603-3820
16
17     INFORMATION FOR SEQ ID NO:  1:
18
19     SEQUENCE CHARACTERISTICS:
20
21     LENGTH:  2161
22
23     TYPE:  nucleic acid
24
25     STRANDEDNESS:  single
26
27     TOPOLOGY:  linear
28
29     US-09-106-038A-1

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Alignment Scores:	
Pred. No.:	2, 2e-21
Score:	369.00
Percent Similarity:	39.05%
Best Local Similarity:	28.44%
Query Match:	16, 70%
DB:	3
Length:	216
Matches:	126
Conservative:	47
Mismatches:	178
Indels:	92
Gaps:	21

US-09-993-234-6_COPY_25_417 (1-393) x US-09-106-038A-1 (1-2161)

QY	3	gltThArgSerProArg-----	CysAspCysAlaGlyAspPheHisLysLysIle	19
Db	358	GGGGACAGGGACAGACAGAAATAGTGTGTGTGCCCAAGGAAATAATATATACACCCCTCAAAAT		
QY	20	GlyLeuPheCysCysAsr9GlYcysProAlaGlnHisTyrLeuLysAlaProCysThrGlu	39	
Db	418	AATTCGATTTGGTGTACCAAGTGGCCACAAAGGAACCTCTTGTCATATGACTGTCCAGGC	477	
QY	40	ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTyrGluAsn	59	
Db	478	CCGGGGCAGGAATACGAGATCGAGGGAGTGTAGAGCCGGCTCTTCACCGCTTCAGAAAC	537	
QY	60	HisHisAsnSerGluCysAlaIleArgCysGlnIleLeuAspGluGlnAlaSerGlnValAla	79	
Db	538	CACGCTCAGA---CACTGGCTCAGCTGCTCTCCAAATGGCGAAAGAAATGGGTCAAGTGGAC	594	
QY	80	LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheVal	99	
Db	595	ATCTCTCTTGTACAGTGGACCGGGACACACGCTGTGTGGTGGCAGAGAAACCACTACCGG	654	
QY	100	GluCys-----GlnValSerGluCysAlaSerSerSerProPheTyrCysGlnPro	116	
Db	655	CATTATTGGAGTGAACACCTTTCACAGGC-----TTCAATTGTCACACCTTC	699	
QY	117	CysLeuAspCysGlyAlaLeuHisArgHisIleThrArgLeuLeuCysSerIleArgAspThr	136	
Db	700	TGCCCTCAAT---GGGACCGCTCAC-----CTCTCCCTGCCAGGAGAAACCAAC	744	
QY	137	AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro	156	
Db	745	ACCGGTGTCACCTTCATGCAGAGGTCTTTCTTAAGAAAGAAACGAGTGTCTCTCT	801	
QY	157	ThrSerThrLeuGlySerCysProGlu---ArgCysAlaIleValCys-----	171	
Db	802	-----ACTAACTGTAAAGAAACCTTGAGATGCAGGAAGTGTGTCCCTACCCACG	849	
QY	172	-----GlyTyrArgGlnMetPheTyrAlaGlnValLeu	182	
Db	850	ATTGAGCATGTTAAGGCACACTGAGGACATCGACACACAGCTGCTGTGGCCCTGGTCAAT	909	
QY	183	LeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrArgHis	202	
Db	910	TTCCTTGTCTTGGCTTTTATCCCTTCCTTCATGTGTTAATGATGCTACCAACGG	969	
QY	203	CysTyrProHisLys-----ProLeuValThrAlaAspGluAla	215	

Db	970	-----TGGAGTCCCAACCTCTACTCCATGTGTTGTGGGAATGACACCTGAAAAAGAGGCG	10298
QY	216	GLYMETGUALALEUTHrProProProAlaThrHisLeuSerProLeuAspSer-----	233
Db	1027	GAGCTTGAAGGAACTACTACTAAAGCC-----CTGGCCCCAAACCCAAAGCTTCACT	10777
QY	234	-----AlaHisThrLeuLeuAlaProProAspSerSerGluHisIleGly	248
Db	1078	CCCACTCCAGGCTTCACCCCAACCTGGGGCTTCAGTCCCGTGGCCAGTTCCACCTTACCC	1137
QY	249	ThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrProGluThrGlnGluAlaLeu	268
Db	1138	TCCTCC-----AGCTCCACCTATACCCCGGTGAC-----	1164
QY	269	CysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro-----	286
Db	1165	TGTCCTCAACTTGGG-----GCTCCCGCAAGAGGTGGACCAACCTAT	1209
QY	287	-----AlaAlaAlaProThrLeuSerPro-----	294
Db	1210	CAGGGGAGTCAACCCCATCTTGCAGACAGCCCTGCTCGCGACCCCATCCCAACCCCTT	1269
QY	295	-----GluSerProAlaGlySerProAlaMetIleLeuGlnProGlyPro--Gln	310
Db	1270	CAGAAGTGGAGGACAGCGCCACAAAGCCTAACAACCTGATGACCCGCGACG	1329
QY	311	LeuTyrAspAlaMetAspAlaValProAlaArgTrpTrpGluPheValArgThrLeu	330
Db	1330	CTGATACCCCGGTGGGAGAAAGTGGCCCCGCTGGCGTGGAAAGAAATTCGTGCGCGCTA	1389
QY	331	GlyLeuArgGlnAlaGluIleGluAlaValGlnValGluIleGlyArg---PheArgasp	349
Db	1390	GGGTGTGACGACCAACGATCGATCGGCTGAGACTGACAGAAACGGGCGTCTGCGCGAG	1449
QY	350	GlnGlnTyrGlnMetLeuTyrAlaGlyTrpArgGlnGlnPro-----AlaGlyLeu	366
Db	1450	GGCGAATACAGCATGCTGGGAGCAGCTGGAGGCGGCGACGCGGCGGCGAGGCCAGCTG	1509
QY	367	GlyAlaValTyrAlaAlaLeuGlnArgMetGlyLeuAspGlyCysValGlnAspLeuArg	386
Db	1510	GAGCTGTGGGACGCTGCTCCGACATGAGCACTGTGCTGGGCTGCTGGAGGACATCGAG	1569
QY	387	SerArgLeu 389	
Db	1570	GAGGCGCTT 1578	
RESULT 14			
US-09-505-250-3			
; Sequence 3, Application US/09505250A			
; Patent No. 6329148			
; GENERAL INFORMATION:			
; APPLICANT: Rosen, Glenn			
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with			
; FILE REFERENCE: Tripicolides and Death Domain Ligands			
; CURRENT APPLICATION NUMBER: US/09/505,250A			
; NUMBER OF SEQ ID NOS: 4			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 3			
; LENGTH: 2161			
; TYPE: DNA			
; ORGANISM: H. sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (256)...(1623)			
US-09-505-250-3			
Alignment Scores:			
Pred. No.: 2.2e-21 Length: 2161			
Score: 369.00 Matches: 126			
Percent Similarity: 39.05% Conservative: 47			

Best Local Similarity: 28.448 Mismatches: 178
Query Match: 16.708 Indels: 92
DB: 4 Gaps: 21

US-09-993-234-6_COPY_25_417 (1-393) x US-09-505-250-3 (1-2161)

QY 3 GlyhyrserProAlaG-----CysAspCysAlaGlyAspPheHisLysLysIle 19
DB 358 GGGGACAGGGGAGAGAGATAGTGTGTGTCGCCAGAGAAATATATATCCACCCCAAAAT 417
QY 20 GlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGlu 39
DB 418 AATTCGATTTCTCTTACCAAGTCCACAAAGAACTTCTGTTCATGACTGCTCAGCC 477
QY 40 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTyrGlnAsn 59
DB 478 CCGGAGGAGATACGAGATGAGAGAGAGTGTGAGAGCGGCTTCACCGCTTCAGAAAC 537
QY 60 HisHisAsnSerGlyCysAlaArgCysGlnAlaCysAspGlnGlnAlaSerGlnValAla 79
DB 538 CACCTCAGA---CACTGCTTCAGCTGCTCCAAATGCCAAAGGAAATGGGTGAGTGGAG 594
QY 80 LeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheAla 99
DB 595 ATCTCTTGTGACAGTGGAGCGGACCGTGTGTGCTGACAGAGAACACAGTACCGG 654
QY 100 GlnCys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnPro 116
DB 655 CATATTTGGAGTAAACCTTTTCCAGTGC-----TTCAATTCGACGCTC 699
QY 117 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLysSerArgArgAspThr 136
DB 700 TGCCTCAAT---GGGACGCTGCAC-----CTCTCTGCTCCAGAGAAACAGAAC 744
QY 137 AspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysPro 156
DB 745 ACCGTGTGCACCTGCTCCATGACGAGTTCTTCTTAAGAGAAAGAGGTGTCTCTGT--- 801
QY 157 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 171
DB 802 -----AGTAAGTGTAAAGAAAGCCTGGAGTCCAGAACTTGTGCTTACCCAG 849
QY 172 -----GlyTyrArgGlnMetPheTyrValGlnValLeu 182
DB 850 ATTGAGATGTTAAGGCACACTGAGACTGAGACGACACAGCGTGGTCCCGCTGCTCAT 909
QY 183 LeuAlaGlyLeuValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyrArgHis 202
DB 910 TTCTTTGTCTTGTGCTTTTATTCCTCTCTTCAATGGTTAATGTATGCTGCTACCAAG 969
QY 203 CysTyrProHisLys-----ProLeuValThrAlaAspGlnAla 215
DB 970 ---TGAAAGTCCAAAGCTCTACTCATTTGTTGTGGAAATGACACACCTGAAAGAGGGG 1026
QY 216 GlyMetGlnAlaLeuThrProProAlaThrHisLeuSerProLeuAspSer----- 233
DB 1027 GAGCTTGAAGAACTACTAAACCC-----CTGGCCCAAAACCAAGCTTCACT 1077
QY 234 -----AlaHisThrLeuLeuAlaProProAspSerSerGlnLysIleCys 248
DB 1078 CCCACCTCCAGGCTTACCCCTGAGGCTTCAAGTCCGAGCCAGTTCACCTTCAAC 1137
QY 249 ThrValGlnLeuValGlyAsnSerThrProGlyTyrProGlnThrGlnGlnAlaLeu 268
DB 1138 TTC-----AGCTCCACTATACCCCGGTGAC----- 1164
QY 269 CysProGlnValThrTyrSerTyrAspGlnLeuProSerArgAlaLeuGlyPro----- 286
DB 1165 TGTCCAAACTTTCG-----GCTCCCGCAGAGAGGTGACACACCTTAT 1209
QY 287 -----AlaAlaAlaProThrLeuSerPro----- 294
DB 1210 CAGGGGCTGACCCCACTCTTGGACAGACCTGCTGCGCTCGAACCCCACTCCCAACCCCTT 1269

QY 295 -----GlnSerProAlaGlySerProAlaMetLeuGlnProGlyPro---Gln 310
DB 1270 CAGAAGTGGAGAGACAGCCGCCACAGACAGACACTGATGATGACCCCGACG 1329
QY 311 LeuTyrAspValMetAspAlaValProAlaArgAlaGlyTyrGlyGlnPheValArgThrLeu 330
DB 1330 CTGTAAGCGCGTGTGGAGAACGTGCCCGTTCGCTGGAAGGAATGTGTGGGGGCGCTA 1389
QY 331 GlyLeuArgGlnAlaGlnIleGlnAlaValGlnValGlnIleGlyArg---PheArgAsp 349
DB 1390 GGGCTGACGACGACACAGATGATGCTGCTGAGCTGCGAAGCGGCGCTGCTGCGCAG 1449
QY 350 GlnGlnTyrGlnMetLeuLysArgTyrArgGlnGlnGlnPro-----AlaGlyLeu 366
DB 1450 GCGCAATACAGCATGCTGGCAGCTGAGAGCGGCGGCGGCGGAGCCAGCGCTG 1509
QY 367 GlyAlaValTyrAlaAlaLeuGlnArgMetGlyLeuAspGlyCysValGlnAspLeuArg 386
DB 1510 GAGCTGTGGGAGCGGCTGCTCGGACATGACCTGCTGCGCTGAGAGCATCGAG 1569
QY 387 SerArgLeu 389
DB 1570 GAGCGCTT 1578

RESULT 15
US-08-321-668-1
Sequence 1, Application US/08321668
Patent No. 5665859

GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
APPLICANT: VARPOLOMEV, Eugene
APPLICANT: BATKIN, Michael

TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
THE TINE RECEPTORS, THEIR PREPARATION AND THEIR USE

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,668
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107268
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-1597
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS

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LOCATION: 256..1620
US-08-321-668-1

Alignment Scores:
Pred. No.: 2.22e-21
Score: 369.00
Percent Similarity: 39.05%
Best Local Similarity: 28.44%
Query Match: 16.70%

Matches: 126
Conservative: 47
Mismatch: 178
Indels: 92
Gaps: 21

US-09-993-234-6_COPY_25_417 (1-393) x US-08-321-668-1 (1-2175)

QY 3 GYThrArgSerProArg-----CysAspCysAlaGlyAspPheHisLysIle 19
DB 358 GGGGACAGGAGAGAGAGATAGTGTGTGCCCAAGAAATATATCCACCCCAAAAT 417
QY 20 GYLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGlu 39
DB 418 AATTCGATTGTGCTTACCAAGTGCACAAAGAACTACTGTGCAATGACTGTCCAGGC 477
QY 40 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsn 59
DB 478 CCGGGGACAGGTACGACTGCAGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAC 537
QY 60 HisHisAsnSerGlyCysAlaArgCysGlnAlaCysAspGlnGlnAlaSerGlnValAla 79
DB 538 CACCTCAGA---CACTGCCTCAGCTGCTCCAAATGCCAAAGAAATGGGTCCAGGTGAG 594
QY 80 LeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal 99
DB 595 ATCTCTTCTTGACAGTGGACCGGGACACCGTGTGTGCTGCAGAGAAACCAAGTACCGG 654
QY 100 GlnCys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnPro 116
DB 655 CATATATGGAGTGAACACTTTTCCAGTGC-----TTCATATTCAGCGCTC 699
QY 117 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 136
DB 700 TGCCTCAAT---GGGACCGTGCAC-----CTCTCCTCCAGAGAAACAGAGAAC 744
QY 137 AspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysPro 156
DB 745 ACCGTGTGCACCTGCATGCAGGTTTCTTTCTTAAGAGAAACGAGTGTCTCTGT--- 801
QY 157 ThrSerThrLeuGlySerCysProGln---ArgCysAlaAlaValCys----- 171
DB 802 -----AGTAACTGTAAAGAAAGCCTGGAGTGCACGAAGTGTGCTTACCCAG 849
QY 172 -----GlyTrpArgGlnMetPheTrpValGlnValLeu 182
DB 850 AWTGAGAAATGTTAAGGCACCTGAGGACTCAGGACACACAGTGTGTCCTGCTCATTT 909
QY 183 LeuAlaGlyLeuValAlaProLeuLeuGlnGlyAlaThrLeuThrTyrThrArgHis 202
DB 910 TTCCTTGTGCTTTCCTTTATCCCTCCTCTTCATGTGTTAATGATACGCTACCAACG 969
QY 203 CysTrpProHisLys-----ProLeuValThrAlaAspGlnAla 215
DB 970 ---TGAAGTCCAAAGCTACTCATGTGTGTGGAAATGACACCTGAAAAAGAGGG 1026
QY 216 GlyMetGlnAlaLeuThrProProAlaThrHisLeuSerProLeuAspSer----- 233
DB 1027 GAGCTGAAGGAACTACTACTAAAGCC-----CTGGCCCAAAACCAAGCTTCAGT 1077
QY 234 -----AlaHisThrLeuLeuAlaProProAspSerSerGlyLysIleCys 248
DB 1078 CCACTCCAGGCTTCACCCCAACCTGGGCTTCAGTCCCGCCAGTTCACCTTCAC 1137
QY 249 ThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrProGlyTrpGlnGlnAlaLeu 268
DB 1138 TCC-----AGCTCCACCTATACCCCGGTGAC----- 1164

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QY 269 CysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro----- 286
DB 1165 TGTCCCAACTTTTGC-----GCTCCCGGACAGAGGTGGACACCACTTAT 1209
QY 287 -----AlaAlaAlaProThrLeuSerPro----- 294
DB 1210 CAGGGGCTGACCCCATCTTGGACAGCCCTGCTCCGACCCCATTCACCAACCCCTTT 1269
QY 295 -----GluSerProAlaGlySerProAlaMetMetLeuGlnProGlyPro---Gln 310
DB 1270 CAGAGTGGAGAGACAGCGCCCAAGCCACAGAGCTGACACTGATGACCCCGGAGAG 1329
QY 311 LeuTyrAspValMetAspAlaValProAlaArgArgTrpLysGlnPheValArgThrLeu 330
DB 1330 CTGTACCGCTGTGGTGGAGACGTGCCCCCTTCCCTGGAAGAAATTCGTGCGGCCCTTA 1389
QY 331 GYLeuArgGlnAlaGlnIleGlnValAlaGlnValGlnIleGlyArg---PheArgAsp 349
DB 1390 GGGCTGAGCGACACAGATCGATCGGCTGTGAGCTGTGAGAACGGGGCTGCTGCGGAG 1449
QY 350 GlnGlnTyrGlnMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeu 366
DB 1450 GCGCAATACAGCATTCGTGGGAGCTGTGAGGCGGACGCGGGGCGGACGCGCACGCTG 1509
QY 367 GYAlaValTyrAlaAlaLeuGlnArgMetGlyLeuAspGlyCysValGlnAspLeuArg 386
DB 1510 GAGCTGCTGGACGCGTGTCCCGACATGACCTGTGCGGCTGCGCTGGAGGACATCGAG 1569
QY 387 SerArgLeu 389
DB 1570 GAGCGCTT 1578

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Search completed: April 6, 2003, 23:29:40
 Job time : 87.3429 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:35:34 ; Search time 4567.25 Seconds
(without alignments)
2504.221 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_417
Perfect score: 2209
Sequence: 1 OGCTSPRCDCAGDFHKKIG.....ERMGLDGCVEDLRSRLQRCG 393

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-O/cqg2.1/USPTO.spool/US0999334/runat.27032003_115455_15349/app_query.fasta.1.2346
-DB=GenEmbl -QFMT=firststep -SUFFIX=rge -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=dl0sum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pic -NOR-ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0999334.ecgl.1.1.8534.0runat.27032003_115455_15349 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb.ba:*
2: gb.htg:*
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5: gb.ov:*
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18: em.hum:*
19: em.mu:*
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21: em.or:*
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24: em.ph:*
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29: em.vi:*
30: em_htg_hum:*
31: em_htg_inv:*
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35: em_htg_rtd:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2209	100.0	1254	6 AR119657	AR119657 Sequence
2	2209	100.0	1254	9 HSU72763	U72763 Human death
3	2209	100.0	1254	9 HSU78029	U78029 Human apopto
4	2209	100.0	1254	9 HSU94501	U94501 Human Lymph
5	2209	100.0	1634	9 HSU74611	U74611 Human Apo-3
6	2209	100.0	1662	6 AX055442	AX055442 Sequence
7	2209	100.0	1662	6 AX201344	AX201344 Sequence
8	2209	100.0	1783	6 AR119656	AR119656 Sequence
9	2199	99.5	1528	9 HSU83597	U83597 Human death
10	2199	99.5	1557	9 HSU75380	U75380 Human apopt
11	2198.5	99.5	1257	9 HSU94502	U94502 Human Lymph
12	2157.5	97.7	1355	9 HSU94503	U94503 Human Lymph
13	2140.5	96.9	1743	6 AX331947	AX331947 Sequence
14	2140.5	96.9	1743	9 HSWSL1	Y03932 H. sapiens m
15	2128	96.3	1669	9 AF026070	AF026070 Homo sapi
16	2114	95.7	1250	6 AX150176	AX150176 Sequence
17	2104.5	95.3	1763	9 AF026071	AF026071 Homo sapi
18	2062.5	93.4	1198	9 HSU94504	U94504 Human Lymph
19	1971.5	89.2	1143	9 HSU94510	U94510 Human Lymph
20	1902.5	86.1	1119	9 HSU94509	U94509 Human Lymph
21	1837	83.2	1087	9 HSU94505	U94506 Human Lymph
22	1530.5	69.3	952	9 HSU94506	U94506 Human Lymph
23	1517.5	68.7	4811	9 AB051851	AB051851 Homo sapi
24	1498.5	67.8	4825	9 AB051850	AB051850 Homo sapi
25	1498.5	67.8	53982	9 AL158217	AL158217 Human DNA
26	1364	61.7	1665	10 AF329969	AF329969 Mus muscu
27	1290.5	58.4	838	9 HSU94507	U94507 Human Lymph
28	1224.5	55.4	1619	10 BC017526	BC017526 Mus muscu
29	1221	55.3	1581	9 AK094463	AK094463 Homo sapi
30	1221	55.3	2053	9 AK094488	AK094488 Homo sapi
31	1036.5	46.9	705	9 HSU94508	U94508 Human Lymph
32	957.5	43.3	816	6 AX335086	AX335086 Sequence
33	957.5	43.3	816	9 HSU83598	U83598 Human death
34	952	43.1	808	9 HSU75381	U75381 Human apopt
35	952	43.1	809	9 HSU94512	U94512 Human Lymph
36	942.5	42.7	196368	2 AL772240	AL772240 Mus muscu
37	673	30.5	97483	2 AC118359	AC118359 Rattus no
38	636	28.8	18015	10 AF134858	AF134858 Mus muscu
39	609	27.6	651	9 HSU83599	U83599 Human alter
40	409.5	18.5	2004	4 MSU19994	U19994 Sus scrofa
41	393.5	17.8	1956	10 MUSU1994	M59377 Murine tumo
42	393.5	17.8	2048	10 MUSU1994	M59377 Murine tumo
43	393.5	17.8	2063	10 MPM55R	X59238 Murine mRNA
44	393.5	17.8	2086	10 BC004599	BC004599 Mus muscu
45	393.5	17.8	2115	10 AF329978	AF329978 Rattus no

RESULT 1

ALIGNMENTS

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Score:	2209.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
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	Matches: 393
	Conservative: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0

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LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
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PRI 15-NOV-1996															
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BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN

Alignment Scores:
Pred. No.: 7.97e-110 Length: 1254
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conserved: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x HS072763 (1-1254)

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DEFINITION Human apoptosis inducing receptor AIR mRNA, complete cds.
ACCESSION U78029
VERSION U78029.1 GI:1778763
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SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE Degli-Esposti, M.A., Dln, W.S., Cosman, D., Smith, C.A. and
Goodwin, R.G.
AIR, A Novel Member of the TNF Receptor Family, Is a Strong Inducer
of Apoptosis
TITLE Unpublished
JOURNAL 2 (bases 1 to 1254)
REFERENCE Degli-Esposti, M.A. and Goodwin, R.G.
AUTHORS Direct Submission
TITLE Submitted (12-NOV-1996) Biochemistry, Immunex Corporation, 51
JOURNAL University St., Seattle, WA 98101, USA
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ORGANISM Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 1634)
Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pittl,R.M., Gray,C.L.,
Goddard,A.D., Bauer,K.D. and Ashkenazi,A.
Apo-3, a new member of the tumor necrosis factor receptor family,
contains a death domain and activates apoptosis and NF-kB
Curr. Biol. (1996) In press
2 (bases 1 to 1634)
Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pittl,R.M., Gray,C.L.,
Goddard,A.D., Bauer,K.D. and Ashkenazi,A.
Direct Submission
TITLE Submitted (15-OCT-1996) Molecular Oncology, Genentech, 460 Pt. San
JOURNAL Bruno Blvd., South San Francisco, CA 94080, USA
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Alignment Scores:
Pred. No.: 1,06e-109 Length: 1634
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conserved: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-993-234-6_COPY_25_417 (1-393) x HSU74611 (1-1634)
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 REFERENCE 1 (bases 1 to 1662)
 Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J.,
 Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L.,
 Tumas, D., Watanabe, C.K. and Wood, W.I.
 Compositions and methods for the treatment of immune related
 diseases
 TITLE JOURNAL Patent: WO 0073452-A 72 07-DEC-2000;
 FEATURES GeneTech, Inc. (US)
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1662)
AUTHORS Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,
Stone,D.M., Watanabe,C.K. and Wood,W.I.
TITLE Compositions and methods for the treatment of tumour
JOURNAL Patent: WO 0153486-A 23 26-JUL-2001;
Genentech, Inc. (US)
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AUTHORS	Chaudhary,P.M. and Hood,L.E.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-JAN-1997) Molecular Biotechnology, University of Washington, 1705 NE Pacific Street, HSB-K360, Seattle, WA 98195,		
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VERSION U75380.1 GI:1695924
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AUTHORS Bodmer, J. L., Burns, K., Schneider, P., Hofmann, K., Steiner, V.,
Thome, M., Bonnard, T., Hahne, M., Schroter, M., Becker, K., Wilson, A.,
French, L. E., Browning, J. L., Macdonald, R. and Tschopp, J.
TRAMP, a novel apoptosis-mediating receptor with sequence homology
to tumor necrosis factor receptor 1 and Fas (Apo-1/CD95)
Immunity 6 (1), 79-88 (1997)
TITLE
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REFERENCE
AUTHORS Bodmer, J. L., Burns, K., Schneider, P., Hofmann, K., Steiner, V.,
Thome, M., Bonnard, T., Hahne, M., Schroter, M., Wilson, A.,
French, L. E., Browning, J. L., Macdonald, R. and Tschopp, J.
Direct Submission
TITLE
JOURNAL Submitted (18-OCT-1996) Institute of Biochemistry, University of
Lausanne, 155 Chemin des Boveresses, Epalinges, CH 1066,
Switzerland
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Location/Qualifiers

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DB 844 TACCCCGAGACCCAGAGAGGCGCTGTGCCAGAGTGACATGTCTGTGGACAGCTGCCCC 903
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
DB 904 AGCAGACTCTTGGCCCCGCTGTGGCGCCACACTCTGCGCAGAGTCCACAGCGGCTGCG 963
QY 301 ProAlaMetLeuLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
DB 964 CAGCCATGATGCTGCAGCGCGGCCCGCCACTCTACGACTGATGAGCGCGTCCAGCG 1023
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuAlaGlyGluAlaGlyValAlaVal 340
DB 1024 CGGCGCTGGAGAGAGTTCGTGCGCCAGCTGGGCTGGCGCAGGACAGATCGAAGCGCTG 1083
QY 341 GluValGluIleGlyArgPheArgAspGlnGlyTyrGluMetLeuLysArgTrpArgGln 360
DB 1084 GAGGTGAGATCGCGGCTTCCGAGACACAGCACTAGAGATGTCTCAAGCGCTGGCCCGAG 1143
QY 361 GlnGluProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
DB 1144 CAGCAGCCCGCGGCGCTCGAGCGGTTTACGCGCCCTGAGCGCATGGGGGTGAGCGCG 1203
QY 381 CysValGluLysPheLysArgSerArgLeuGlnArgGlyPro 393
DB 1204 TGGGTGGAAGACTTGGCGACGCCCTGACAGCGAGGCCCG 1242

RESULT 11
HSU94502      1257 bp      mRNA      linear      PRI 15-MAY-1997
LOCUS
DEFINITION
Human lymphocyte associated receptor of death 1b mRNA.
ACCESSION
U94502.1
VERSION
U94502.1 GI:2071950
KEYWORDS
SOURCE
ORGANISM
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1257)
Screation/G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J., and Bell,J.I.
IARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL
MEDLINE
97272273
PUBMED
9114039
REFERENCE
2 (bases 1 to 1257)
Screation/G.R.
Direct Submission
TITLE
Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
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1. 1257
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HeLa"

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CDS
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TNF-R1; contains a death domain"
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/product="lymphocyte associated receptor of death 1b"
/protein_id="AAC51307.1"
/db_xref="GI:2071951"
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DCGCLPGEYEHEDGCSCTSTIGSCPERCAVCGRQNFVYVLLAGVLPILLTA
LVTTTHCMFHKPLVTADAGMEALTPPAHLSPIDSHHTLAPDSSEKICTVO
LVSMTGPQYPTQLEALCPQVMTMDLPRLALGPAAPTLSPSPAGSPAMVQGP
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AVYALERMGIDGVEDLRSLRQGP"
misc_feature
708..711
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Accession Number U94501, probably represents alternative
3' splice site"
BASE COUNT      202 a      421 c      408 g      226 t
ORIGIN
Alignment Scores:
Pred. No.:      2,91e-109      Length:      1257
Score:          2198.50      Matches:      393
Percent Similarity: 99.75%      Conservative: 0
Best local Similarity: 99.75%      Mismatches: 0
Query Match:      99.52%      Indels:      1
DB:              9      Gaps:      1
US-09-993-234-6_COPY_25_417 (1-393) x HS094502 (1-1257)
QY      1  GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db      73  CAGGGCGGACATCGTAGGCCCAAGGTGTACTGTGGCGGTGACTTCCAAAGAGATTGGT 132
QY      21  LeuphCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db      133  CTGTTTGTGTGACAGAGCGTGGCCAGCGGCGACTCGAAGGCCCTTGCACGGAGGCC 192
QY      41  CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTyrPgluAsnHis 60
Db      193  TGCAGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTGGCTGGGAGAACAC 252
QY      61  HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db      253  CATTAATCTGAATGTGCCCGCTGCCAGGCTGTGTAGACAGGCTCCAGGTGGCGCTG 312
QY      81  GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
Db      313  GAGAACTGTCAGAGCGTGGCGACACCGCGTGTGCTTAAGCCAGGCTGGTTCTGGAG 372
QY      101  CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db      373  TGCAGGTCACCAATGTGTACAGCTTACACCTTCTACTGCCAACACATGCTTACACTGC 432
QY      121  GlnAlaLeuHisArgHisThrArgLeuLeuLeuCysSerArgAspThrAspCysGlyThr 140
Db      433  GGGGCGCTGCACCGCCACACAGGCTACTGTGTCCCGCAGAGATACAGACTGTGGAC 492
QY      141  CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db      493  TGCCTGCGTGGCTTCTAAGAACATGGGATGGCTGCGTCTGCTGCCACAGCAACCTG 552
QY      161  GlySerCysProGluArgCysAlaAlaValCysGlyTyrParGlnMetPheTyrValGln 180
Db      553  GGGAGCTGTCCAGAGCGCTGTGCCCTGTGTGCTGGAGAGCAATGTCTGGGCTCAG 612
QY      181  ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrTyr 200
Db      613  GTGTCCTGGCTGGCTGTGTGTCCCTCTGCTTGGGGCCACCTGACCTACACATAC 672
QY      201  ArgHisCysTyrProHisLysProLeuValThr---AlaAspGluAlaGlyMetGluAla 219
Db      673  CGCCACTGCTGGCCTCACAAAGCCCTGTACTGCAGAGATGAGTGGATGGAGGCT 732
QY      220  LeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuAla 239
Db      733  CTGACCCACACACCGGCCACCATGTGTACCCCTTGGAGAGGCCACACCTTTACCA 792
QY      240  ProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerThrPro 259
Db      793  CCTCTGACAGAGAGAGAAATCTGCACCGTCCAGTTGGTGGTAAACATGACCTGG 852
QY      260  GlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTyrSerTyrAspGlnLeu 279
Db      853  GGCTACCCCGAGACCAGAGAGCGCTGTCCCGCAGAGTGAATGCTCTCGGGACAGTTG 912
QY      280  ProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGly 299
Db      913  CCCACAGAGCTTGTGGCCCGCTCTGCGCCACACTCTGCCAGAGTCCCCACCGCGC 972
QY      300  SerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValPro 319
Db      973  TCGCCAGCCATGATCTCTGACGCGGCGCCGACGCTCTACGAGATGAGACGGGTCCA 1032
QY      320  AlaArgArgTyrPlyGluPheValArgThrLeuGlyLeuArgGluAlaGlyIleGluAla 339
Db      1033  GCGCGGCGCTGGAAGAGTGTGTCGCGACGCTGGGGGCTGGCGGAGAGATCGAAGCC 1092
QY      340  ValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTyrArg 359
Db      1093  GTGAGGTGGAGATCGCGCGCTCCGAGACCGAGTACGATCTCAAGCGCTGGCGGC 1152
QY      360  GlnGlnGlnProAlaGlyLeuGlyValAlaValTyrAlaAlaLeuGluArgMetGlyLeuAsp 379
Db      1153  CAGCAGCAGCGCGCGCGCTCGGAGCCGTTTACGGCGCCCTTGAGAGCATGGGGCTGGAC 1212
QY      380  GlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db      1213  GGCTGCTGGAAGACTGTGGCGAGCGCGCTGCGAGCGCGCGCGCCG 1254
RESULT 12
LOCUS      HS094503      1355 bp      mRNA      linear      PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 2 mRNA, alternatively
spliced, complete cds.
ACCESSION      U94503
VERSION      U94503.1
KEYWORDS      GI:2071952
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 1355)
AUTHORS      Screaton, G.R., Xu, X.N., Olsen, A.L., Cowper, A.E., Tan, R.,
McMichael, A.J., and Bell, J.I.
TITLE      LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
PROC. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL      JOURNAL
MEDLINE      97272273
PUBMED      9114039
REFERENCE      2 (bases 1 to 1355)
AUTHORS      Screaton, G.R.
TITLE      Direct Submission
JOURNAL      Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
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/cell_type="lymphocyte"
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GREGGNHPTPTSCFOGSCRMALAMSSCLGRP"
599..700
/note="Insertion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable retained intron leading
to premature transcriptional termination"

BASE COUNT 223 a 441 c 451 g 240 t

ORIGIN

misc-feature

Alignment Scores:

Pred. No.: 4,87e-107 Length: 1355
Score: 2157.50 Matches: 392
Percent Similarity: 91.80% Conservative: 0
Best Local Similarity: 91.80% Mismatches: 1
Query Match: 97.67% Indels: 35
DB: Gaps: 1

US-09-993-234-6_COPY_25_417 (1-393) x HSU94503 (1-1355)

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Db 73 CAGGGGGGAGCTGTAAGCCCGAGGTGTGACTGTGCGGTGACTTCACAGAAGATTGGT 132

QY 21 LeuPheCysAspArgLysCysProAlaGlyHisLysLeuLysAlaProCysThrGluPro 40
Db 133 CTGTTTGTTCAGAGAGCTGCCAGCGGGGCACTACTGAGGCCCTTCCACAGAGACC 192

QY 41 CysGlyAspSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 193 TGGGGAGACTCCACCTGCTGTGTGTCCCAAGACACCTTCTGGCTGGGAGAACCCAC 252

QY 61 HisAspSerGlyCysAlaArgCysGlnAlaCysAspGlyGlnAlaSerGlnValAlaLeu 80
Db 253 CATTAATTTCGAATGTCCCGCTGCCAGGCTGTGATGACAGGCCCTCCAGGTGGCGCTG 312

QY 81 GluAspCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 313 GAGAACTGTTCAGACAGTGGCCGACACCCGCTGGCTGTAAAGCAGAGCTGGTTGTGAG 372

QY 101 CysGlnValSerGlnCysValSerSerSerProPheThrCysGlnProCysLeuAspCys 120
Db 373 TGCAGAGTACCAATGTGTCTGACAGATTACCTTCTACTGTCCACCAAGCCCTAGACTGC 432

QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 433 GGGGGCCCTCACCAGCCACACAGCGCTACTGTCTCCCGAGAGATTACTACTGTGGACC 492

QY 141 CysLeuProGlyPheThrGlnHisGlyAspGlyCysValSerCysProHisSerThrLeu 160
Db 493 TCCCTGCCCGCTTCTATGATCATGAGCATGGCTGGCTCTGCCCCAGACACCGCTG 552

QY 161 GlySerCysProGlyArgGlyAlaAlaValCysGlyTrpArg 174
Db 553 GGGAGCTGTCCAGAGCGCTGTGCTGTGTGGCTGGAGGACAGAGTAGTGTGTGTCTGCT 612

QY 174 174

Db 613 GGGAAATGCGAGTGGGAGAACTGGGATGACCGAGGAGCGGGGTGAGAGGGGCGCAAC 672

QY 175 -----GlnMetPheTrpValGlnValLeuLeuAlaGlyLeu 186
Db 673 CACCCAGACACCCAGAGCTGTTCAGTGTGTTGGTCCAGAGTGTCTGTGCTGGCTG 731

QY 187 ValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyrArgHisCysTrpProHis 206
Db 732 CTGTCTCCCTCTCTGCTGGGCGCCACCTTACTTACATACCGGACATGCTGGCTCAC 791

QY 207 LysProLeuValThrAlaAspGluAlaGlyMetGlnAlaLeuThrProProAlaThr 226
Db 792 AACCCCTGTGTACTGATGATGAAGCTGGATGAGAGCTGTGACCCACCGAGCGGCACC 851

QY 227 HisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAspSerSerGlyLys 246
Db 852 CATCTGTACCTTGGACAGCGCCACACCTTCTAGCACCTTCTACACACTGTGAAG 911

QY 247 IleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTrpProGluThrGlnGlu 266
Db 912 ATCTGACCGCTTCAGTTGTGGGTAAACAGCTGAGACCCCTGGTACCCCGAGACCCAGAG 971

QY 267 AlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro 286
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QY 287 AlaAlaAlaProThrLeuSerProGlySerProAlaGlySerProAlaMetLeuGln 306
Db 1032 GCTGTGCGCCACACTCTGCGCAGAGTCCCGAGCGGCTGCGCACCATGATGTGACAG 1091

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Db 1092 CCGGGCCCGAGCTGTACAGACGTGATGACGCGGCTGCCACCGGGCGCTGGAAAGGACTTC 1151

QY 327 ValArgThrLeuGlyLeuArgGluAlaGlyIleGluAlaValGlnValGluIleGlyArg 346
Db 1152 GTGCGCACCTGTGGGCTGGCGGAGCAGAGATCCAGACCGGTGAGATCGGCCCGC 1211

QY 347 PheArgAspGlnGlyTrpGlnMetLeuLysArgTrpArgGlnGlnProAlaGlyLeu 366
Db 1212 TTCGAGACACAGCATGATGCTCAAGCGTGGCGCAGACGAGCGCGGGCGCTTC 1271

QY 367 GlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg 386
Db 1272 GAGCGCGTTTACGCGCGCTGGAGGCGCATGGGGCTGGAGCGGTGGAGAACCTTGGCC 1331

QY 387 SerArgLeuGlnArgGlyPro 393
Db 1332 AGCCGCTGACAGCGGCGCCG 1352

RESULT 13
AX331947 1743 bp DNA linear PAT 09-JAN-2002
LOCUS AX331947
DEFINITION Sequence 2456 from Patent WO0194629.
ACCESSION AX331947
VERSION AX331947.1 GI:18122581
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
REFERENCE
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrikan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 2456 13-DEC-2001;
Avalon Pharmaceuticals (US)
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source location/Qualifiers
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BASE COUNT 347 a 543 c 549 g 304 t
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Alignment Scores:
Pred. No.: 5.16e-106 Length: 1743
Score: 2140.50 Matches: 389

Percent Similarity: 91.10% Conservative: 0
Best Local Similarity: 91.10% Mismatches: 4
Query Match: 96.90% Indels: 35
DB: 6 Gaps: 1

US-09-993-234-6_COPY_25_417 (1-393) x AX331947 (1-1743)

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QY 21 LeuPheCysArgGlyCysProAlaGlyHisIleLysAlaProCysThrGluPro 40
Db 201 CTGTTTGTTCAGAGGCTGCGCCAGCGGAGCAGTCTGAAGGCCCTTGACAGGAGCC 260
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluHis 60
Db 261 TGGCGCAACTCCACTGCTGCTGTGTGCCACAGACACTTCTTGCCCTGGAGAACAC 320
QY 61 HisAsnSerGlyCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 80
Db 321 CATAAATCTGAATGCGCCGCTGCGAGCCGTGATGAGCAGGCCCTCCAGGTGGCGCTG 380
QY 81 GluAsnGlySerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 381 GAGAACTGTTAGCAGTGGCCGACACCGGCTGTGCTTAAGCCAGGCTGTTGGAG 440
QY 101 CysGlnAlaSerGlnCysValSerSerSerProPheTrpCysGlnProCysLeuAspCys 120
Db 441 TGGCAGGTGACCAATGTGTGACGAGTTCACCTTCTACTCCACCACTGCTAGACAGC 500
QY 121 GlnAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 501 GGGGCGCTGACCGCCACACAGCGCTACTCTGTTCCCGCAGAGATACGACTGTGGAGC 560
QY 141 CysLeuProGlyPheTrpGlyHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 561 TGCTGCTGCTGCTCTGTATGAACATGAGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTG 620
QY 161 GlnSerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 621 GGGAGCTGTCCAGAGCGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 680
QY 174 174
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Db 741 CACCCAAACACCACAGCTGCTTTCAGTG-TCGTGGGTCCAGGTGCTCTGCTGCTGCTT 799
QY 187 ValValProLeuLeuLeuGlyAlaThrLeuThrTrpTrpArgHisCysTrpProHis 206
Db 800 GTGCTGCCCTGCTGCTGCTGGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 859
QY 207 LysProLeuValThrAlaAspGlnAlaGlyMetGlnAlaLeuThrProProAlaThr 226
Db 860 AAGCCCTGTGTTACTGAGATGAGCTGGATGAGGCTGTGACCCACACCGGCCAC 919
QY 227 HisLeuSerProLeuAspPheSerAlaHisThrLeuLeuAlaProProAspSerSerGlyLys 246
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QY 367 GlnAlaValTrpAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGlnLysAspLeuArg 386
Db 1340 GGAGCGCTTACCGCGCCCTGGAGGCAATGGGCGCTGACAGCGTGTGCTGGAAGACTTGGCC 1399
QY 387 SerArgLeuGlnArgGlyPro 393
Db 1400 AGCCGCTGACAGCTGTGGCCG 1420
RESULT 14
LOCUS HSWSL1 1743 bp mRNA linear PRI 16-DEC-1996
DEFINITION H. sapiens mRNA for WSL-LR, WSL-S1 and WSL-S2 proteins.
ACCESSION Y09392
VERSION Y09392.1 GI:1669690
KEYWORDS WSL-1 gene; WSL-1R protein; WSL-S1 protein; WSL-S2 protein.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1743)
AUTHORS Kilsdonk, J., Raven, T., Jiang, Y. P., Goeddel, D. V., Gilles, K. M., Pun, K. T., Grinham, C. J., Brown, R., and Farrow, S. N.
TITLE A death-domain-containing receptor that mediates apoptosis
JOURNALS NATURE 384 (6607), 372-375 (1996)
MEDLINE 97088617
PUBMED 8934525
REFERENCE 2 (bases 1 to 1743)
AUTHORS Kilsdonk, J.
TITLE Direct Submission
JOURNALS Submitted (12-NOV-1996) J. Kilsdonk, GLAXO-Wellcome, Medicines Research Centre, Gunnels Wood Road, Stevenage, SG1 2NY, UK
FEATURES
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QY	174	-----	174
D	681	GGGAATGCCCGTGGGAGAACGTGGGATGGACCGGAGGGGAGCGGCTGAGAGGGGGCCAC	740
QY	175	-----glnmetPheTrpValGlnValLeuAlaGlyLeu	186
D	741	CACCCACACACCCACAGACTGCTTTCACTG-TTCGTGGCTCACAGTGTCTGCTGGCTGCT	799
QY	187	ValValProLeuIleuGluGlyAlaTrpLeuThyTrpThrTyraArgHisCysTrpProHis	206
D	800	GTGGTCCCCCTCTGCTTGGGGCCACCCGTGACCTTACACATTACCGCCACGCTGGCTCAC	859
QY	207	LysProLeuValThrAlaAspGluAlaGlyMetGlnAlaLeuThrProProAlaTrp	226
D	860	AAGCCCTGTTACTCATCATGATGAAAGTGGGATGGAGAGCTGTACCCACCACCGCCAC	919
QY	227	HistLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAspSerSerGlyLys	246
D	920	CATCTGTCACTTGTGGACAGCGCCACACCCCTTACACCTCTGTACACGCTGAGTAGAG	979
QY	247	IleCysThrValGlnIleuValGlyAsnSerTrpThrProGlyTrpProGluTrpGlnGlu	266
D	980	ANCTGACCGCTCATAGTGGTGGGTAAACAGCTGACCCCTGGCTTACCCGAGACCCAGGAG	1039
QY	267	AlaLeuCysProGluValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro	286
D	1040	GGGCTGTGCCCCACAGTGCATGTCTGTGGACCACTGTCCACAGACAGACTCTTGGCCCC	1099
QY	287	AlaAlaAlaProThrLeuSerProGluSerProAlaGlySerProAlaMetIleuGln	306
D	1100	GCTGTGGCGCCACACTCTCGCCCANAGTCCCAGCCGGCTGCCACGCCATGTAGCTGCAG	1159
QY	307	ProGlyProGluLeuTrpAspValMetAspAlaValProAlaArgArgTrpIleGluPhe	326
D	1160	CCGGCCCGCCAGACTCTACGACGTGATGTGACGGCGGTCCAGCGCGGCTGGANAAGAGTTCC	1219
QY	327	ValArgTrpIleuGlyLeuArgGluAlaGluIleGluAlaValGlnValGluIleGlyArg	346
D	1220	GTGGCGACGCTGGGCTGGCTGGCGAGGACAGATCGAAGCCGTGGAGGTGGAGATCGCTCTC	1279
QY	347	PheArgAspGlnGlnTrpGluMetLeuLysArgTrpArgGlnGlnGluProAlaGlyLeu	366
D	1280	TTCGAGACACAGCATGACGATGCTCAAGACACTGGCCGACAGACACCCCGGGGCTTC	1339
QY	367	GlyAlaValAlaTrpAlaAlaLeuGluLysMetGlyLeuAspGlyCysValGluAspLeuArg	386
D	1340	GGAGCGGTTTACGGCGCCCTGGAGGCGATGGGGCTGGACGGCTGCTGGAGAAGACTTGGCGC	1399
QY	387	SerArgLeuGlnArgGlyPro 393	
D	1400	AGCGCGCTGCAGCGGTGGCCG 1420	
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DEFINITION	Homo sapiens death receptor 3 beta (DR3) mRNA, complete cds.		
ACCESSION	AF026070		
VERSION	AF026070.1	GI:2570830	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
	Wierzbicka,K., Ribeiro,P., Charlot,C., Renard,N., Colfflier,B. and		
	Salles,G.		

TITLE A new death receptor 3 isoform: expression in human lymphoid cell lines and non-Hodgkin's lymphomas
JOURNAL Biochem. Biophys. Res. Commun. 242 (2), 376-379 (1998)
MEDLINE 98113360
PUBMED 9446802
REFERENCE 2 (bases 1 to 1669)
AUTHORS Marzocha, K., Ribeiro, P., Renard, N., Charlot, C., Colflier, B. and Sallies, G.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-1997) Hematology, CHRE Hospitalier Lyon-Sud, Chemin du Grand Revoyet, Pierre Benite 69495, France
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BASE COUNT 329 a 532 c 513 g 295 t
ORIGIN
Alignment Scores:
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DB: 9 Gaps: 2
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QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 201 CTGTTTGTGGAGAGGCTGCCCGCGGGGCACTGAAAGCCCTTGGACGAGGAGCC 260
QY 41 CysGlyLysSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGlnAsnHis 60
Db 261 TGGCGCAACTCCACCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 320
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
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QY 81 GluAsnGlySerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 381 GAGAACTGTTCAGCAGTGGCGGACACCGCGCTGTGTAAAGCAGGCTGTGTGTGTGTGTGT 440
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120

Db 441 TGGAGGTCAAGCCAAATGTGTCAGCACTTCAACCTTTACTGACCACCAATGCTAGACTGC 500
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QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSer----- 158
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QY 159 -----ThrLeuGlySerCysProGlnArgCysAlaAlaValCysGlyTyr 173
Db 620 GTCCCTTGACAGAGCAACCGCTGGAGGCTGTCCAGAGGCTGTGCTGTGTGTGTGTGTGT 679
QY 174 ArgGln-----MetPheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLe 191
Db 680 AGCAGAGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 739
QY 191 uLeuGlyAlaThrLeuThrTyrThrTyrArgHisCysTrpProHisLysProLeuValTh 211
Db 740 GCTTGGGGGCCACCTGACCTACACATACCGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 799
QY 211 rAlaAspGlnAlaGlyMetGlnAlaLeuThrProProAlaThrHisLeuSerProLe 231
Db 800 TGCAGATGAAGCTGGATGAGGCTGTGACCCACACCGCCACCAATGCTGACCTT 859
QY 231 uAspSerAlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCysThrValG 251
Db 860 GGAACAGCGCCACACCTTCTAGCACCCTTCGACAGCAGTGAAGAATCTGACCGTCA 919
QY 251 nLeuValGlyAsnSerTrpThrProGlyTyrProGlyuThrGlnAlaLeuCysProG 271
Db 920 GTTGGTGGGTAAACAGCTGAGCCCTGTGCTACCCGAGACCCAGAGAGGGGCTGTCCGCA 979
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Db 980 GGTACATATGGTCCGGAGACGCTGGCCAGAGAGCTTGTGGCCCGCTGCTGCGCCAC 1039
QY 291 rLeuSerProGluSerProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLe 311
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QY 311 uTyrAspValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuG 331
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QY 331 yLeuArgGlnAlaGluIleGlnAlaValGlnValGlnIleGlyArgPheArgAspGlnG 351
Db 1160 GCTCGCGAGGCAAGATCGAAGCCGTGAGAGTGGATTCGCTCTTCCGACAGACAGCA 1219
QY 351 nTyrGluMetLeuLysArgTrpArgGlnGlnProAlaGlyLeuGlnAlaValTyrAl 371
Db 1220 CTAGAGATGCTCAAGACATGCGCCGACAGCAGACCCCGGCGCTCGAGCGCTTTACGC 1279
QY 371 aAlaLeuGlnArgMetGlyLeuAspGlyCysValGlnAspLeuArgSerArgLeuGlnAr 391
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QY 391 gGlyPro 393
Db 1340 TGGCCCG 1346

Search completed: April 6, 2003, 21:07:51
Job time : 4591.25 secs

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GenCore version 5.1.4-p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:33:09 ; Search time 365.927 Seconds

(without alignments)
2418.610 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_417

Perfect score: 2209
Sequence: 1 QGSTRSPRCDACAGDFHKKIG.....ERMGLDGCVEDLSRLQGRP 393

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-DB-N.geneseq.101002 -OFMT-fastgap -SUFFIX-rng -MINMATCH-0.1 -LOPCBL-0
-LOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-blossum62 -TRANS-human40.cdl
-LIST-45 -DOCNLIG-200 -THR-SCORE-pct -THR-MAX-100 -THR-MIN-0 -ALIGN-15
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-YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	2209	100.0	1254	AA189427	Death domain conta
2	2209	100.0	1254	AA189427	Death domain conta
3	2209	100.0	1254	AA189427	Human death domain
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ALIGNMENTS

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AA189427:
02-MAR-1998 (first entry)
Death domain containing receptor DR3 cDNA.
Death domain containing receptor: DR3; human; apoptosis;
Inflammation; NF-kappaB; ds.
Homo sapiens.
Key sig_peptide location/Qualifiers
/*tag- a


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FH Key Location/Qualifiers
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FT /product- "Death domain containing receptor DR3"
FT mat_peptide /tag- b
FT /tag- 73..1251
FT /tag- c
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XX 06-JAN-1999.
XX
XX 12-MAR-1997; 97JP-0057503.
XX
XX 06-FEB-1997; 97US-0037341.
XX 12-MAR-1996; 96US-0013285.
XX 17-OCT-1996; 96US-0028711.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI) UNIV MICHIGAN.
XX
XX MPI: 1999-124390/11.
XX P-RSDB; AAW5538.
XX
XX PT New death domain containing receptor and recombinant vector -
XX optionally comprising leader sequence
XX
XX PS Claim 6; Fig 3; 50pp; Japanese.
XX
XX CC The invention provides nucleotide sequences encoding death domain
XX containing receptor polypeptides DR3-VI and DR3. The DR3-VI cDNA clone
XX is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
XX contained in ATCC deposition No. 97757. Recombinant vectors comprising
XX the nucleic acid sequences and optionally the leader sequences are
XX used for the recombinant production of the proteins. The present
XX sequence represents a cDNA encoding the death domain containing
XX receptor polypeptide (DR3).
XX
XX SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:
Pred. No.: 2,19e-117 Length: 1254
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x AAX00925 (1-1254)
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QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 133 CTGTTTGTGTGACAGAGCTGCCAGCGGGACACTGAAAGGCCCTTGACAGGAGCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTTPGluAsnHis 60
DB 193 TGGCGCAACTCCACCTGCTGTGTGTCCCAACACACTTCTTGCCCTGGGAGAACAC 252
QY 61 HisAsnSerGlyCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 253 CATTAATTCGTAATGTCGCCCTGCGACAGCCTGTATAGCAGAGCCTCCAGAGTGGCCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTTPPheValGlu 100
DB 313 GAGAACTGTTTCAGACAGTGGCGGACACCCGCTGTGTGTAAGCCAGGCTGTTGTGGAG 372
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120

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DB 373 TGCAGGTCACCCCAATGTGTGACAGTTCACCCCTTCTACTGCCAACCAATGCTAGACTGC 432
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DB 433 GGGGCCCTGACCGGCCACACAGGCTACTGTGTCCCGCAGAGTACTGACTGTGGAGCC 492
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 493 TGCTGCTGCTGCTGTATGAAACATGGGATGGTGGCTGGCTGCTGCCACAGACCCCTG 552
QY 161 GlySerCysProGluArgCysAlaValCysGlyTTPArgGlnMetPheTyrValGln 180
DB 553 GGGAGCTGTCCAGAGCCCTGTGCGCTGTGTGCTGGAGCAGATGTTGTGGCTCAG 612
QY 181 ValLeuLeuAlaGlyLeuValAlaProLeuLeuGlnGlyAlaThrLeuThrTyrThrTyr 200
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QY 201 ArgHisCysTTPProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
DB 673 CGCCACTGCTGGCTCACAAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 732
QY 221 ThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuAlaPro 240
DB 733 ACCCCACACCGCGCCACCATCTGTCACTTGGACACCGCCACACCTTCTAGCACT 792
QY 241 ProAspSerSerGlyLysIleCysThrValGlnLeuValGlyAsnSerTTPThrProGly 260
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QY 261 TyrProGlnThrGlnGluAlaLeuCysProGlnValThrTTPSerTTPAspGlnLeuPro 280
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QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
DB 913 AGCAGACTCTTGGCCCGCTGTGCGCCACACTCTCCAGAGATGCCAGCCGCGCTGC 972
QY 301 ProAlaMetLeuLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
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DB 1213 TGCSTGGAAGACTTGGCGAGCGCGCTGACAGCGGCGCCG 1251

RESULT 3
AAC68777
ID AAC68777 standard; cDNA; 1254 BP.
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XX AAC68777;
XX
XX 20-FEB-2001 (first entry)
XX
XX Human death domain containing receptor DR3 coding sequence.
XX
XX Human: death domain containing receptor; DR3; cancer;
XX autoimmune disorder; inflammation; cardiovascular disorder; infection;
XX neurodegenerative disease; angiogenesis; ss.
XX
XX Homo sapiens.
OS

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XX XX W0200064465-A1.
PN 02-NOV-2000.
XX 21-APR-2000; 2000MO-US10741.
XX 22-APR-1999; 9905-0130488.
PR 28-MAY-1999; 9905-0136741.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNITV MICHIGAN.
PA (YUGG/) YU G.
PA (NIJ/) NI J.
PA (GENT/) GENTZ R L.
PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX
PI YU G, NI J, Gentz RL, Dillon PJ, Dixit VM;
XX
XX MPI; 2000-687263/67.
DR P-PDB; AAB36265.
XX
XX Treating graft-versus-host disease, cancer, immunodeficiency or an
PT autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent -
XX
XX Example 2B; Fig 2; 273pp; English.
XX
XX The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-V1. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC atherosclerosis, ischemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune diseases such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.
XX
SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:
Pred. No.: 2,19e-117 Length: 1254
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x AAC68777 (1-1254)

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DB 73 CAGGGGGGACATCGTAGGCCAGGCTGTGACTGCGCGTAGCTTCACAAAGAGATTGGT 132
QY 21 LEUPHCYASCYARGLCYSPROALAGLYHISTYLEULYSALAPROCYSTRHGIUPO 40
DB 133 CTGTTTGTGGCAGAGGCTGCCAGCGGACACTACCTAAGGCCCTTGCACGAGGCC 192
QY 41 CYSGLYASNSERTHCYSLAVALCYSPROGLINASPPHLEULALATRPGLUASNHS 60
DB 193 TCGGGCACTCCACCGCTTGTTGTGTCCCAAGACACTTCTTGGCCCTGGGAGAACCC 252
QY 61 HISASNSEGLCYSLAVALCYSGINALCYASAPGLUGINALASERGLNVALALEU 80
DB 253 CATTAATTCGAAATGTCGCCGCTGCCAGGCTGTGATGACAGAGCCCTCCAGTGGCGCTG 312
QY 81 GUASNCSYSERLAVALLAASPPHARGCYSGLYCYSLYSPROGLYTRPHEVALGIU 100
DB 313 GAGAACTGTTCAGACAGTGGCCGACCCGCTGTGGCTGAACCCAGGCGTTTGTGGAG 372
QY 101 CYSGLINALEISERGLNVALSERSERPROPHETRYCYGLINPROCYSLAUSPCYS 120
|||||

DB 373 TGCAGGTGACAGCCATGTGTACAGAGATTCAACCTTCTACTGCCACACCATGCTAGACTGC 432
QY 121 GLYALALEUHSARGHISTHARGLEULCYSSERARGARGLAPTHRASPYSGLYTHR 140
DB 433 GGGGCGCTGCACGCCACACACGCTACTCTGTCCCGCAGAGATGACTGCTGGGAGCC 492
QY 141 CYSLEUPROGLYPHETRYGLIUNHISGLYASPGLYCYSAVALSERCYSPPROHSPERTHLEU 160
DB 493 TGCCTGCTGCTCTTCTGTGAACATGGGATGGCTGCTGTCTGTGCCCCACAGCACCTCC 552
QY 161 GLYSERCYSPROGLIUNHARGCYSAVALAVALCYSGLYTRPARGLINMETPHETRPVALGI 180
DB 553 GGGAGCTGTCCAGAGCGCTGTCCGCTGTCTGTGGCTGAGGAGAGANTTCTGTGGTCCAG 612
QY 181 VALLEULNALAGLYLEUVALAVALPROLEULLEULGLYALATHRLEUTHRYTRHTRYR 200
DB 613 GTGCTCTGCTGCTGCTGTGGTGTCCCTCTCTCTCTGTTGGGCGCACCTGACCTACACATAC 672
QY 201 ARGHISCYSTRPPOHISLSPROLEUVALTHRALASPGIUNHISGLYMETGLIUNHIS 220
DB 673 CGCCACTGTGCTGCTGCACAAAGCCCTGTGTACTGCAATGATGAGCTGGATGGAGCTCTG 732
QY 221 THPROPROALATHRHSLEUSERPROLEUASPSERLAHISTHRLLEULALAPRO 240
DB 733 ACCCCACACCGCGCCACCCATCTGTACACCTTGAGACAGCCGCCACACCTTCTAGACACT 792
QY 241 PROASPSERGLIUNHISGLYSTRHVALGINLEUVALGLYASNSETRTPHTRPROGLY 260
DB 793 CTTGACAGCAGTAGAAGATCTCACCGCTCCACTGTGGTGAACAGCTGGAGCCCTGCG 852
QY 261 TYRPROGLIUNHISGLYALALEUCYSPROGLINVALTHRTRPSERTRPASPGINLEUPRO 280
DB 853 TACCCGAGAGCCAGAGAGGGCTCTCCCGCAGATGACATGCTCCGGACACAGTTGCC 912
QY 281 SERHARALALEUGLYPROALALALAPROHRLLEUSERPROGLIUSERPROALAGLYSER 300
DB 913 AGCAGAGCTCTTGGCCCGCTGCTGCGCCACACTCTCCGACAGAGCCCGCGGCTGCG 972
QY 301 PROALAMETLEULINLEUPROGLIUNHISLSPROGLINLEUTHRALASPSERLAVALLAVAL 320
DB 973 CCAGCCATGATGCTGCAGCGCGGCGCCGACGCTTACGAGCTGATGAGCGCGGTCCAGCG 1032
QY 321 ARGARGTRPLYSGLIUNHISVALARGTHRLLEUGLYLEUARGIUNHISGLYALALEU 340
DB 1033 CGGCGCTGTGAAGAGATGCTGTGCGACGCTGGGCTGCGGAGGACAGATCGAAGCCGTG 1092
QY 341 GLIUNHISGLIUNHISGLYARGHARGHARGASPGININTYRGLIUNHISLVALARGITRPARGLIN 360
DB 1093 GAGGTGAGATGCGCGCTTCCGAGACAGCAGTAGAGATGCTCAAGCGCTGGCGCCAG 1152
QY 361 GINGLINPROALAGLYLEUGLYALAVALLYTRALALALEUGIUNHISGLYMETGLYLEUASPGLY 380
DB 1153 CAGACGCCGCGGGCGCTGGAGCCGTTTACGGGCGCTTGAGCCGATGGGCTGGAGCCG 1212
QY 381 CYSVALGIUNHISLEUARGSERARGLEUGLINARGGLYPRO 393
DB 1213 TCGGTGGAAGACTGTGCGAGCCGCTGACGCGGCGCG 1251

RESULT 4
AAT91180
ID AAT91180 standard; cDNA; 1634 BP.
XX
AC AAT91180;
XX
DT 14-APR-1998 (first entry)
XX
DE Human apoptosis protein Apo-3 cDNA clone FH20.57.
XX
KW Apo-3; apoptosis; human; therapy; drug screening; ss.
XX
OS Homo sapiens.
XX
FH key Location/Qualifiers

FT CDS 89..1342
FT sig_peptide /*tag- a
FT 89..160 /*tag- b
FT /note= "determined by hydropathy analysis"
FT mat_peptide 161..1339
FT /*tag- c
XX
XX W09737020-A1.
XX
XX 09-OCT-1997.
XX
XX 31-MAR-1997; 97WO-US05230.
XX
XX 23-SEP-1996; 96US-0710802.
XX 01-APR-1996; 96US-0625328.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ;
XX
XX WPI; 1997-503105/46.
XX
XX
XX Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis
XX in mammalian cells
XX
XX Example 1; Page 45-46; 70pp; English.
XX
XX cDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see
XX W6709), designated Apo-3, that stimulates or induces apoptotic
XX activity in mammalian cells. It was isolated from a human foetal
XX heart cDNA library by screening with probes (see T91183-84) based
XX on an EST sequence (GenBank locus W71984) that showed homology to
XX the intracellular domain of human TNFR1 and CD95. Amino acid
XX residues 1-181 of Apo-3 are identical to another novel apoptosis
XX polypeptide, Apo-2LI (see W6708). Nucleic acids encoding Apo-3
XX can be used diagnostically for tissue-specific typing and to
XX produce recombinant Apo-3 polypeptides, especially the
XX extracellular domain (amino acids 1-198) or death domain (amino
XX acids 338-417). Apo-3 can be used to induce apoptosis or
XX NF-kappa-B- or JNK-mediated gene expression for therapeutic
XX purposes. Non-human transgenic animals containing cells that
XX express Apo-3 nucleic acid, and knockout animals containing
XX cells that have an altered Apo-3 gene, can be used in drug
XX screening and development.
XX
XX Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 2.92e-117 Length: 1634
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 gaps: 0
US-09-993-234-6_COPY_25_417 (1-393) x AAT91180 (1-1634)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 161 CAGGCGCGGACCTGACCCCGAGGTGACTGTCCGGTGTCTCCACAAAGAAATTTGGT 220
QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 221 CTGTTTGTTCAGACGCTGCCAGCGGGGACATACCTGAAGGCGCCCTGTGACGAGGCC 280
QY 41 CysGlyLysSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGlnAsnHis 60
DB 281 TGCAGCACTCCACCTCTGTGTGTGCCCAAGACACCTTCTGGCTGGAGAACACAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 341 CATATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCCAAGTGGCGTG 400

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 401 GAGAACTGTTCCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCAGGCTGTTGTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 461 TGCAGGCTCAGCACAATGTGTGAGCAGTTCACCCCTTCTACTGCACCAATGCTAGACTGC 520
QY 121 GlnAlaLeuHisArgHisThrArgLeuLeuYssSerArgArgAspThrAspCysGlyThr 140
DB 521 GGGGCGCTGCACCGCCGACACAGGCTACTCTGTTCGCCAGAGATACTGACTGTGGAGCC 580
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 581 TGCCTGCCTGCTCTAATGAACATGGGAGATGGCGTGGCTGCTGCCACAGCAGCAGCTGC 640
QY 161 GlySerCysProGluThyGlyCysAlaAlaValCysGlyTyrParGlnMetPheTrpValGln 180
DB 641 GGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGCTGAGGAGAGATGTTCTGGGCTCCAG 700
QY 181 ValLeuLeuAlaGlyLeuValAlaProLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
DB 701 GTGCTCTGCTGCGCTGTGTGTGCTCCCTGCTGCTGTGGGCGCCACTGACTACACATAC 760
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGlnAlaGlyMetGlnAlaLeu 220
DB 761 CGCCACGCTGCTGCTCCACACACCCCTGCTTCTGCTGACATGAAGCTGGATGGAGCTCTG 820
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuAlaPro 240
DB 821 ACCCCACACCGCGCCACCCATCTGTACCCCTTGAGACGCGCCACACCCCTTGACACT 880
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlnAsnSerTrpThrProGly 260
DB 881 CTTAGACGACATGAGATGTGACCGCTCCAGTTGGGGTAAACATGATGACCTGACCTTGGC 940
QY 261 TyrProGlnThrGlnAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
DB 941 TACCCGAGACCCAGAGAGCGCTGTGCCCGCAGGATGATGCTCTGGAGACCATGTGGCC 1000
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
DB 1001 AGCAGAGCTCTTGGCCCGCTGCTGCGCCACACTCTGCGCAGATGTCCTCCAGCGGCTCG 1060
QY 301 ProAlaMetLeuGlnProGlyProGlnLeuThrAspValMetAspAlaValProAla 320
DB 1061 CCAGCCATGATGCTGACGCGCGCGCCGCGAGCTCTACGACGATGAGAGCGGCTCCAGCG 1120
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlnAlaGluIleGlnAlaVal 340
DB 1121 CGGCGGTGGAAGGAGTGTGTCGCGCAGCTGGGGCTGCCGAGGACGAGATGGAAGCCCTG 1180
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
DB 1181 GAGGTGAGATCGCGCTTCCGAGACCCAGCATGATGATGATGATGATGATGATGATGATG 1240
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaIleGlnValGlnMetGlyLeuAspGly 380
DB 1241 CAGCAGCCCGGGGCTCTGGAGCGGTTTACCGGCGCTGGAGCGCATGGGCTGGAGCGCG 1300
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
DB 1301 TGCGTGGAAGACTTGGCGAGCGGCTGTGAGGCGGCGCG 1339
RESULT 5
AAH27782
ID AAH27782 standard; DNA; 1634 BP.
XX
XX AAH27782;
AC
XX
XX 15-AUG-2001 (first entry)
XX

DE	Human genomic DNA encoding a rheumatoid arthritis associated protein.
XX	
KW	Rheumatoid arthritis; transmembrane protein; human; ds.
OS	Homo sapiens.
FH	Key
FT	CDS
FT	/tag=
FT	/product= "Rheumatoid arthritis associated protein"
XX	
PN	WO200132921-A2.
PD	
XX	10-MAY-2001.
PF	
XX	01-NOV-2000; 2000WO-JP07690.
PR	
XX	01-NOV-1999; 99JP-0310805.
PA	(SHIO/) SHIOZAWA S.
PI	Shiozawa S, Konishi Y;
XX	
DR	WPI: 2001-308750/32.
DR	P-PSTDB; AAB97370.
PT	
PT	Diagnosing rheumatoid arthritis by probing digested human genomic DNA
XX	or comparing expression of mRNA or polypeptide of a region of
XX	transmembrane protein -
PS	Claim 1; Page 14-18; 21pp; Japanese.
CC	
CC	This invention relates to a method of diagnosing chronic rheumatoid
CC	arthritis by digesting human genomic DNA with EcoRI and hybridizing it
CC	with a probe containing a fragment of the present sequence which
CC	represents DNA encoding a transmembrane protein. The method is used for
CC	the diagnosis of chronic rheumatoid arthritis, and for developing new
CC	treatments.
SQ	Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;
Alignment Scores:	
Pred. No.:	2,92e-117 Length: 1634
Score:	2209.00 Matches: 393
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	Gaps: 0
US-09-993-234-6_COPY_25_417 (1-393) x AA#27782 (1-1634)	
OY	1 GINGLYGLYTHARGSERPROARGCYSAPRCYSALAGIYAAPHNHIALYSLILEGLY 20
Db	161 CAGGGCGGACMCAGTGGGCCCAAGGTGTACTGTCTGCCGGTGACTTCACAAGAAGATTGGT 220
OY	21 LEUPHECYSARGGLVCSPROMLAGLNIHSTRYLEULYSALARPCSYSTHGILUPRO 40
Db	221 CGTTTGTGTGAGAGGCTGCCACAGGGGGCACTACCCTGAAGGCCCTTGCAAGGAGCCC 280
OY	41 CYSGIYAASERTHCYSLEUVALCYSPROGLNASPRHRPHLEUALATRPGLUANMHS 60
Db	281 TGCGGCAACTCCACCTGCCCTGTGTGTGCCAACAGACACTTCTGGCCTGGGAGAACAC 340
OY	61 HISAENSRGLUCYALAIRGCYSGLINLIACYSAAPGIUGINALASERGLNVALALEU 80
Db	341 CATAAITTTGTAATGATGCCCCGCTGCCAGGCTGTGATGAGCAGGGCCCTCCAGGTGCGGTG 400
OY	81 GLUASNCSERRALAVALAIASPRTHARGCYSGLYCYSPLROGLTYTRPHEVALGLU 100
Db	401 GAGAACTGTTCAGCAGTAGTGGCCGACACCCGCTGTGGCTTAAGCCAGGCTGGTTTGTGGAG 460
OY	101 CysGINVALserGINcysVALserSerSerProPhETyTyCysGLINProCysLEUaspCys 120

Db	461	TGGCAGGTCGAGCCATGTGTGTGACGAGTTCACCCCTTACTGCTCCACCACTATGCCACTGCTGC	520
Qy	121	GLYAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr	140
Db	521	GGGGGCGCTGCACCGGCGCACACAGGCTACTCTGTTCCCGCAGAAATCTGACTGTGGGACC	580
Qy	141	CysLeuProGlyPheThrGluHisGlyAspGlyCysValysValSerCysProHisSerThrLeu	160
Db	581	TGCGTCCCTGGCTTTATGAACATGGGATGGCTGCTGTCTGTCGCCACAGACACCTTG	640
Qy	161	GlySerCysProGluArgCysAlaAlaValCysGlyTyrPargGlnMetPheTyrValGln	180
Db	641	GGAGACTGTCACAGACGCGTGTGCCGCTGTGTGGCTGGAGGAGCAAGTTCGTGGCTCAG	700
Qy	181	ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyValaThrLeuThrTyrThrTyr	200
Db	701	GTGCTCTCGGGCTGGGCTGTGTGGTCCCTCTCGCTGGGGCCACCTGTACATCACTATAC	760
Qy	201	ArgHisCysTyrProHisLysProLeuValThrAlaAspGlnAlaGlyMetGlnAlaLeu	220
Db	761	CGCCACTGCTGGCTCTCACAGCCCCCTGTACTGTCAAGATATACCTGGATGGAGGCTTG	820
Qy	221	ThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro	240
Db	821	ACCCACACACCGGCGCACCACTCTGCACCTTGAGACAGCCGACACACCTTCAGACCT	880
Qy	241	ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerThrPheProGly	260
Db	881	CCTGCACACACTGAAAGATGTGCACCGTCACTGGTGGATGAACGCTGGACCCCTGGC	940
Qy	261	TyrProGlnThrGlnGlnAlaLeuCysProGlnValaThrTyrSerTyrAspGlnLeuPro	280
Db	941	TACCCCGAGACCCGAGAGGCGCTGTGCCGACAGGTGACATGGTCTGGGACCACTGTGCC	1000
Qy	281	SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer	300
Db	1001	AGCAAGGCTCTTGGCCCCCGCTGCTGGCCGACACCTCTCGCAGAAAGTCCCAACCGGCTCG	1060
Qy	301	ProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla	320
Db	1061	CCAGCAGTATGTCGTGACGCGGGGCGGCACACTCTACAGACTATGACCGCGGTCCACGC	1120
Qy	321	ArgArgTrrPlyGluPheValaThrThrLeuGlyLeuArgGlnAlaGluIleGlnAlaVal	340
Db	1121	CGGGCGCTGGAAAGGAGTTCGTGCGCAGCGCTGGGGCTCGCGAGGACAGATCGAAGCCGTG	1180
Qy	341	GluValGluIleGlyArgPheArgAspGlnGlnTyrGlnMetLeuLysArgTrrPargGln	360
Db	1181	GAGGTGGAGATCGGCCCTTCCAGACACACACTACGAAATGCTCAAGCGCTGGCGCAG	1240
Qy	361	GlnGlnProAlaGlyLeuGlyAlaValaTyrAlaAlaLeuGlnArgMetGlyLeuAspGly	380
Db	1241	CAGCAGCGCCGGGGGCGTCGGAGCGCTTACGCGGGCCCTGAGACGCATGGGGCTGGACCGC	1300
Qy	381	CysValGluAspLeuArgSerArgLeuGlnArgGlyPro	393
Db	1301	TGCGTGGAAAGACTTGGCGACCGCCGTCGACAGCGGCGCCG	1339
RESULT 6			
AAL47186			
ID	AAL47186 standard; cDNA; 1634 BP.		
XX	AAL47186;		
XX	AC		
XX	DT		
XX	22-AUG-2002 (first entry)		
XX	Human rheumatoid arthritis associated DR3 gene related cDNA #1.		
DE	Human rheumatoid arthritis associated DR3 gene related cDNA #1.		
XX	Human rheumatoid arthritis associated DR3 gene related cDNA #1.		
KM	Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;		
XX	gene therapy; gene; ss.		
XX	Homo sapiens.		
OS	Homo sapiens.		

EH Key Location/Qualifiers
FT CDS 89..1342
FT /*tag= a
FT /product= "AAO17879"
PN WO200234912-A1.
XX
XX
XX 02-MAY-2002.
XX
XX 24-OCT-2001; 2001WO-JP09313.
XX
XX 24-OCT-2000; 2000JP-0334296.
XX 27-MAR-2001; 2001JP-0090346.
XX 30-MAR-2001; 2001JP-0099990.
XX
XX (NEMI-) NEM IND RES ORG.
XX (SHIO/) SHIOZAWA S.
XX
XX Shiozawa S, Konishi Y;
XX
XX WPI; 2002-417132/44.
XX P-PSDB; AAO17879.
XX
XX
XX Genomes, particularly DR3 genomic DNA, participating in rheumatoid
XX arthritis via mutation, useful in evaluating disease onset and its
XX possibility and providing therapy and remedies -
XX
XX Example 1; Page 66-69; 84pp; Japanese.
XX
XX The present invention relates to the human DR3 gene, which is associated
XX with rheumatoid arthritis. Certain mutations in the gene can be linked to
XX the disease. The sequences can be used to evaluate disease onset and its
XX possibility and to provide therapy and remedies. The present sequence is
XX a coding sequence described in the exemplification of the invention.
XX
XX Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other:
XX
XX
XX Alignment Scores:
XX Pred. No.: 2,92e-117 Length: 1634
XX Score: 2209.00 Matches: 393
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX Gaps: 0
XX
XX US-09-993-234-6_COPY_25_417 (1-393) x AAL47186 (1-1634)
OY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 161 CAGGGCGGACACTGTAAGCCCGAGGTGTGACTGTGCCGGTACTTCCACAAAGATTTGCT 220
OY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 221 CTGTTTGTGCAGAGGCTGCCACAGGGGCACTACTGTAAGGCCCTTGCACGGAGCCC 280
OY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 281 TGGCGCACTCCACTGCTGTGTGTGTCGCCCAAGACACTTCTTGGCGGAGAACAC 340
OY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 341 CATATTCTGAAATGTCGCCGCTGCAGGCTGTGATGACAGGCTCCACAGGTGGCGCTG 400
OY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
DB 401 GAGAACTGTTCAGAGTGGCCGACACCCGCTGTGCTGTAACCCAGGCTGTTTGGAG 460
OY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 461 TGGCAGGTCCAGCCAAATGTCAGAGTTACACCTTCTACTGCAACCATGCTAGACTGC 520
OY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
|||||

DB 521 GGGGCCCTGCACCCGACACAGGCTACTCTGTCCCGAGAGATGACTGTGGAGCC 580
OY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 581 TGGCTGGCTGGCTTCTATTAACATGGCGATGGCTGGTCTCTCCGCCACAGACACCTTG 640
OY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrArgGlnMetPheTrpValGln 180
DB 641 GGGAGCTGTCCAGACGCGCTGCCGCTGCTGTGGCTGGAGCAGATGTTCTGGGCTCAG 700
OY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyr 200
DB 701 GTGCTCTGGCTGGCTGTGTGTGTGCTCCCTGCTGGTGGGCGACCTGTGACACATAC 760
OY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
DB 761 CGCCACTGTGGCTTCACAGGCCCTGGTACTGCAAGATGAAGCTGGATGGAGGCTCTG 820
OY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
DB 821 ACCCCACACCGGACCCATCTGTACCCCTTGACAGCGCCACACCTTCTAGACCT 880
OY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
DB 881 CCTGACAGCAGTGAAGATGTGCACCGTCGATGGTGGTGAACGCTGGACCCCTGGC 940
OY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
DB 941 TACCCGAGACCCAGAGGCGCTGTCCCGAGGTGATGCTCTGGGACCACTTGGCCC 1000
OY 281 SerArgAlaLeuGlyProAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
DB 1001 AACAGAGCTCTGGCCCTGCTGCTGCGCCACACTCTCCGACAGTCCACCGGCTCG 1060
OY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
DB 1061 CCAGCATGATGCTGTGAGCGGGGCGGCGGCTTACGAGTGAATGACCGGCTGCCAGG 1120
OY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGlyIleGluAlaVal 340
DB 1121 CGGCGCTGGAAGAGTCTGCTGCGACGCTGGGCTGCGGAGGACAGATGCCAACCGCTG 1180
OY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
DB 1181 GAGGTGAGATGCGGCGCTTCCGAGACAGACAGTACGATGCTCAAGCGCTGGCCAG 1240
OY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetLysAspGly 380
DB 1241 CAGCAGCCCGGCGGCTGCGGACCGTTTACGGGCGCTGAGCGCATGCGGCTGGAGCG 1300
OY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
DB 1301 TGGCTGGAAGACTTGGCGACGCGGCTGCGAGCGGCGCCG 1339
RESULT 7
AAC91477
ID AAC91477 standard; cDNA; 1662 BP.
XX
XX AAC91477;
AC
XX 21-MAR-2001 (first entry)
DT
XX
XX Human PRO779 cDNA.
DE
XX
XX Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW antirheumatic; cardiant; antiandemic; immunosuppressive; antithyroid;
KW antidiabetic; nocotropic; neuroprotective; hepatotropic; virocidic;
KW antiallergic; antiasthmatic; immune related disorder;
KW hepatobiliary disease; autoimmune disease; allergy; ss.
OS Homo sapiens.
XX
XX WO200073452-A2.
PN

XX 07-DEC-2000.
 PD 02-JUN-2000; 2000MO-US15264.
 PF
 XX
 PR 02-JUN-1999; 99MO-US12252.
 PR 20-JUL-1999; 99US-0144732.
 PR 20-JUL-1999; 99US-0144758.
 PR 28-JUL-1999; 99US-0146222.
 PR 01-SEP-1999; 99MO-US20111.
 PR 15-SEP-1999; 99MO-US21090.
 PR 15-SEP-1999; 99MO-US21547.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99MO-US28313.
 PR 01-DEC-1999; 99MO-US28634.
 PR 09-DEC-1999; 99US-0170262.
 PR 20-DEC-1999; 99MO-US30911.
 PR 05-JAN-2000; 2000MO-US00219.
 PR 06-JAN-2000; 2000MO-US00376.
 PR 11-FEB-2000; 2000MO-US03565.
 PR 18-FEB-2000; 2000MO-US04341.
 PR 18-FEB-2000; 2000MO-US04342.
 PR 22-FEB-2000; 2000MO-US04414.
 PR 24-FEB-2000; 2000MO-US04914.
 PR 15-MAR-2000; 2000MO-US06884.
 PR 20-MAR-2000; 2000MO-US07377.
 PR 21-MAR-2000; 2000MO-US07532.
 PR 30-MAR-2000; 2000MO-US08439.
 PR 17-MAY-2000; 2000MO-US13705.
 PR 22-MAY-2000; 2000MO-US14042.
 XX
 PA (GENTH) GENENTECH INC.
 PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tamas D, Watanabe CK;
 PI Wood WI;
 PI
 XX
 DR WPI: 2001-025253/03.
 DR P-PSDB: AAB50918.
 PT
 PT Thirty three nucleic acids encoding PRO polypeptides which are useful
 PT in the diagnosis and treatment of immune related disorders, e.g.
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 PT thyroiditis and diabetes mellitus.
 XX
 PS Claim 48: Fig 33; 218pp; English.
 XX
 CC The present sequence is one of thirty three nucleic acids encoding PRO
 CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
 CC antagonists are useful for treating and diagnosing immune related
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases
 CC (such as infectious, autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
 CC food hypersensitivity and urticaria), immunological diseases of the
 CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
 CC and hypersensitivity pneumonitis), transplantation associated diseases
 CC including graft rejection and graft-versus-host diseases.
 XX
 SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;
 Alignment Scores:

Pred. No.:	2,97e-117	Length:	1662
Score:	2209.00	Matches:	393
Percent Similarity:	100.008	Conservative:	0
Best Local Similarity:	100.008	Mismatches:	0
Query Match:	100.008	Indels:	0
DB:	22	Gaps:	0

US-09-993-234-6_COPY_25_417 (1-393) x AAC91477 (1-1662)

QY	1	GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly	20
DB	175	CAGGCGCGACCTCAGCTACCCAGGCTGACGTCCGGTGACTCCACAGAACATTGGT	234
QY	21	LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro	40
DB	235	CTGTTTGTTCAGAGGCTGCCAGCGGGGACTACTGAAAGCCCTTCACAGGAGCC	294
QY	41	CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTyrGluAsnHis	60
DB	295	TGCGCAACTCCACCTGCTGTTGTGTCCCAAGACACCTTTCGGCTGGAGAACCC	354
QY	61	HisAsnSerGlyCysAlaArgCysGlnAlaCysAspIleGlnAlaSerGlnValAlaLeu	80
DB	355	CATTAATTCGAATGTCGCCCTGCGCAGGCTGTGATAGCAGGCTCCAGGTGGCGCTG	414
QY	81	GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu	100
DB	415	GAGAACTGTCAGCAGGCGCCGACACCCGCTGTGGCTGTAAAGCCAGGCTGTTGGAG	474
QY	101	CysGlnValSerGlnCysValAlaSerSerProPheTyrCysGlnProCysLeuAspCys	120
DB	475	TGCCAGGTCCAGCAATGTGCAGAGTTCAACCTTTCACGACCAACATCCATGACTGC	534
QY	121	GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr	140
DB	535	GGGGCGCTGCAGCCGACACACGCGTACTGTGCCGCGAGATGACTGCTGGGACC	594
QY	141	CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu	160
DB	595	TGCTGCTGCTGCTTCTATGAAATGCGAGTGGCTGTGCTGCCACGACGACACCTG	654
QY	161	GlySerCysProGlyArgCysAlaAlaValCysGlyTyrArgGlnMetPheTyrValGln	180
DB	655	GGGAGCTGTCCAGAGCGCTGCGCTGTGCGTGGCGAGCAGATGTTCTGGGTCCAG	714
QY	181	ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrTyr	200
DB	715	GTCTCTCTGCTGCTGCTTGTGTCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG	774
QY	201	ArgHisCysTyrProHisLysProLeuValThrAlaAspGlnAlaGlyMetGlnAlaLeu	220
DB	775	CGCAGCTGCTGGGCTCAGAACGCCCTGGTACTGAGATGAACTGGATGAGGCTCTG	834
QY	221	ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro	240
DB	835	ACCCACACACCGGCGCCATCTGTCAACCTTGGACAGCGCCACACCTTTCAGACCT	894
QY	241	ProAspSerSerGlyLysIleCysThrValGlnLeuValGlyAsnSerThrPheProGly	260
DB	895	CTGACAGACAGTAGAAGATCTGCACCTGCAGTGTGGTGAACAGCTGACCCCTGCG	954
QY	261	TyrProGlyThrGlnGlnAlaLeuCysProGlnValThrTyrSerThrAspGlnLeuPro	280
DB	955	TACCCGGAACCCAGAGAGCGCTGCTCCGCGAGGTACATGTCTCTGGAGACAGTGGCC	1014
QY	281	SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGlySerProAlaGlySer	300
DB	1015	ACGAGAGCTCTTGGCCCGCTGCTGGCCACACCTCTCCAGAGTCCACCGCGCTCG	1074
QY	301	ProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla	320
DB	1075	CCAGCCATGATGCTCGAGCGCGGCGCGAGCTCTACGAGCTGATGAGCGCGGTCCAGCG	1134

QY 321 ArgArTrpIysGluPheValArgThrLeuGlyLeuArgGluAluIleGluAlaVal 340
| | | | |
DB 1135 CGGCGCGGAGAGAGAGTTCGCGCCAGCCCTGGGCTGGCGCAGCAGATCGAGCCGTG 1194
QY 341 GluValGluIleGlyArgPheArgAspGlnIleTyrGluMetLeuLysArgTrpArgGln 360
| | | | |
DB 1195 GAGGTGGAGATCGGCGCTTCGAGACACAGATGCTCAAGCCCTGGCGCAG 1254
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
| | | | |
DB 1255 CAGCAGCCCGCGGCGCTGGAGCGCTTACGCGGCGCTGGAGCGCATGGGCTGGAGCGC 1314
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
| | | | |
DB 1315 TGGGTGGAGACTTGGCGCAGCCGCTGACGCGCGCCG 1353
RESULT 8
ABK40265
ID ABK40265 standard; cDNA; 1662 BP.
XX
AC ABK40265;
XX
DT 15-JUL-2002 (first entry)
XX
DE cDNA encoding human PRO779 polypeptide.
XX
KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukemia; neuronal disorder; stromal disorder; blastocytic disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder;
KW gene therapy; cytostatic; neuroprotective; gene; ss.
XX
OS Homo sapiens.
XX
PN MO200153486-A1.
XX
PD 26-JUL-2001.
XX
PE 11-FEB-2000; 2000MO-US03565.
XX
PR 08-MAR-1999; 99MO-US05028.
PR 11-MAR-1999; 99US-123972P.
PR 11-MAY-1999; 99US-133459P.
PR 02-JUN-1999; 99MO-US12252.
PR 22-JUN-1999; 99US-140650P.
PR 20-JUL-1999; 99US-140653P.
PR 26-JUL-1999; 99US-144758P.
PR 28-JUL-1999; 99US-145698P.
PR 17-AUG-1999; 99US-146222P.
PR 31-AUG-1999; 99US-149395P.
PR 01-SEP-1999; 99MO-US20111.
PR 15-SEP-1999; 99MO-US21090.
PR 30-NOV-1999; 99MO-US28313.
PR 01-DEC-1999; 99MO-US28301.
PR 01-DEC-1999; 99MO-US28634.
PR 05-JAN-2000; 2000MO-US00219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ,
PI Marsters SA, Pan J, Pilleri RM, Roy MA, Smith V, Stone DM,
PI Watanabe CK, Wood WI;
XX
DR WPI: 2002-205567/26.
DR P-PSDB; AUB6139.
XX
PT Thirty five nucleic acids encoding PRO polypeptides, useful for
PT treating benign or malignant tumours, leukaemias and lymphoid
PT malignancies, inflammatory, angiogenic and immunologic disorders -
XX
PS Claim 50; Fig 23; 302pp; English.
XX
CC The present invention relates to the isolation of novel human PRO

CC polypeptides and the polynucleotide sequences encoding them. The
CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
CC useful for treating benign or malignant tumours (e.g. renal, kidney,
CC bladder, breast, etc), leukaemias and lymphoid malignancies, other
CC disorders such as neuronal, glial, astrocytal, hypotalamic, granular,
CC microphagal, stromal and blastocytic disorders, inflammatory, immune
CC and angiogenic disorders. The polynucleotide sequences are also
CC useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
CC polypeptides of the invention.
XX
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;
Alignment Scores:
Score: 2.97e-117 Length: 1662
Percent Similarity: 100.00 Matches: 393
Best Local Similarity: 100.008 Mismatches: 0
Query Match: 100.008 Indels: 0
DB: 24 Gaps: 0
US-09-993-234-6_COPY_25_417 (1-393) x ABK40265 (1-1662)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
| | | | |
DB 175 CAGGCGCAGCTAGTCCAGCCAGGTGTGACTGTCCGGTGCATTCACAMAGATTGGT 234
QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
| | | | |
DB 235 CTGTTTGTTCACAGAGGTGCCAGCGGCGACACTGAAAGGCCCTTGACGAGGCC 294
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
| | | | |
DB 295 TGGCGCAACTCAGCTGCTGTGTGTCGCCAAGACACTTCTGGCTGGAGACAC 354
QY 61 HisAsnSerGluCysAlaIleArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
| | | | |
DB 355 CATTAATCTGAAATGTGCCCGCTGCCAGGCTGTATGAGAGGCTCCCAAGTGGCGCTG 414
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
| | | | |
DB 415 GAGAACTGTTACAGAGTGGCCGACACCCGCTGTGCTGTAAAGCAGGCTGTGTGGAG 474
QY 101 CysGlnValSerGlnCysValAsnSerSerProPheTyrCysGlnProCysLeuAspCys 120
| | | | |
DB 475 TGCAGGTCAGCAGCAATGTGTGACGAGTTCACCTTCTATGCTCCCAACATGCTAGACTGC 534
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
| | | | |
DB 535 GGGGCGCTGCACCCGACACACAGGCTACTGTTCGCCCAAGATACGACTGTGGGACC 594
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
| | | | |
DB 595 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCTGCTGCCACAGCACCTTG 654
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
| | | | |
DB 655 GGGAGCTGTCCAGAGCGGTGTGCCGCTGTGTGGCTGGAGGCAAGTGTGGGCTCAG 714
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyr 200
| | | | |
DB 715 GTGCTCTGTGGCTGTGCTGTGCTCCCTCTGCTGTGGGCGCACCTGACATACATAC 774
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
| | | | |
DB 775 CGCAGCTGCTGCTCAGACAGCCCTGTGTACTGACATGAAGCTGGGATGAGGCTGTG 834
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
| | | | |
DB 835 ACCCAGACAGCGGCGACCCATCTGACCTTGGAGACGCGCCACACCTCTAGACACT 894
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
| | | | |
DB 895 CCTGACAGCACTGAGAAAGATCTGCACCGCTCAGTTGTGGGTAAACAGCTGAGACCTGGC 954

Db	963	ACCCACACCGGCGCACACCATCTGTACACCTTGTGAGACGGCCACACACCTTCTAGCACT	1022
Qy	241	ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly	260
Db	1023	CTGTACAGCGTGAAGAATCTCACCGTCCAGTTGGTGGTAAACGCTGGACCTTGCC	1082
Qy	261	TyrProGlnThrGlnGlnIleLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro	280
Db	1083	TACCCGAGACCCAGGAGGCGCTCTCCCGCAGGTGACATGGTCTCGGAGCCAGTTGGCC	1142
Qy	281	SerArgIleLeuGlnProIleAlaIleProThrLeuSerProGlnUserProIleGlySer	300
Db	1143	AGCAGACCTTTGGCCCGCGTGTGGGCCACACTCTGCCAGAGATCCCAACCGGCTCG	1202
Qy	301	ProIleMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProIle	320
Db	1203	CCACCCATGATGCTGCAGACCGGCGCGCAGCTCTACAGATGATGAGCGGGTCCACGCG	1262
Qy	321	ArgArgTrpIrypSerGluPheValArgThrIleuGlyLeuArgGluIleGluIleVal	340
Db	1263	CGGGCTGGGAAGAGATTCTGCGCCAGCGTGGGGCTGCGGAGGACAGATCGAACCCGTG	1322
Qy	341	GluValGluIleGlyArgPheArgAspGlnGlnIleTyrGluMetLeuLysArgTrpArgGln	360
Db	1323	GAGGTGAGATCGGCGGCTTCCAGACCCAGCATGACGATCTCAAGCGCTGGCGCCAG	1382
Qy	361	GlnGlnProIleGlyLeuGlnIleValIleTyrAlaIleLeuGlnIleArgMetGlyLeuAspGly	380
Db	1383	CAGCAGCCCGCGGGCCCTCGGAGCCGTTACGGGGCCCTGAGACGATGGGGCTGGACGCC	1442
Qy	381	CysValIleLysPheArgSerArgLeuGlnArgGlyPro	393
Db	1443	TGCGTGGAAAGACTTTCGCGCACCCGCTGCAGCGCGGCCG	1481
RESULT 10			
AAK00924			
ID	AAK00924	standard; cDNA; 1783 BP.	
XX	XX	AAK00924;	
AC	AC		
DT	DT	25-MAR-1999 (first entry)	
XX	XX		
DE	DE	Death domain containing receptor polypeptide (DR3-V1) encoding cDNA.	
XX	XX		
KW	KW	Death domain; receptor; DR3-V1; DR3; recombinant; ds.	
XX	XX		
OS	OS	Homo sapiens.	
XX	XX		
FH	FH	Location/Qualifiers	
FT	FT	CDS	198..1484
FT	FT	CD5	198..1484
FT	FT	FT	/tag- a
FT	FT	FT	/product- "Death domain containing receptor DR3-V1"
FT	FT	FT	sig_peptide
FT	FT	FT	mat_peptide
FT	FT	FT	mat_peptide
XX	XX		
XX	XX	Jp11000170-A.	
XX	XX		
PD	PD	06-JAN-1999.	
XX	XX		
PE	PE	12-MAR-1997;	97JP-0057503.
XX	XX		
PR	PR	06-FEB-1997;	97US-0037341.
PR	PR	12-MAR-1996;	96US-0013285.
PR	PR	17-OCT-1996;	96US-0028711.
XX	XX		
PA	PA	(HUMA-) HUMAN GENOME SCI INC.	
PA	PA	(UMMI) UNIV MICHIGAN.	
XX	XX	WPI: 1999-124390/11.	
DR	DR	P-PSDB; AAM95337.	
DR	DR		

xx	New death domain containing receptor and recombinant vector - optionally comprising leader sequence
xx	Claim 2; Fig 1, 2; 50pp; Japanese.
cc	The invention provides nucleotide sequences encoding death domain containing receptor polypeptides DR3-VI and DR3. The DR3-VI cDNA clone is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is contained in ATCC deposition No. 97757. Recombinant vectors comprising the nucleic acid sequences and optionally the leader sequences are used for the recombinant production of the proteins. The present sequence represents a cDNA encoding the death domain containing receptor polypeptide (DR3-VI).
xx	
so	Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;
sd	
Alignment Scores:	
Pred. No.:	3 21e-117 Length: 1783
Score:	2209.00 Matches: 393
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	Gaps: 0
US-09-993-234_6_COPY_25_417 (1-393) x MAX00924 (1-1783)	
OY	1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Dd	303 CAGGGCGGCCTCGTAGGCCCGAGGTGTACACTGCCGCTACTTCCACMAAGATTGGT 362
OY	21 LeuPheCysCysArgGlyCysProAlaGlyHisIstyrLeuLysAlaProCyssthGluPro 40
Dd	363 CTGTTTGTTTCACAGAGCTGCCACGGGGCACATCACTTAAGAGCCCCCTTCACGGAAGCCC 422
OY	41 CysGlyAasnSerThrCysLeuValCysProAlasprhrPheLeuAlatrGluAasnHis 60
Dd	423 TCGGGCAACTCCACTGCTTGTGTGTCTCCAAACAACACTTCTTGCTGGGAGAACAC 482
OY	61 HisAasnSerGlyCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Dd	483 CATATTGTGATGATGGCCCGCTGCCAAGCCCTGTATAGACAGGCTCCAGTGGCCGTG 542
OY	81 GluAasnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrrPheValGlu 100
Dd	543 GAGAAGCTGTACAGCAGTGGCGACACCAGCGTGTGGGTAAAGCCAGGCTGTTTGGAG 602
OY	101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Dd	603 TGCCAGGTCACAGCATGTGTACAGCAGTTCACTTCACTGACCACACATGCTTAGACTGC 662
OY	121 GlyAlaLeuHisArgHisThrArgLeuLeuLysSerArgrArgAspThrAspCysGlyThr 140
Dd	663 GAGGCGCTGACACCGGCACACAGGCTACTCTGTTCGCCGACAGATGACTGTGGGACC 722
OY	141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProTrnSerThrLeu 160
Dd	723 TGCCGCGCTGGCTTCTAAGACATGGCGATGGCTGCGGTGTCCTGCCACAGACACCTG 782
OY	161 GlySerCysProGlyArgCysAlaAlaValCysGlyTrrArgGlnMetPheTrrPvalGln 180
Dd	783 GGGACCTCTCCAGAGCGCTGTGGCGCTCTGTGTGGCTGGAGGCGAGATGTTCTGGGTCCAG 842
OY	181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTrrTrrTyr 200
Dd	843 GTGGCTCTGGGCTGGCTTGTGTGTGCTCCCTCTGCTTGGGGCCACCCCTGACCTACATAC 902
OY	201 ArgHisCysTrrProHisLysProLeuValThrAlaAspGlnAlaGlyMetGlnAlaLeu 220
Dd	903 CGGCACCTGCTGGCTGCACAAACCCCTGTTACTGTACATGAAGCTGGGATGGAGGCTGTG 962
OY	221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuAlaPro 240

Db 963 ACCCCACCACCGCCACCATCTGTCTACCCCTTGAGACAGCCGCCACACCTTCTAGACACT 1022
QY 241 ProAspSerSerGluTyrIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 1023 CTTGACAGAGAGTGAAGATCTGCACCGCTCAGTTGGTGGATACACTGGACCCCTGGC 1082
QY 261 TyrProGlnThrGlnGlnAlaLeuGlyProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 1083 TACCCAGAGACCCAGAGAGGCGCTCTGCGCCAGGTGACATGCTTGGGAGACAGTTGCC 1142
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 1143 AGCAGAGCTTGTGGCCCGCTGCTGCGCCACACTCTCCGCAAGTCCCAAGCCGCTCG 1202
QY 301 ProAlaMetLeuLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 1203 CCAGCCATGATGCTGACAGCCGCGCCGACCTTACGACATGATGACGCGGCTCCAGCG 1262
QY 321 ArgArgTyrPylGlnPheValArgThrLeuGlyLeuArgGlnAlaGluIleGlnAlaVal 340
Db 1263 CGGCGCTGGAGAGAGTTCGTCGCGACGCTGGGCTGCGGAGAGATCGAAGCCCTG 1322
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGlnMetLeuTyrAspGln 360
Db 1323 GAGGTGAGATCGCGCGCTTCCGAGACACACATACGAGATGCTCAAGCCCTGCGCCAG 1382
QY 361 GlnGlnProAlaGlyLeuGlnAlaValTyrAlaAlaLeuGlnArgMetGlyLeuAspGly 380
Db 1383 CACACACCGCGCGCTTCCGAGCGCTTACGCGCGCTTGGAGCGATGGGCTGGAGCGG 1442
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1443 TGGGTGGAAGACTTGGCGACCGCCCTGACAGCGGCGCG 1481
RESULT 11
AAC68776
ID AAC68776 standard; cDNA; 1783 BP.
XX
AC 68776;
XX
20-FEB-2001 (first entry)
XX
Human death domain containing receptor DR3-VI coding sequence.
XX
Human: death domain containing receptor; DR3-VI; cancer;
XX
autoimmune disorder; inflammation; cardiovascular disorder; infection;
XX
neurodegenerative disease; angiogenesis; ss.
XX
Homo sapiens.
XX
W0200064465-A1.
XX
02-NOV-2000.
XX
21-APR-2000; 2000WO-US10741.
XX
22-APR-1999; 99US-0130488.
XX
28-MAY-1999; 99US-0136741.
XX
(HUMA-) HUMAN GENOME SCI INC.
XX
(UNMT) UNIV MICHIGAN.
XX
(YUGG) YU G.
XX
(NIJG) NI J.
XX
(GENT) GENTZ R L.
XX
(DILL) DILLON P J.
XX
(DIXI) DIXIT V M.
XX
YU G, NI J, Gentz RL, Dillon PJ, Dixit VM;
XX
WPI: 2000-687263/67.
XX
P-PSDB: AAB36264.
XX
Treating graft-versus-host disease, cancer, immunodeficiency or an

PT autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent -
XX
PS Example 1; Fig 1; 273pp; English.
XX
CC The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-VI. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arthritis, ischemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.
XX
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other:

Alignment Scores:
Pred. No.: 3,21e-117 Length: 1783
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x AAC68776 (1-1783)
QY 1 GlnGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisTyrIleGly 20
Db 303 CAGGGGCGGACCTCGAGCCCGCAGGTGTGACTGTGCGGAGCTTCCACAAAGATGTGT 362
QY 21 LeuPheCysCysArgGlyCysProAlaGlnHisTyrLeuValAspCysThrGlnPro 40
Db 363 CTGTTTGTGGAGAGGCTGCCAGGGGGGCACTACTTAAGCCCTTGCCAGAGCCC 422
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 423 TCCGGCACTCCACCTGCTGTGTGCCCAAGACACCTTCTTGGCGGAGAAACAC 482
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnGlnAlaSerGlnValAlaLeu 80
Db 483 CATTAATTCGATGTGCCCGCTGCCAGGCTGTGTGATGACAGAGCCCTCCAGGTGCGCTG 542
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
Db 543 GAGAACTGTTCAGAGTGGCCGACACCGCTGTGCTGTAAACCAAGCGCTTGTGGAG 602
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 603 TCCAGAGTCAGCAATGTGTGACAGTTCACCCCTTCTACTGCCAACCAATGCTTAGACTGC 662
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 663 GGGGCGCTGCACCGCCACACAGGCTACTCTGTCCCGAGAGATGACTGTGGAGC 722
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 723 TGCCTGCTGTGCTTATGAACATGATGATGCTGCTGCTGCTGCCACAGAGACCCCTG 782
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrPheGlnMetPheTrpValGln 180
Db 783 GGGAGCTGTCCAGAGCGCTGTGCCCTGTGTGCTGTGAGAGCAATGCTTGTGGCTCAG 842
QY 181 ValLeuLeuAlaGlyLeuValAlaPheLeuLeuGlnGlyAlaThrLeuThrTyrThrTyr 200
Db 843 GTGCTCGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 902
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGlnAlaGlyMetGlnAlaLeu 220
Db 903 CGCCACTGTGCTCCACAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 962
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuAlaPro 240

Db 963 ACCCCACACCGCCACCATCTGTACACCTTGGACAGCCGCCACACCTTCTAGACACT 1022
Qy 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 1203 CCTGACAGCACTGAGAAAGATGTGCACGCTCAGTTGGTGGTAAACAGTGCACCCCTGCG 1082
Qy 261 TyrProGlnThrGlnGlnAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 1083 TACCCCGAGACCCAGAGGCGCTCTGCCCGCAGGTGACATGGTCTCGGAGCAGATTGCC 1142
Qy 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGlnSerProAlaGlySer 300
Db 1143 AGCAGAGCTCTTGGCCCGCGCTGCTGCGCCACACTCTGCCAGAGTCCCGACCGGCTCG 1202
Qy 301 ProAlaMetLeuLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 1203 CCACGCAATGATGCTGCAGCGCGCGCGCAGCTTACAGCAGTGAAGAGCGGCTCCACAGC 1262
Qy 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1263 CGGCGCTGGAAAGAGATTGCTGCGCAGCTGGCGCTGCGCGCAGCAGAGATGAAAGCCGTG 1322
Qy 341 GluValGluIleGlyArgPheArgAspGlnGlnIleTyrGluMetLeuLysArgTrpArgGln 360
Db 1323 GAGGTGGAGATCGCGCTTCCGAGACGACGATGAGATGCTACAGCTGGCGCCAG 1382
Qy 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1383 CAGCAGCGCGCGCGCGCTCGGAGCGGCTTACGCGCGCTGAGCGCATGGGCTGAGCGCGC 1442
Qy 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1443 TGCCTGGAAAGACTTGCAGACCGCGCTGCGCAGCGCGCGCGC 1481
RESULT 12
AAV28700
ID AAV28700 standard; cDNA: 1847 BP.
AC AAV28700;
XX 20-AUG-1998 (first entry)
DT Human apoptosis inducing receptor coding sequence.
XX
DE Apoptosis inducing receptor; AIR protein; human; cell death regulator;
XX Type I transmembrane protein; tumour cell death; autoimmune disease;
KM therapy; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 236..1489
FT /tag= a
FT /product= AIR
XX
XX W09814565-A1.
XX
XX 09-APR-1998.
XX
XX 03-OCT-1997; 97MO-US17876.
XX
XX 04-OCT-1996; 96US-0044456.
XX
XX (IMMUNEX CORP.
XX
XX Perkins PA;
XX
XX WPI: 1998-240077/21.
XX
XX P-PSDB: AAW57045.
XX
XX DNA encoding apoptosis inducing receptor - which is Type I
XX PT transmembrane protein, useful for regulating cell death
XX

PS Claim 2; Page 28-30; 45pp; English.
XX
CC This sequence encodes the human apoptosis inducing receptor (AIR) of the
CC invention. AIR is a type I transmembrane protein, soluble forms of which
CC can be used to regulate cell death in a therapeutic setting. Soluble AIR
CC can also be used in vitro to block apoptosis or AIR-expressing cells, or
CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain
CC of AIR can be used to develop assays for inhibitors of AIR-induced cell
CC death, which is useful to regulate cell death in a therapeutic setting as
CC well as in vitro. Agonists of AIR activity can be used to kill tumour
CC cells that express AIR, or T cells expressing AIR in autoimmune diseases.
XX
S0 Sequence 1847 BP; 316 A; 605 C; 579 G; 347 T; 0 other:

Alignment Scores:
Pred. No.: 3,33e-117 Length: 1847
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 19

US-09-993-234-6_copy_25_417 (1-393) x AAV28700 (1-1847)
Qy 1 GlnGlyLysThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 308 CAGGCGCGCAGCTGTAAGCCCGCAGGTGTGACTGTGCGGAGACTTCCACAAGAAATGGT 367
Qy 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 368 CTGTTTGTGAGAGGCTGCGCAGCGGCGCCTGACCTGAAAGCCCTTGCACGAGGCC 427
Qy 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 428 TCGCGCAACTCCACCTGCTGCTGTGTGCTCCCAAGCACACTTGTGCTCGGAGAAACAC 487
Qy 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 488 CATATTCATGATGTGCCCGCTGCGCAGCGCTGTGATGAGACAGCGCTCCACAGTGGCGGTG 547
Qy 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
Db 548 GAGAACTGTTCAGAGTGCGCGCCGACACCGCTGTGCTGTAAACAGCGGTGTGTGGAG 607
Qy 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 608 TGCCAGGTACGACCATGTGTGCTGACAGTTCACCTTCTTACGCCAACCATGCTTAAGACTGC 667
Qy 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 668 GGGGCGCTGCACCGCCACACAGCGCTACTGTTCGCCAGAGATACGATGTGGAGCC 727
Qy 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 728 TGCTGTGCTGTGTATGATGACATGGCATGGCTGCTGCTGCCACGAGGACCGCTG 787
Qy 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrPargGlnMetPheTrpAlaGln 180
Db 788 GGGAGCTGTCCAGACCGCTGTGCCCTGTGTGCTGAGGCAATGTTCGGGTCCAG 847
Qy 181 ValLeuLeuAlaGlyLeuValAlaProLeuLeuLeuGlyAlaThrLeuThrTyr 200
Db 848 GTGCTGTGCGTGGCGCTGTGTGCTCCCTGCTGTGGGGGACCGCTGACATAC 907
Qy 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 908 CGCCACTGCTGCTCACAAGCGCTGTACTGAGATGAAGCTGGAGTGAAGCTCTG 967
Qy 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
Db 968 ACCCCACACCGCGCCACCATGTGCACCTTGGACAGCGCCACACCTTACACACT 1027
Qy 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260

Db 201 CTGTTTGTTCAGAGGCTCCCAAGGCGGCGACTACCTGAAGGCCCTTCGACGAGGCC 260
 QY 41 CysG1YasnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
 Db 261 TGGGGCAACATCCATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 320
 QY 61 HisAsnSerIleuValAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
 Db 321 CATAAATTCCTAATGTCCCTCCCTGACGCGCTGTGATGACAGAGGCTCCAGAGTGGCGCTG 380
 QY 81 GluAsnSerSerAlaValAlaAspThrArgCysGlyCysIleProGlyTrpPheValGlu 100
 Db 381 GAGAACTGTTCAGAGGAGGCGGACCGGCTGTGCTGTAAAGCAGGCTGGTTGTGTGAG 440
 QY 101 CysGlnValSerGlnCysValSerSerSerProPheTrpCysGlnProCysLeuAspCys 120
 Db 441 TGGCAGGTTCAGCCAAATGTGTACAGATGTTCACCTTCACAGCCCAACATGCTAGACTGC 500
 QY 121 G1YAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
 Db 501 GGGGCGCTGCACGCGCCACACAGCGCTACTCTGTCCCGCAGAGATGACTGCTGGGACC 560
 QY 141 CysLeuProGlyPheTrpGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
 Db 561 TGCCTGCTGACCTGTATGAACATGCGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 620
 QY 161 G1YSerCysProGluArgCysAlaAlaValCysGlyTrpArg----- 174
 Db 621 GGGAGCTGTCCAGAGGCGCTGTGCGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 680
 QY 174 ----- 174
 Db 681 GGGAAATGCGGTGGAGAACTGGGATGGACCGAGGCGGCGGTGAGAGAGGGGCGCAAC 740
 QY 175 -----GlnMetPheThrValGlnValLeuLeuAlaGlyLeu 186
 Db 741 CACCCAAACCCACACCACTGCTTCAAGTG--TTCTGGGTCCAGAGGTGCTGGCTGGCTT 799
 QY 187 ValValProLeuLeuLeuGlyAlaThrLeuThrTrpTrpArgHisCysTrpProHis 206
 Db 800 GTGGTCCCTCTCGCTGTGGGGCCACCTGACCTACACATACCCGCACTGCTGGCTCTAC 859
 QY 207 LysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrProProProAlaThr 226
 Db 860 AAGCCCTGGTACTGACAGATGAAGCTGGATGAGGCTGACCCACACCGCGCAC 919
 QY 227 HisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAspSerSerGlyLeu 246
 Db 920 CATCTGTACCTGTGGACAGCGCCACACCTTCTACACCTCTGTACAGAGTGAAGAG 979
 QY 247 IleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTrpProGlyTrpGlnGlu 266
 Db 980 ATCTGCACCTCCAGTTGGTGGGTGAACAGCTGACCCCTGGCTACCCCGAGACCCAGAG 1039
 QY 267 AlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro 286
 Db 1040 GCGCTGTCCCGCAGGTGATGCTCTGGGACCAAGTTGCCACAGAGGTCTTGGGCC 1099
 QY 287 AlaAlaAlaProThrLeuSerProGluSerProAlaGlySerProAlaMetMetLeuGln 306
 Db 1100 GCTGTGTGCGCCACACTCTGTGCGAGATGCCACCGGCTGCGCAGCATGATCTCTCAG 1159
 QY 307 ProGlyProGlnLeuTrpAspValMetAspAlaValProAlaArgArgTrpGlyGluPhe 326
 Db 1160 CCGGGCCCGCAGCTCTACAGCTGATGACCGGCTCCACGCGCGCGCTGGAAGAGATT 1219
 QY 327 ValArgThrLeuGlyLeuArgGluAlaGluLeuAlaValGluValGluLeuGlyArg 346
 Db 1220 GTGGGACCGTGGGGGTGCGCGAGAGATCGAAGCCGCGGAGGTGAGATGCGTCTC 1279
 QY 347 PheArgAspGlnGlnTrpGluMetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeu 366
 Db 1280 TTCGAGAACGACGATGATGATGCTCAAGCATGTGCGCGCAGCAGACCGCGCGGCGCTC 1339

QY 367 G1YAlaValTrpAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg 386
 Db 1340 GGAGCCCGTTTACGGCGCCCTGAGCCGATGGGGGTGGAGCGGCTGCGGAAGACTTGGCC 1399
 QY 387 SerArgLeuGlnArgGlyPro 393
 Db 1400 AGCCGCTGCAGCGTGGCCCG 1420
 RESULT 14
 ID AAF83770 standard; DNA: 1250 BP.
 AC AAF83770;
 DT 06-AUG-2001 (first entry)
 DE Nucleotide sequence of human TR3 gene.
 KW TR3; cell proliferation; leukemia; immunosuppressive; cytostatic; dermatological; antiarthritic; antidiabetic; neuroprotective; cardiant; antithyroid; antiinflammatory; antiallergic; T-cell-inhibitor; ds.
 OS Homo sapiens.
 FH Key
 FT CDS
 FT 1..1250
 FT /tag- a
 FT /transl_except- "(pos:481..482, aa:Asp)"
 FT /note- "this codon has an apparent 1 nucleotide deletion which alters the reading frame"
 FT /transl_except- "(pos:558..559, aa:Cys)"
 FT /note- "this codon has an apparent 1 nucleotide deletion which alters the reading frame"
 FT /transl_except- "(pos:638..639, aa:Leu)"
 FT /note- "this codon has an apparent 1 nucleotide deletion which alters the reading frame"
 FT /transl_except- "(pos:718..719, aa:Met)"
 FT /note- "this codon has an apparent 1 nucleotide deletion which alters the reading frame"
 FT sig_peptide 1..72
 FT /tag- b
 FT mat_peptide 73..1247
 FT /tag- c
 PN W0200135995-A2.
 XX 25-MAY-2001.
 PD 17-NOV-2000; 2000MO-US31692.
 XX 19-NOV-1999; 99US-0166583.
 PA ('TITV') TITTLE T V.
 PA (WEGM/) WEGMANN K W.
 PI Tittle TV, Wegmann KW.
 DR WPI: 2001-343711/36.
 DR P-PSDB: AAB84941.
 PT Composition for treatment of T-cell mediated disease e.g. arthritis, cancer comprises a biologically active TR3-specific binding agent especially a monoclonal antibody -
 PS Disclosure: Page 72: 77pp; English.
 CC The invention relates to a composition comprising a biologically active TR3-specific binding agent (I) that binds to TR3 and inhibits the proliferation of cells expressing TR3. (II) identified by the methods are useful for treating a subject suspected of having a disease associated with a proliferation of cells expressing TR3 especially leukemias or lymphomas or a T-cell mediated disease especially autoimmune diseases

CC such as myasthenia gravis, systemic lupus erythematosus, rheumatoid
 CC arthritis, diabetes, multiple sclerosis, sarcoidosis, myocarditis,
 CC thyroiditis and tumours. (1) is also useful for treating a subject
 CC suspected of having graft-versus-host disease, rejection of a
 CC transplanted organ such as heart, liver, lung, kidney, pancreas, bowel,
 CC skin or an appendage, or inflammatory diseases, allergies and contact
 CC dermatitis. The present sequence represents the nucleotide sequence of
 CC human TR3 gene.

XX Sequence 1250 BP; 201 A; 419 C; 406 G; 224 T; 0 other;

Alignment Scores:

Pred. No.:	7,77e-111	Length:	1250
Score:	2094.00	Matches:	389
Percent Similarity:	98.98%	Conservative:	0
Best Local Similarity:	98.98%	Mismatches:	4
Query Match:	94.79%	Indels:	4
DB:	22	Gaps:	0

US-09-993-234-6_COPY_25_417 (1-393) x AAF83770 (1-1250)

QY 1 GlnGlyLysThrArgSerProArgCysAlaGlyAspPheHisLysIleGly 20
 Db 73 CAGGCGCGCACTGCTACCCAGAGGTGACCTGCGCTTCCAGAGAGATTGCT 132
 QY 21 LeuPheCysArGgIyCysProAlaGlyHisIleuLysAlaProCysThrGluPro 40
 Db 133 CTGTTTGTGTCAGAGAGGCTCCAGCGGGCAGCTGAGAGGCCCTTCAGCGAGACC 192
 QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGlnAsnHis 60
 Db 193 TGGCGCAACTCCACCTGCTGTGTGTCCAGAGACCTCTTGGCTGGAGAACAC 252
 QY 61 HisAsnSerIuLysAlaArGyCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 80
 Db 253 CATAAATTCGAATGTGCTCCCTCCAGGCTGTGATGAGACAGCCCTCCAGGTGGCGCTG 312
 QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
 Db 313 GAAACTGTTCACAGCTGCGCGGACCCGCTGCTGCTGTAAGCCAGCTGTTGTGGAG 372
 QY 101 CysGlnValSerGlnCysValSerSerSerProPheThrCysGlnProCysLeuAspCys 120
 Db 373 TGCAGAGTCAGCCAAATGTGTCACAGTTCACCTTCTACGCCAACATGCTTACAGCTGC 432
 QY 121 GlyAlaLeuHisArgHisIleThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
 Db 433 GGGGCCCTGCACCGCCACACACGCTACTCTGTCCCGCAGAGATAC -GACTGTGGAGC 491
 QY 141 CysLeuProGlyIlePheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
 Db 492 TGGCTGCTGGCTTCTATGACATGCGCATGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 551
 QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
 Db 552 GCGAGAGGT -CCAGAGCGCTGCGCGCTGTGCTGAGGAGAGATGCTTGGCTCAG 610
 QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
 Db 611 GTGCTCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 669
 QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGlnAlaGlyMetGlnAlaLeu 220
 Db 670 CGCGCACTGCTGGCTCACAAGCCCTGCTTACTGCAAGAGAGAGAGAGAGAGAGAGAGAG 728
 QY 221 ThrProProAlaThrHisLysSerProLeuAspSerAlaHisIleThrLeuLeuAlaPro 240
 Db 729 ACCCCACACACCGCCACCATCTGTACCCCTTGAGAGAGGCCACACCTTCTACACCT 788
 QY 241 ProAspSerSerGlnLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
 Db 789 CCTGACACAGTGAAGAATCTGCACCGCTCCAGTTGTGTGTAACAGCTGAGCCCTGGC 848

QY 261 TyrProGlnThrGlnGlnAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
 Db 849 TACCCAGAGACCAGAGAGCCCTTGGCCGAGGTGACATGCTTGGAGACAGTTCGCC 908
 QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
 Db 909 AGCAGACTCTTGGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 968
 QY 301 ProAlaMetLeuLeuGlnProGlyProGlnLeuThrAspValMetAspAlaValProAla 320
 Db 969 CCAAGCATGATGTGTCAGCGGGGCCCTCAGCTTACAGCTGATGAGAGCGGCTCCAGCG 1028
 QY 321 ArgArgTrpLysGlnPheValArgThrLeuGlyLeuArgGlnAlaGlnIleGlnAlaVal 340
 Db 1029 CGGCGCTGGAAGAGTCTGCTGCGCAGCTTGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1088
 QY 341 GluValGlnIleGlyArgPheArgAspGlnIleTyrGlnMetLeuLysArgTrpArgGln 360
 Db 1089 GAGGTGAGATCGGCCCTTCCAGACACAGCATGAGATGCTCAAGCGCTGCGGCCAG 1148
 QY 361 GlnGlnProAlaGlyLeuGlnAlaValTyrAlaAlaLeuLysArgMetGlyLeuAspGly 380
 Db 1149 CAGCAGCCCGCGGCTCGGAGCCGTTTACGCGGCCCTGGAGGCAATGGGGCTGAGCGC 1208
 QY 381 CysValGlnAspLeuArgSerArgLeuGlnArgGlyPro 393
 Db 1209 TGGGTGAAGACTTGGCGCAGCGCGCTGACGCGGGGCCG 1247

RESULT 15

AA147185
 ID AA147185 standard; DNA; 4825 BP.

AC AA147185;

DE 22-ANG-2002 (first entry)

XX Human DR3 gene associated with rheumatoid arthritis.

KW Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;

XX gene therapy; gene; ds.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

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/note= "this sequence contains introns"

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128..635

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636..756

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974..1108

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/number= 3

1109..1476

/*tag= g

/number= 3

1477..1644

/*tag= h

/number= 4

1645..1742

/*tag= i

/number= 4

1743..1821

exon

intron

exon

intron

exon

intron

exon

intron

exon

intron

exon

intron

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PN      WO200234912-A1.
XX      02-MAY-2002.
XX      24-OCT-2001; 2001WO-JP09313.
XX      24-OCT-2000; 2000JP-0324296.
PR      27-MAR-2001; 2001JP-0090546.
PR      30-MAR-2001; 2001JP-0099990.
XX      (NEMT-) NEW IND RES ORG.
PA      (SHIO/) SHIOZAWA S.
XX      Shiozawa S, Konishi Y;
PI      WPI; 2002-417132/44.
XX      DR
XX      Genomes, particularly DR3 genomic DNA, participating in rheumatoid
PT      arthritis via mutation, useful in evaluating disease onset and its
PT      possibility and providing therapy and remedies -
XX      Claim 1; Page 64-66; 84pp; Japanese.
XX      The present invention relates to the human DR3 gene, which is associated
CC      with rheumatoid arthritis. Certain mutations in the gene can be linked to
CC      the disease. The sequences can be used to evaluate disease onset and its
CC      possibility and to provide therapy and remedies. The present sequence is
CC      the gene of the invention.
XX      Sequence 4825 BP; 921 A; 1378 C; 1521 G; 1005 T; 0 other;
SQ

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Alignment Scores:

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Pred. No.:      2,76e-76      Length:      4825
Score:          1498.50      Matches:      389
Percent Similarity: 28.46%      Conservative: 0
Best Local Similarity: 28.46%      Mismatches: 4
Query Match:      67.84%      Indels:      978
DB:              24      Gaps:      8

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US-09-993-234-6_COPY_25_417 (1-393) x AAL47185 (1-4825)

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QY      21 LeupheCysCysArgGlyCysProAla----- 29
DB      729 CTGTTTGTGTGCAGAGCTGCCAGCGGGTAAAGTGGCCACAGGGGTGGAGAGCCATGGG 788
QY      29 ----- 29
DB      789 GCAGGCGAGGCTGGAGAGCTGGCGGCGACGCCCGGAGAGTAAGAGAGAGCTGGCAGGGGA 848
QY      29 ----- 29
DB      849 GGTAGGGGTAGCTGACAGAGAAAGTAGGAGCTGGAGAGAAAGAGGAGGAGGAGGAGG 908
QY      29 ----- 29
DB      909 TGGAGACAGGTCGGGGGTTGCTGGGACGCCCTGCTGCTGACCCCTGACCCCTGGTTC 968
QY      30 ----GlyHisTyrIleuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuVa 48
DB      969 CACAGGCGACTAAGCTGAGAGGCCCTTTCAGCGGAGGCCCTGCGGACACTCCACCTGCTTGT 1028
QY      48 ICysProGlnAspThrPheLeuAlaTyrPgluAsnHisAsnSerGluCysAlaArgCys 68
DB      1029 GTGTCCCGCAGACACACTCTTGGCGCTGGGAGACACACATAATCTGAAATGTGCCCGGTG 1088
QY      68 sGlnAlaCysAspGlu----- 73
DB      1089 CCAGGCGCTGTAGTACAGAGGCTGAGGGCTTCTCAGTCTTGGCAGGAGTTCCTAAGGA 1148
QY      73 ----- 73
DB      1149 CAGGCGTTTGAAGGAAGAGTGGCTGGGCGCCCAAACTTGGGTGTGAGAGTCTGCA 1208
QY      73 ----- 73
DB      1209 CCCAAGCTTGGCAGAACCTCCACCCCTGATCTCTCAGGGGTGGCCCTTGGCCCTTCT 1268
QY      73 ----- 73
DB      1269 CTCTCGGTGACCTCCATCTCTCATATGCTGCTGGCTGGCTGGCTGAATCTCTG 1328
QY      73 ----- 73
DB      1329 AGCTTCTCTCTTTTAAAGGTAAGCCCTGTAACCTGTCTGTCTTGGCTAATTTCTGTCT 1388
QY      73 ----- 73
DB      1389 ATTAATCTGGATAATGCTCTGCTGCTCATATGGAGGCTTTGGGCGCTGACTACTCT 1448
QY      74 -----GlnAlaSerGlnValAlaLeuGlnAsnCysSerAl 85
DB      1449 ACTCCCACTCTCCCTGCACCCCAAGCC--TCCAGAGTGGCGGTGAGAACTGTTCAGC 1507
QY      85 aValAlaSerThrArgCysGlyCysLysArgGlyThrPheAlaGlyCysGlnValSerG1 105
DB      1508 AGTGGCCGACACCCGCTGTGCTGTAACAGGCTGGTGTGTGGAGTGTCCAGGTAGGCA 1567
QY      105 nCysValSerSerSerProPheTyrCysGlnProCysLeuAspCysGlyAlaLeuHisArg 125
DB      1568 ATGTGTGAGAGTTCACCTCTTACTGCAACATGCTTAACAGTGGGGGCGCTGACAGG 1627
QY      125 gHisThrArgLeuLeuCysSer----- 132
DB      1628 CCACACAGCGCTACTCTGTGA--GTACCCSSACSSAGAGGCTCTACTCCSAGACSSCTT 1686
QY      132 ----- 132
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QY 224 -----Pro-Ala 225
Db 3965 GGGTAAGGGGCTTACTTGGCAAGCAGGGCTGACCTGGGCCCTTGGCTTCCAGGCC 4024
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Db 4025 ACCCATCTGTACCCCTTGGACAGCGCCACACCTTGTAGACCTCTGACAGCAGTGAG 4084
QY 246 LysIleCysThrValGlnLeuValGlnAsnSerThrProGlyThrProGlyThrGln 265
Db 4085 AAGATCTGCACCGTCCAGTTGGTGGTAACGCTGACCCCTGTACCCCGAGACCCAG 4144
QY 266 GluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeu--- 284
Db 4145 GAGCGGCTTGCCCGCAGGTGACATGTGCTGGGACAGTTGCCAGAGAGCTTGTGT 4204
QY 284 ----- 284
Db 4205 AAGGACATCAGTGGCTTGAAGCCTTGACCCATTCTCTGTGCGGTGGGAATTGTG 4264
QY 284 ----- 284
Db 4265 GTTTCACACAGCTGTCCCTTCTGCCCCCTTAACAGAGAGTCCGCCCTATGCCCTGACC 4324
QY 284 ----- 284
Db 4325 CACCGATCCAGCGGGCTTACGCCCTGGGGTACCAGCAGAACGCCCTGACTGTGCCTC 4384
QY 285 -----GlyProAlaAla 288
Db 4385 CCGACCCGCGGCCACGATGCCCAATTGGCTCTCTGTGGCCCTGCCCGCCGCTGCT 4444
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Db 4445 GCGGCCACACTCTCTGCGCAGAGTCCCGCGGCTGCGCAGCCATGATGTCTGACGCCGGGC 4504
QY 309 ProGlnLeuTrpAspValMetAspAlaValProAlaArgTrpLysGluPheValArg 328
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Db 4565 ACGCTGGGGCTGCGCGAGGAGAGATGCAAGCCGTGGAGGTGAGATCGCGCGCTCCGA 4624
QY 349 AspGlnGlnTrpGlnMetLeuLysArgTrpArgGlnGlnProAlaGlyLeuGlyAla 368
Db 4625 GACGACGAGTACGAGATGCTTAAAGCTGGCGCCAGCAGACCCGCGGCGCTCGAGGCC 4684
QY 369 ValTrpAlaAlaLeuGlnArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArg 388
Db 4685 GTTACGCGGGCCCTGAGAGCGCATGGGGCTGAGCGGCTGCGTGAAGACTTGGCAGCGCCG 4744
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Search completed: April 6, 2003, 16:52:30
Job time : 436.927 secs

26

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GenCore version 5.1.4.p5.4578
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OM protein - nucleic search, using frame-plus-p2n model

Run on: April 6, 2003, 21:08:18 ; Search time 149.643 seconds
(without alignments)
2303.655 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_417

Perfect score: 2209
Sequence: 1 OGCTSPRCDCAGDFHKKIG.....ERMGDGCVEDLRSRLQGRP 393

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Dgapop 6.0 , Fgapext 7.0
Dgapop 6.0 , Dextext 7.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186658

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-FGAPEXT=7 -FGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications_NA:

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- 2: /cgnt2.6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgnt2.6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgnt2.6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 12: /cgnt2.6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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- 14: /cgnt2.6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2209	100.0	1254	10	US-09-333-966-3 Sequence 3, Appl1
2	2209	100.0	1634	9	US-10-081-280-9 Sequence 9, Appl1
3	2209	100.0	1634	9	US-10-112-793-9 Sequence 9, Appl1
4	2209	100.0	1634	9	US-10-112-193-11 Sequence 11, Appl1

5	2209	100.0	1634	10	US-09-993-234-9 Sequence 9, Appl1
6	2209	100.0	1783	10	US-09-333-966-1 Sequence 1, Appl1
7	2140.5	96.9	1743	9	US-09-954-531-1389 Sequence 1389, Ap
8	1498.5	67.8	10797	9	US-10-092-154-1577 Sequence 1577, Ap
9	1498.5	67.8	10797	10	US-09-764-847-1577 Sequence 1577, Ap
10	957.5	43.3	816	10	US-09-964-824A-292 Sequence 292, App
11	952	43.1	1438	9	US-10-081-280-5 Sequence 5, Appl1
12	952	43.1	1438	9	US-10-112-793-5 Sequence 5, Appl1
13	952	43.1	1438	10	US-10-112-193-5 Sequence 5, Appl1
14	952	43.1	1438	10	US-09-884-733-5 Sequence 5, Appl1
15	952	43.1	1438	10	US-09-993-234-5 Sequence 5, Appl1
16	666	30.1	433	9	US-10-081-280-2 Sequence 2, Appl1
17	666	30.1	433	9	US-10-112-793-2 Sequence 2, Appl1
18	666	30.1	433	9	US-10-112-193-2 Sequence 2, Appl1
19	666	30.1	433	10	US-09-884-733-2 Sequence 2, Appl1
20	666	30.1	433	10	US-09-993-234-2 Sequence 2, Appl1
21	383.5	17.4	2130	10	US-09-917-800A-1601 Sequence 1601, Ap
22	383.5	17.4	2440	10	US-09-970-532-1 Sequence 1, Appl1
23	369.5	16.7	2173	9	US-09-898-234-14 Sequence 14, Appl1
24	369.5	16.7	2173	9	US-09-899-429A-24 Sequence 24, Appl1
25	369.5	16.7	2173	9	US-09-792-356-14 Sequence 14, Appl1
26	369.5	16.7	2173	10	US-09-899-422-14 Sequence 14, Appl1
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31	369	16.7	2111	10	US-09-880-107-2360 Sequence 2360, Ap
32	369	16.7	2141	9	US-09-898-234-16 Sequence 16, Appl1
33	369	16.7	2141	9	US-09-899-429A-26 Sequence 26, Appl1
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37	330	14.9	191	9	US-09-796-692-2549 Sequence 2549, Ap
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39	256	11.6	1334	9	US-09-792-356-11 Sequence 11, Appl1
40	256	11.6	1334	10	US-09-899-422-11 Sequence 11, Appl1
41	256	11.5	1334	9	US-09-899-429A-21 Sequence 21, Appl1
42	229	10.4	1704	12	US-10-020-787-1 Sequence 1, Appl1
43	226.5	10.3	1724	10	US-09-924-231-1 Sequence 1, Appl1
44	226.5	10.3	1724	10	US-09-934-289A-14 Sequence 14, Appl1
45	216.5	9.8	1834	10	US-09-934-289A-41 Sequence 41, Appl1

ALIGNMENTS

RESULT 1
US-09-333-966-3
Sequence 3, Application US/09333966
Patent No. US2002009773A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Retner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: 06-FEB-1997
APPLICATION NUMBER: NO. US2002000973A1 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steife, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-09-333-966-3

Alignment Scores:
Pred. No.: 9.64e-190 Length: 1254
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

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DB 133 CCGTTTGTGTCAGAGCGTCCCGAGGGGCGACTACCTGAGGCCCTTGCGAGGAGCC 192

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QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
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QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
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QY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
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DB 1153 CAGCAGCCCGCGGCGCTCGAGAGCGCTTACGCGCGCCCTGAGGCGCATGGGGCTGGAGCGG 1212
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DB 1213 TGCCTGGAAGACTTGGCGACGCGCTGACGCGGCGCGG 1251

RESULT 2
US-10-081-280-9
Sequence 9, Application US/10081280
Patent No. US20020165157A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270

FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-081-280-9
Alignment Scores:
Pred. No.: 1,31e-189 Length: 1634
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrParGlnMetPheTyrValGln 180
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QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuGlnGlyAlaThrLeuThrTyrThrTyr 200
DB 701 GTGCTCTGCTGCTGCTGTGGTCCCTGCTGCTGGGCGCCAGCTGACTACACATAC 760
QY 201 ArgHisCysTyrProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
DB 761 CGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 820
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240

DB 821 ACCCGACCGCGCCACCATCTGTACACCTTGGACACCGCCACACCTTCTAGACACT 880
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DB 881 CCTGACACAGCTGAGAAATCTGACCTGACCTGAGTGGGTAAACAGCTGACCCCTGCG 940
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTyrPheTyrAspGlnLeuPro 280
DB 941 TACCCCGAGACCCAGAGGCGCTCTGCCGAGAGTGAATGTTCTGAGACAGTTGCC 1000
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
DB 1001 AGCAGAGCTTGGCGCCCGCTGCTGCGCCACACTCTGCGCAAGATCCCGACGGCTCG 1060
QY 301 ProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
DB 1061 CCAGCATGATGCTGCACCGCGCCCGGCGAGCTTACAGACGTGATGAGCGCGTCCACCG 1120
QY 321 ArgArgTyrLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
DB 1121 CGGCGCTGGAAGAGTTGTGTCGACGCTGGGGCTGCGCGAGAGATGCAAGCCGTG 1180
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGlnMetLeuLysArgTyrParGln 360
DB 1181 GAGTGGAGATCGGCGCTTCCGAGACAGCAGTACGAGATGCTCAACCGCTGGCGCCAG 1240
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
DB 1241 CAGCAGCGCGCGCGCTGCGAGCGCTTACCGCGCTGAGCGCATGGGCTGAGACGCG 1300
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
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RESULT 3
US-10-112-793-9
Sequence 9, Application US/10112793
Publication No. US20020192729A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-112-793-9

Alignment Scores:
Pred. No.: 1.31e-189 Length: 1634
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x US-10-112-793-9 (1-1634)

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DB 161 CAGGGCGGCACTCTTACCCAGGTGTGACTGTGCGGTGACTTCCACAGAGATTGTT 220
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DB 281 TGGGGCAACACCACTGCTGTGTGTGCCCCAAGACACTTCTGGGCTGGAGAACAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 80
DB 341 CATTAATCTTAATGTGCGCCCTGCGAGGCTGTGATAGCAGGCGCTCCAGGTGGCCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 401 GAGAACTGTTCCAGACAGCGCGGACACCGCGTGGGTGTAAGCCAGGCTGTTGTGAG 460
QY 101 CysGlnValSerGlnCysValLysSerSerProPheTrpCysGlnProCysLeuAspCys 120
DB 461 TGGCAAGTCCAGCAATGTGTCAGCTACCTTCTACGCGCACCACTGCTGAGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 521 GGGGCGCTGACCGCCACAGCGGCTACTCTGTCCCGAGACATCTGACTGTGGACC 580
QY 141 CysLeuProGlyPheTrpGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
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QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
DB 641 GGGAGCTGTCCAGAGCGGTGCTGCTGCTGCTGAGGAGAGATGTTCTGGGCTCCAG 700
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTrpTrp 200
DB 701 GGTGCTCTGCGGCGCTTGTGCTCCCTCTGCTTGGGGCCACCTTGACCTTACACTAC 760
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
DB 761 CGCCACTGCTGGCTCACAAGCCCTGGTGTACTGAGATGAAGCTGGATGAGGCTGTC 820
QY 221 ThrProProAlaThrHisIleuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
DB 821 ACCCAACACCGGCAACCCATCTGTACCCCTTGAGACAGGCGCCACACCTTGTAGACCT 880
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlnValAsnSerTrpThrProGly 260
DB 881 CCGTACAGAGTGAAGATGTGCAACCGCTGAGTGTGGTGAACGCTGAGACCCCTGGC 940
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
```

```
DB 941 TACCCGAGACCAGAGAGCGCTCTGCCCGCAGGTGACATGTCTGGAGCACTGCC 1000
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
DB 1001 AGCAGAGCTCTTGGCCCGCGCTGCGCCACACTCTGCGCAGAGTCCCAAGCGGCTGC 1060
QY 301 ProAlaMetLeuGlnProGlyProGlnLeuTrpAspValMetAspAlaValProAla 320
DB 1061 CCAGCCATGATGTGACAGCGGCGCCGACAGCTACAGACATGATGATGAGACCGGCTCCAG 1120
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
DB 1121 CGGCGCTGGAAGAGGTTGTCGCGACCTGCGGCTGCGCCAGAGCAGATCGAAGCCGCTG 1180
QY 341 GluValGluIleGlyArgPheArgAspGlnGluTrpGluMetLeuLysArgTrpArgGln 360
DB 1181 GAGGTGAGATCGGCGCTCTCCAGACACAGTACAGATGCTCAAGGCTGAGCGCCAG 1240
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
DB 1241 CAGCAGCCCGCGGCGCTCGGAGCGGCTTACCGGCGCTGAGAGGCAATGGGGCTGAGACGC 1300
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
DB 1301 TGGCTGGAAGACTTGGCGACCGCGCTGCGACGCGGCGCCG 1339
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RESULT 4

US-10-112-193-11

Sequence 11, Application US/10112193

Publication No. US20030004313A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-3 POLYPEPTIDE

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/112,193

FILING DATE: 28-Mar-2002

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/928,069

FILING DATE: 11-Sep-1997

APPLICATION NUMBER: 60/026943

FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1052R1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 1634 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-10-112-193-11

Alignment Scores:

Pred. No.: 1.31e-189 Length: 1634

Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x US-10-112-193-11 (1-1634)

QY 1 GlnGlyLysThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 161 CAGGGGGGCACTGCTACCCAGGTGAGCTGCTCCGGTGACTTCCACAGAAATTTGGT 220
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 221 CTGTTTGTGTCAGAGGCTGCCAGCGGGGACACTGAAAGGCCCTTTCAGCAGGAGCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 281 TGGGGCAACTGCACCTGCTGTGTGTCCACAGACACTTCTTGGCTGGGAACCCAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnGlnAlaSerGlnValAlaLeu 80
DB 341 CATAAATTCTGAATGTGCCCGCTGCCAGGCGCTGATGAGCAGGCGCTCCAGTGGCGTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
DB 401 GAGAACTGTTCCAGACGTGGCGGACACCCGCTGTGTAAGCAGCGCTGTTGTGAG 460
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 461 TGGCGAGTGCACCAATGTGTGACGATTCACCTTCTACTGCGCAACCAATGCTGAGCTGC 520
QY 121 GlnValLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 521 GGGGCGCTGCACCGCCACACACGCGTACTGTTCCCGCAGAGTACTGATGTGGGACC 580
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 581 TGCTGCTGCTGCTTCTATGAACATGCGGATGGCTGCTGCTGCCACAGCAGACCTTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrTrpArgGlnMetPheTrpValGln 180
DB 641 GGGAGGTGTCAGAGCGCTGCGCTGTGTGTGCGAGCGAGATGTTCTGGGCTCAG 700
QY 181 ValLeuLeuAlaGlyLeuValAlaProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
DB 701 GTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 760
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
DB 761 CGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 820
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
DB 821 ACCCCACACCGCGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 880
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTyrThrProGly 260
DB 881 CTTGACAGCAGTGAAGATCTGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 940
QY 261 TyrProGluThrGlnGlnAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
DB 941 TACCCCGAGACCCAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1000
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
DB 1001 AGCAGACTCTTGGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1060
QY 301 ProAlaMetLeuLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValAlaPro 320
DB 1061 CAGACCAATGATGCTGACCGCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1120
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340

DB 1121 CGCGCTGGAAGAGTTCTGTCGACGCTGGGCTGCCGAGAGAGATCGAAGCCGTG 1180
QY 341 GluValAlaGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTyrArgGln 360
DB 1181 GAGGTGAGATGCGCGCTTCCGAGACCAAGTACGATGCTCAACGCTGCGCCAG 1240
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
DB 1241 CAGACCGCGCGGCGCTGCGAGCGCTTACCGCGCGCTGCGAGCGCATGCGGCTGACGCG 1300
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
DB 1301 TGCCTGGAAGACTTGGCAGCGCGCTGCGAGCGCGCGCG 1339

RESULT 5

US-09-993-234-9

Sequence 9, Application US/09993234

Patent No. US20020146768A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/993,234

FILING DATE: 19-No. US20020146768A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,683

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Marachang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1007P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5416

TELEX: 910/371-7168

TELEFAX: 415/952-9881

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 1634 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-993-234-9

Alignment Scores:
Pred. No.: 1,31e-189 Length: 1634
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x US-09-993-234-9 (1-1634)

QY 1 GlnGlyLysThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 161 CAGGGGGGCACTGCTACCCAGGTGAGCTGCTCCGGTGACTTCCACAGAAATTTGGT 220

QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuValaProCysThrGluPro 40
|||||
Db 221 CTGTTTGTTCAGAGGCTGCCACCGGGGCACTACTGAAAGGCCCTTCAGACGAGCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTyrGluAsnHis 60
|||||
Db 281 TGGGGCAACTCACCCTGCTGTGTGTCTCCCAAGACACTCTTGTGGCTGGGAGAACAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnGlnAlaSerGlnValaLeu 80
|||||
Db 341 CATATTCTGAAATGTCCTGCGCAGGCTGTGATGAGCAGGCGCTCCAGAGTGGCGCTG 400
QY 81 GluAsnCysSerAlaValaAlaAspThrArgCysGlyCysLysProGlyTyrPheValaGlu 100
|||||
Db 401 GAGAACTGTTCAGCAGTGGCGGACACCGGCTGTGCTAAGCAGGCTGGTGTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAsnCys 120
|||||
Db 461 TGGCAGGTGAGCCAAATGTGTAGCAGTTCAACCTTCTACTCCCAACATGCTTACTGTC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuLeuLeuSerArgAspThrAspCysGlyThr 140
|||||
Db 521 GGGGCTCTGCACCGCCACACAGGCTACTCTGTTCCCGCAGAGTACTGACTGTGGAGCC 580
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
|||||
Db 581 TGCCTGCTGCTGCTTCTTGAACATGGCAGATGGCTGCTGCTGCTGCTGCTGCTGCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValaCysGlyTyrArgGlnMetPheTyrValGln 180
|||||
Db 641 GGGAGTGTCCAGAGGCTGTGCGGCTGTGTGTGGCTGGAGGAGATGTTCTGGGTCTAG 700
QY 181 ValLeuLeuAlaGlyLeuValaValaProLeuLeuLeuGlyAlaThrLeuThrTyrThr 200
|||||
Db 701 GTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 760
QY 201 ArgHisCysTyrProHisLysProLeuValThrAlaAspGlnAlaGlyMetGlnAlaLeu 220
|||||
Db 761 CGGCACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 820
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
|||||
Db 821 ACCCCACACCGGCGCACCATCTGTACCTTGTGACAGGCGCCACACCTCTAGACACT 880
QY 241 ProAspSerSerGluLysLysIleCysThrValGlnLeuValGlyAsnSerThrProGly 260
|||||
Db 881 CCGAAGAGAGTGAAGATCTGACCGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 940
QY 261 TyrProGluThrGlnGlnAlaLeuCysProGlnValThrTyrSerThrAspGlnLeuPro 280
|||||
Db 941 TACCCCGAAGACCCAGAGGCGCTGCTGCGCAGGTGACATGGTCTGGGAGACAGTTGCC 1000
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
|||||
Db 1001 AGCAGAGCTCTTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1060
QY 301 ProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
|||||
Db 1061 CCAGCCATGATCTGACAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1120
QY 321 ArgArgTyrPylsGluPheValaArgThrLeuGlyLeuArgGlnAlaGlyIleGlnAlaVal 340
|||||
Db 1121 CGGCGCTGGAAGAGTGTGTCGCGCAGCGTGGGGCTGGCGGAGCAGAGATCAACCGCG 1180
QY 341 GluValGlnIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTyrArgGln 360
|||||
Db 1181 GAGGTGGAGATGGCGCTGCTCCGAGACAGCAGTACGAGATCTCAAGCGCTGGCGCCAG 1240
QY 361 GlnGlnProAlaGlyLeuGlyValaValaTyrAlaAlaLeuGlnGluArgMetGlyLeuAspGly 380
|||||
Db 1241 CAGCAGCCCGCGGCTGCGAGCCCTTTACGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1300
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393

Db 1301 TGCCTGGAAGACTTGCAGAGCGGCTGCTGACGCGGCGCG 1339

RESULT 6

US-09-333-966-1

Sequence 1, Application US/09333966

Patent No. US20020009773A1

GENERAL INFORMATION:

APPLICANT: Yu, Guo-Liang

APPLICANT: Ni, Jian

APPLICANT: Dixit, Vishva

APPLICANT: Gentz, Reiner L.

APPLICANT: Dillon, Patrick J.

TITLE OF INVENTION: Death Domain Containing Receptors

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., NW, Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: US/09/333,966

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/815,469

FILING DATE:

APPLICATION NUMBER: No. US20020009773A1 Yet Assigned

FILING DATE: 06-FEB-1997

APPLICATION NUMBER: US 60/028,711

FILING DATE: 17-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/013,285

FILING DATE: 12-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1783 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: both

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 198..1481

US-09-333-966-1

Alignment Scores:

Pred. No.: 1,46e-189

Score: 2209.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 10

US-09-993-234-6_COPY_25_417 (1-393) x US-09-333-966-1 (1-1783)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20

Db 303 CAGGGCGGCACTGTGACCCAGGTGACTGTCCGGTGTACTCCACAAAGATTGGT 362
QY 21 LeuPheCysArqglYcysProAlaGlyH1stYLeuYsAlaProCysThrGluPro 40
Db 363 CTGTTTGTTCAGAGGCTGCCAGGGGGACACTGAAGGCCCTTGCAGCGAGACC 422
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTTPGluAsnHis 60
Db 423 TGGCGCAACTCCACTCTGTGTGTCCCAAGACACTCTTGGCTGGGAGAAACAC 482
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 483 CATTAATTCATAATGTGCCCTGTCCAGGCTGTGATGAGAGGGCTTCCAGGTGCCGTG 542
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTTPPheValGlu 100
Db 543 GAGAACTGTCAGACAGTGGCGACACCCGCTGTGCTGAAGCCAGGCTGTTGTGGAG 602
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 603 TGGCAGCTCAGCCAAATGTCTCAGCAGATTCAACCTTCTACTGCCAACCATGCTGAGACTGC 662
QY 121 G1yAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 663 GGGGCTCTGCACGCGCACACAGGCTACTGTCTCCGCAAGATGACTGTGGAGACC 722
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 723 TGCCTGCTGCTGCTTCTATGAACATGGGAGATGGCTGCTGCTGCCACAGACACCTG 782
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTTPArgGlnMetPheTTPValGln 180
Db 783 GGGAGCTGTCCAGAGGCTGTGCGCTGTGTGTGGAGAGAGATGTTCTGGGTGCAG 842
QY 181 ValLeuLeuAlaGlyLeuValAlaProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 843 GTGTCTGCTGTGCTGTGTGTGCTCCCTGCTGTGGGCGCACCTGACTTACATAC 902
QY 201 ArgHisCysTTPProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 903 CGGCACGTGCGGCTCAACAAGCCCTGTACTGACATGAAGTGGGATGGAGGCTCTG 962
QY 221 ThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
Db 963 ACCCCACACCGGCGCACCCACTGTCTCACCCTTGGACAGCGCCACACCTTCTGACACT 1022
QY 241 ProAspSerSerGluYsHisCysThrValGlnLeuValGlyAsnSerTTPThrProGly 260
Db 1023 CCTGACACAGTGAAGATCTGACACCTCAGTTGGTGAACAGCTGGACCTGGGC 1082
QY 261 TyrProGluThrGlnGlnAlaLeuCysProGlnValThrTTPSerTTPAspGlnLeuPro 280
Db 1083 TACCCCGAAGACCGAGAGGGGCTGTGCCGAGGTGACATGTCTCTGGAGCACTTGGCC 1142
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 1143 AGCAGACTCTTGGCCCGCTGTGCTGCCCACTCTGCCAGAGATGCCCGCGGCTGC 1202
QY 301 ProAlaMetLeuLeuGlnProGlyProGlyLeuValAspValMetAspAlaValProAla 320
Db 1203 CAGCCCAATGATGTGCGAGCGGGGCGCGAGCTTACAGACGATGAGAGCGGCTCCACGG 1262
QY 321 ArgArgTTPYsGluPheValArgThrLeuGlyLeuArgGluAlaGlyLeuAlaVal 340
Db 1263 CGGGCGTGAAGAGATGTCGTGGCAGCTGTGGGCTGGCGGAGAGATGGAAGCCGTG 1322
QY 341 GluValAluLeuGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTTPArgGln 360
Db 1323 GAGGTGAGATCGGCGCTTCCGAGACAGACAGATGAGATGCTCAAGCGCTGCGCGCAG 1382
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluValGlyMetGlyLeuAspGly 380
Db 1383 CAGCAGCCCGCGGCTCGGAGCGCTTACGCGGCTTGGAGCGCATGGGCTGGAGCGGC 1442

QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1443 TGCCTGGAAGACTTGGCGAGCGGCTGCGAGCGGCGCCG 1481

RESULT 7
US-09-954-531-1389
; Sequence 1389, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954, 531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233, 133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234, 009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234, 034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234, 509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234, 567
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1389
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-1389

Alignment Scores:
Pred. No.: 2,01e-183 Length: 1743
Score: 2140.50 Matches: 389
Percent Similarity: 91.10% Conserved: 0
Best Local Similarity: 91.10% Mismatches: 4
Query Match: 96.90% Indels: 35
Gaps: 1

US-09-993-234-6_COPY_25_417 (1-393) x US-09-954-531-1389 (1-1743)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysLeuGly 20
Db 141 CAGGGCGGCACTGTGACCCAGGTGACTGTCCGGTGTACTCCACAAAGATTGGT 200
QY 21 LeuPheCysArqglYcysProAlaGlyH1stYLeuYsAlaProCysThrGluPro 40
Db 201 CTGTTTGTTCAGAGGCTGCCAGGGGGACACTGAGAGGCCCTTGCAGCGAGGCC 260
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTTPGluAsnHis 60
Db 261 TGGCGCAACTCCACTCTGTGTGTCCCAAGACACTTCTTGGCTGGGAGAAACAC 320
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 321 CATTAATTCATAATGTGCCCTGTCCAGGCTGTGATGAGAGGGCTCCAGAGTGGCGCTG 380
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTTPPheValGlu 100
Db 381 GAGAACTGTCAGACAGTGGCGACACCCGCTGTGCTGAAGCCAGGCTGTTGTGGAG 440
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 441 TGGCAGCTCAGCCAAATGTCTCAGCAGATTCAACCTTCTACTGCCAACCATGCTGAGACTGC 500
QY 121 G1yAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 501 GGGGCTCTGCACGCGCACACAGGCTACTGTCTGCCAGAGATGACTGTGGAGACC 560
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160

Db	561	TCGCTGGCTGGCTTCTATGAACATGGCGAATGGGTGGCTCTCTGCCCCAGCAGCACCTG	620
QY	161	GlySerCysProGluArgCysAlaAlaValCysGlyTyrParg	174
Db	621	GGGAGCTGTCAGAGACGCTGTGCCGTGTCTGTGGCTGGAGCAGATAGTGGTGTCT	680
QY	174		174
Db	681	GGGAATGCGCGTGGAGAACTGGGGAATGGACCGAGGGGAGCGGGGTGAGGAGGGGGCCAAAC	740
QY	175	-----GlnMetPheTyrValGlnValIleuLeuAlaGlyLeu	186
Db	741	CACCCAAACACCACCACTGCTTCCAGTG- TTCTGGGTCCAGATGCTCTGTGCTGGCTT	799
QY	187	ValValAlaProIleuLeuGlyAlaIleThrIleuThrTyrThrTyrArgHisCysTyrProHis	206
Db	800	GTGTGTCCCTCCCTGGCTTGGGGCCACCTGACCTTACACATACCGGCACAGCTGGGCTCAC	859
QY	207	LysProIleuValThrAlaAspGluAlaGlyMetGluAlaIleuThrProProAlaThr	226
Db	860	AAGCCCGGTGTACTGCAGATGAAGCGTGGGATGAGAGCTGTGACCCACACCGGCGCAC	919
QY	227	HisIleuSerProIleuAspSerAlaHisThrIleuLeuAlaProProAspSerIleuLys	246
Db	920	CATCTGTACCTTGGAGACAGCGCCACACCTTCTAGCACCTCTGACAGCAGTAGAGAG	979
QY	247	IleCysThrValGlnIleuValGlyAsnSerTyrThrProGlyTyrProGluThrGlnIu	266
Db	980	ATTCGACACCGTCCAGTTGGTGGGGTAACAGCTGAGACCCCTGGCTACCCGAGACCGAGGAG	1039
QY	267	AlaIleuCysProGluValIleThrTyrPserTyrPaspGlnIleuProSerArgAlaIleuGlyPro	286
Db	1040	GGCGTCGCGCCGAGGAGCAATGGTCTCTGGAGCACCTTCCAGCAGACCTTCTGGCCCC	1099
QY	287	AlaAlaAlaProThrIleuSerProGluSerProAlaGlySerProAlaMetIleuGln	306
Db	1100	GCTGCTGGCGCCACACACTCTGCGCCAGATCCCCAGCCGGGCTCGCCAGCCATGATCTCGAG	1159
QY	307	ProGlyProGluIleuTyrAspValMetAspAlaValProAlaArgArgTyrPlysGluPhe	326
Db	1160	CCGGGCGCCGAGCTCTACGACCGATGATGAGACCGCGGTCCCGACGGGGCGTGGAAAGAGTTTC	1219
QY	327	ValArgThrIleuGlyLeuArgGluAlaGlnIleGluAlaValGluIleGlyArg	346
Db	1220	GTGGCGACGCGGGGGCTGGCCGAGGACGAGATGAAAGCCGTGGAGGTGGAATCGCTCTC	1279
QY	347	PheArgAspGlnGlnTyrGluMetLeuLysArgTyrPArgGlnGlnIleProAlaGlyLeu	366
Db	1280	TTCCGAGACGACGATGAGATGATGCTCAACACTGGCGGCAGAGCAGCAGCCGCGGGGCTTC	1339
QY	367	GlyAlaValTyrAlaAlaIleuGlnArgMetGlyIleuAspGlyCysValGlnAspLeuArg	386
Db	1340	GGAGCGCGTTTACGGCGCCGTGGAGCGCATGGGGCTGTGACGGCTGTGGAAAGACTTGGCGC	1399
QY	387	SerArgLeuGlnArgGlyPro	393
Db	1400	AGCCGCGTGCAGCGTGGCCCG	1420
RESULT 8			
US-10-092-154-1577			
: Sequence 1577, Application US/10092154			
: Publication No. US20030054375A1			
: GENERAL INFORMATION:			
: APPLICANT: Rosen et al.			
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies			
: FILE REFERENCE: PC009C1			
: CURRENT APPLICATION NUMBER: US/10/092,154			
: NUMBER FILING DATE: 2002-03-07			
: CUMBER OF SEQ ID NOS: 2003			
: Prior Application removed - See File Wrapper or Palm			
: SOFTWARE: PatentIn Ver. 2.0			
: SEQ ID NO 1577			

Length: 10797	Type: DNA	Organism: Homo sapiens	US-10-092-154-1577
Alignment Scores:			
Pred. No.:	7,87e-125	Length: 10797	
Score:	1498.50	Matches: 389	
Percent Similarity:	28.46%	Conservative: 0	
Best Local Similarity:	28.46%	Mismatches: 4	
Query Match:	67.84%	Indels: 978	
DB:	9	Gaps: 8	
US-09-993-234-6_COPY_25_417 (1-393) x US-10-092-154-1577 (1-10797)			
QY	1	glnGlygLyThrAtgSerProAtgCysAspCysAlaGlyAspPheHisLysLysIleGly	20
Db	5268	CAGGCGGCACTCGTACCCAGGTGACTGTGCGGTACTTCCAAAGAAGATTGGT	5322
QY	21	LeuPheCysCysAAgGlyCysProAla-----	29
Db	5328	CTGTTTGTTCAGAGGCTGCCACGGCGGTAAATGGGCAACAGGGGTTGGAGAGGATGGG	5387
QY	29	-----	29
Db	5388	GCAGCAGGCTGAGAGAGTGGCGGGCAGGCCGGAGATGAAGAGAGGCTGCAGAGGA	5447
QY	29	-----	29
Db	5448	GGTAGGGGTAGCGTACACAGAGAATAGGAGACTGGAGAGAAAGAGGAGGAGGGCAGGG	5507
QY	29	-----	29
Db	5508	TGGAAAGCAGGTCCGGGGTGTCTGGGACGCCCTTGCCCTGACCCCTGCTGTTC	5567
QY	30	---GlyHisrLeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuVa	48
Db	5568	CACAGGGCACTACTGAAAGGCCCTTACAGGAGGCCCTGGGCAACTCCACTGCTGT	5622
QY	48	ICysProGlnAspThrPheLeuAlaTrpGluAsnHisLysAsnSerGluCysAlaArgCys	68
Db	5628	GTGTCCCAACACACTTCTTGCCCTGGGAGAACCAACATAATTGTGAATGTGCCCGTG	5687
QY	68	sgLAlaLcysAspLlu-----	73
Db	5688	CCAGGCGCTGATAGCAGAGGGTGAGGGGCTTTCAGTCTTGGCAGGAGTCTTAAGA	5747
QY	73	-----	73
Db	5748	CAGGCTTTCGAAGGAAGTGGCTGGCTGGGCCCAAACTTGGGGTGTGAGGGTCTGTGA	5807
QY	73	-----	73
Db	5808	CCCACTTGGCAGAACCTTCCACCTGATCTCTTCACAGGTTGCCCTTGGCCCTTCTCT	5867
QY	73	-----	73
Db	5868	CTTCTGTGTGACTTCCCATCTCCATGTGCTTGGCCCTGTGGTGGGCTTAATCTCG	5927
QY	73	-----	73
Db	5928	AGCTTCTCTTTTATAGGATAGCCCTGATACCTGTCTGTCTTTCGCTATTTCTGTCTCC	5987
QY	73	-----	73
Db	5988	ATTATCTTGGGATTAATGCTCTGCTCTTCATGGGAGCCTTGGCCCTGACTTAACCTCC	6047
QY	74	-----GlnAlaSerGlnValAlaLeuGluAsnCysSerAl	85
Db	6048	ACTGCCATCTCCCTGGACCCGCCACAGGC-TCGCCAGGTGGCGCTGGAGAAGTGTTCAGC	6106
QY	85	aValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGluCysGlnValSerG	105

QY 223 ----- 223
Db 8324 CTGCCCTCAAGGGGCTCTCAGTCACTGAGTTCAGATTCTGACAGAGAGCTAAAGTT 8383
QY 223 ----- 223
Db 8384 CAATGGAAGAGAGCCCATGTTGTGGGGGACAAAGAGAGAGAGAGAGAGAGAGAGAG 8443
QY 223 ----- 223
Db 8444 TCAAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 8503
QY 223 ----- 223
Db 8504 GTCAATGGGGGGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8563
QY 224 ----- Pro-Ala 225
Db 8564 GGGTAAGGGGCTTACTTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 8623
QY 226 ThrlstleuSerProleuAspSerAlaHisThrlleuAlaProAspSerSerGlu 245
Db 8624 ACCCATCTGCTACCCCTGGACAGGCGCCACACCTTCTAGACCTCTGACAGCAGTGTAG 8683
QY 246 LysileCysThrValGlnleuValGlnAsnSerThrProGlyTyrProGlyThrGln 265
Db 8684 AAGATCTGCACACCTTCCAGTTGGTGGTAACTGAGAGAGAGAGAGAGAGAGAGAGAGAG 8743
QY 266 GluAlaLeuCysProGlnValThrlPserTyrAspGlnleuProSerArgAlaLeu 284
Db 8744 GAGCGCTGTGCCCGCAGAGTGACATGTCTCTGGACAGAGTTGCCACAGAGCTCTGTGT 8803
QY 284 ----- 284
Db 8804 AAGGACATCAGTGGCCCTGAGCCCTTGCACCCCAATCTCTGTCTGCGGTGGAGATTGTG 8863
QY 284 ----- 284
Db 8864 GTTTCACAACGTGTCTCCCTTTCGCCCTTAACCTGACGAGTCCGCCATGATGCCCTGACC 8923
QY 284 ----- 284
Db 8924 CACGGATCCAGCGGGCTTACGCCCTGGGGTACCCGACGAGAGAGAGAGAGAGAGAGAG 8983
QY 285 ----- GlyProAlaAla 288
Db 8984 CCGACCGCGGCGCCACGTAACCCCAATTGGCTCTCTGCTGAGCCCTGCCAGGCGCCGCTGCT 9043
QY 289 AlaProThrleuSerProGlnSerProAlaGlySerProAlaMetleuGlnProGly 308
Db 9044 GCGCCCACTCTCGCCAGAGTCCCGAGCGGCTCCCGACCATGTATGCTGACGCGCGGC 9103
QY 309 ProGlnleuTyrAspValMetAspAlaValProAlaArgArgTyrPylsGluPheValArg 328
Db 9104 CCGCACTCTAGACGTGTATGAGCGGGTCCAGCGCGGCTGGAAGAGAGTTCGTGCGGC 9163
QY 329 ThrleuGlyleuArgGluAlaGluGluAlaValGluAlaGluGluGluGluGluGluGlu 348
Db 9164 AGCGTGGGCTGCGGAGGAGAGAGATGAGAGCGGTGAGAGTGGAGATGCGCGCTTCCGA 9223
QY 349 AspGlnGlnTyrGlnMetleuLysArgTyrPargGlnGlnGlnProAlaGlyleuGlyAla 368
Db 9224 GACCAAGCATAGAGATGCTCAAGCCCTTGGCCCGACAGCAGCAGCAGCAGCAGCAGCAG 9283
QY 369 ValTyrAlaAlaLeuGluArgMetGlyleuAspGlyCysValGluAspLeuArgSerArg 388
Db 9284 GTTTCAGGGGCGCTGAGAGCATGGGGCTGAGCGGCTGGTGGAGAGACTTGGCAGCGCC 9343
QY 389 leuGlnArgGlyPro 393
Db 9344 CTGCAAGCGCGGCGCG 9358
RESULT 9

US-09-764-847-1577
Sequence 1577, Application US/09764847
Patent No. US20020132767A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PAM or file wrapper
NUMBER OF SEQ ID NOS: 2003
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 1577
LENGTH: 10797
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-847-1577
Alignment Scores:
Pred. No.: 7,87e-125 Length: 10797
Score: 1498.50 Matches: 389
Percent Similarity: 28.46% Conservative: 0
Best Local Similarity: 28.46% Mismatches: 4
Query Match: 67.84% Indels: 978
Gaps: 8
US-09-993-234-6_COPY_25_417 (1-393) x US-09-764-847-1577 (1-10797)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysLysLys 20
Db 5268 CAGGGGGGACACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5327
QY 21 LeuPheCysAspArgGlyCysProAla 29
Db 5328 CTGTTTGTGTGACAGAGCTGCTCCAGCGGGTAACTGACACAGGAGTGGAGAGCATGGG 5387
QY 29 ----- 29
Db 5388 GCAGGAGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5447
QY 29 ----- 29
Db 5448 GGTAGGGGTAGGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5507
QY 29 ----- 29
Db 5508 TGGAAGCAGAGTGGGGGTTGCTGGGACAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 5567
QY 30 ----- GlyHisTyrLeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuVal 48
Db 5568 CACAGGGGACACTACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5627
QY 48 LysProGlnAspThrPheLeuAlaTyrPheLysHisHisAsnSerGluCysAlaArgCys 68
Db 5628 GTGTCCCAAGACACTTCTTGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5687
QY 68 sGlnAlaCysAspGlu 73
Db 5688 CAGAGGCTGTGATGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5747
QY 73 ----- 73
Db 5748 CAGGCTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5807
QY 73 ----- 73
Db 5808 CCGACCTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5867
QY 73 ----- 73
Db 5868 CTTCCTGTGACCTTCCCATCTCTCAGATGAGCTTGGCCTGTGGCTGAGCTTAATCTCTG 5927
QY 73 ----- 73

Db	5928	AGCTTCCTCTTTTTTAAAGGTAGACCCCTGACCTGACCTGCTGCTCTTTGGCCATTTTCTGCTCC	5987
Oy	73	-----	73
Db	5988	ATTATCTTGGGATAAAGCCCTTCGCTCCATGAGGAGCCCTTGGCCCTGACTAACTCC	6047
Oy	74	-----	85
Db	6048	ACTGCCCATCTCCCTGCACCCCCCACCACGCC -TCCAGGTGGCGCTGGCAACTGTTACGC	6106
Oy	85	aValAlaAspThrArgGsgLysAlaSerProGlyTrpPheValGluCysGlnValSerG1	105
Db	6107	AGTGGCCGACACCCGGCTGTGGCTGAAGCAGGAGCTGGTTTGGAGTCCAGGTCACCA	6166
Oy	105	nCysValSerSerSerProPheTrcYsgLInProCysLeuAspCysGlyAlaLeuHisAr	125
Db	6167	ATGTGTAGCAGATTCACCTCTTACAGCCACCATGCTACGACTCGGGGCCCTGCACCG	6226
Oy	125	gHisThrArgLeuLeuCysSer-----	132
Db	6227	CCACACACGGGTACTGCTGTGA -GTACCCCAACCAAGGCTCTTACTCCAGACCCCTT	6285
Oy	132	-----	132
Db	6286	CTCCCTGCTGACCCACTCCTGTCCATGAGTGAAGCATCCCTCTCGATTCAGAGTTC	6345
Oy	133	-ArgArgAspThrAspCysGlyTrhCysLeuProGlyPheTrcGlnHisGlyAspGlyCy	152
Db	6346	CCGAGAGATATCTACGTGTGGAGACGCTGCTGCTCTTATGAACATGGCATGGCTG	6405
Oy	152	sValSerCysProThSer-----	158
Db	6406	CGTGTCTGTGCCCCACGTA -ATTCTAGCTGTGCTGGAGTGAAGGAGCGCGCTGGAG	6464
Oy	158	-----	158
Db	6465	CAGAGCAGGGGCTGGGGTGGGCGAGGTGCTGCTGTTCAGAAATAGNAGAGGGGATAG	6524
Oy	158	-----	158
Db	6525	GGAGGAGGAGACCTTGGCCCTGTGATGGTGGGCCCCCACTTCAGCAAACTAGATGCA	6584
Oy	158	-----	158
Db	6585	AAAGAGCAATCTGGATCCGCCCTTAGCCAGATACATAAGGATTTGCTTCATTTCAGC	6644
Oy	158	-----	158
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Oy	158	-----	158
Db	6705	GTCAATTGTATATAGCTTTAAACTTGGGCTGAGAGGAGTGTGAGCTGAGTGAACATATG	6764
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Db	6765	ATCGTGCACCTGCACCTTCACCTGGGCAACAGACGACACTATTAAATTAATTAATAAA	6824
Oy	158	-----	158
Db	6825	TATTAAATCTATTAAATATTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	6884
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Db	6945	CTCTGATGTGTGTCCTCTTCTGCAACATGGGATTTAGCAGCTAATTCACAGGCTTT	7004
Oy	158	-----	158

Db	7005	GATCAGAGGTAAGGACTTTCCTGTAGCTATTCAAAGCTTTTTTTTTTTTTTTTTTTTTTTT	7064
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Db	7065	TTTTTGAGATGAGACTTGTCTCTGTCCACCCAGGCTGAGATGCAGTGCACGATCTGGCT	7124
OY	158	-----	158
Db	7125	CAGTACAACCTCTGTCTGCTGGGTTCAAGTATTTCTCTGCCTCAGCTCCCAAGTACT	7184
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Db	7185	GGGACTACAGAGGCCACACACACCCCGGTAATTTTTTGTATTTTGTAGAGACGG	7244
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Db	7245	GTTTCACCGCTTTAGCCAAAGATGCTTGATCAGCAGACCTGTGTATCCACCGCCTTGG	7304
OY	158	-----	158
Db	7305	CCTCCCAAAGTCTGGGATTACAGGATGAGCCACCGCGCCGCTCCATTCAAGTCTT	7364
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Db	7365	TATTGAATATCTGCTATGTTCTACACACTGTTCTAGTGTCTGGGATGCACAGGGACA	7424
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Db	7425	AAATAGCAAAATCCCTGCTCTTTGGGGTGACATTCTAGTACCTTTCATGTAGTCTA	7484
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Db	7485	GAAAGACTAGTGAATATATGTCTGTGTGTTTACCAGGGACACAATGACAGAAATTC	7544
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Db	7545	TTGGTAGAGTGAGAGGCTTGGGAGGAAAGGTCTTAGATGAGCAGATGCTGGCA	7604
OY	158	-----	158
Db	7605	GTTCTTAGGAGCCCTCCTGGCATGCACCCCTCATCCCTCAGGCGCACCCCGTCCCTTG	7664
OY	159	-----Thleuglysercystrprogluarqcyalaalavalcygslgtprhg-----	174
Db	7665	CAGGAGCACCTGTGGGAGCTGTCCAGAGCGCTGTGCCCTGTGTGTGCTGAGAGCAG	7724
OY	174	-----	174
Db	7725	TAGTGTGTCTGGGAATCCAGTGGAGAACTGGGATGACACGAGGGAGCGGGTGA	7784
OY	175	-----Glmethperrpvalglvalle	182
Db	7785	GGAGGGGGGCAACCAACCAACCAACCAACGCTGTTCAAGTG-TTCTGGGTCCAGGTCT	7843
OY	182	uLeuualaglyleuvalvalProleuLeuLeuglyalathrLeuthrTYrThrTYrArgHl	202
Db	7844	CCTGCTGGCCCTTGTGTCTCCCTCTCTGTGGGGCCACCTGACCTACATACCGCA	7903
OY	202	scysTriProhliysProleuvalthr-----	211
Db	7904	CTGCTGGCTTACAAGCCCTGGTTACTGTGTAATACACACACCAACACAGCACCAGA	7963
OY	211	-----	211
Db	7964	AGCCGGGGGTGAGATGGGTAGGCCAGAGTCTACTAACCCGTGATACAGAAGGGAAACT	8023
OY	211	-----	211
Db	8024	GAGCAGGAGAGTGTGGGTGCAGAGAACCTTAGAGAGAGTGTACAGACCCAGGTCCA	8083
OY	212	-----Alasptglualaglym	217
Db	8084	GGAGGCTTGCTGTGGCTGACCGCAATCTCTGTGTCTGTACACAGATGAAGTGGGA	8143

Db 417 GGGGCGCTGCACCCGACACAGCGCTACTCTGTTCCCGCAGAGATGACTGTTGGAC 476
Qy 141 CysLeuProGlyPheThyrgluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 477 TGCGTGGCTGCTCTATGAACATGATGGGCTGCTGCTCAGCAATAGCAAGAGGGATAGG 536
Qy 161 GlySerCysProGluArgCysAlaValCysGlyThrPargln-MetPheTrpValGly 180
Db 537 -----GCTGTGCTGGGATGAGGAGGAGGCGCTGGGAGCA 572
Qy 180 nValLeuAlaGlyLeuValProLeu-----Laugl 193
Db 573 GAGAGGGGAGCCTGGGCTGGGCGAGCTGCTGCTCAGCAATAGCAAGAGGGATAGG 632
Qy 193 yAlaThrLeuThrTyThrArgHisCysTrpPro-----HisLysProLeuVa 210
Db 633 GAGG-----AGGAGCGCTTGGCTGGATGGGAGGGGCGCCACTTCA 674
Qy 210 lThAlaAspGluAlaGlyMetGluAlaLeuThrProProAlaThrHisLeuSerPr 230
Db 675 GGCACAACTTAGTGCAG--AAGAGCAATCTGGATCCGCTTAGCCAGATACATAGGATA 733
Qy 230 olAuAspSerAlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCysThrVa 250
Db 734 TTTCCTTCACTTTCACCCAGCATTCCTCCCGAGCATCTAGCCAGATATTACAGATGT 793
Qy 250 lGlnLeuValGlyAsnSer 256
Db 794 AACCTCTGCGCGAATTCT 812

RESULT 11
US-10-081-280-5
Sequence 5, Application US/10081280
Patent No. US20020165157A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-081-280-5

Alignment Scores:
Pred. No.: 8,98e-77 Length: 1438
Score: 952.00 Matches: 163
Percent Similarity: 93.71% Conservative: 1
Best Local Similarity: 93.14% Mismatches: 3
Query Match: 43.10% Indels: 8
Gaps: 1
DB: 9

US-09-993-234-6_COPY_25_417 (1-393) x US-10-081-280-5 (1-1438)

Qy 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 449 CAGGCGGACCTCTAGCCCGCAGGCTGACGTGCTCCGGTGACTTCCACAAAGATTGCT 508
Qy 21 LeuPheCysAspGlyCysProAlaGlyHisThrLeuValAspProCysThrGluPro 40
Db 509 CTGTTTGTTCACAGAGCTGCCAGCGGGGCACTAGCTGAAGGCCCTTGACGAGGCC 568
Qy 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 569 TGGGCAACTCAGCTGCTGCTGTGTCCCAAGACACTTCTTGCGTGGAGAACAC 628
Qy 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 629 CATTAATCTGAATGTGCCCGCTGCCAGGCTGTATGAGAGCGCCCTCCAGGTGGCGCTG 688
Qy 81 GluAsnGlySerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 689 GAGAACTGTTGACGAGGCGGACACCCGCTGTGCTGTAAAGCAGGCTGTTGTGGAG 748
Qy 101 CysGlnValSerGlnCysValSerSerProPheThrCysGlnProCysLeuAspCys 120
Db 749 TGGCAGGTCACCAATGTGTGACGAGTTCACCTTACTGCAACATGCTGACTGAGACTGC 808
Qy 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 809 GGGGCGCTGCACCCGACACACAGCGCTACTCTGTTCCCGCAGATAGTACTGAGTGGAC 868
Qy 141 CysLeuProGlyPheThyrgluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 869 TGCGTGGCTGCTCTATGAACATGATGGGCTGCTGCTCAGCAATAGCAAGAGGGATAGG 928
Qy 161 GlySerCysProGluArgCysAlaValCysGlyThrPargln 175
Db 929 -----GCTGTGCTGGGATGAGGAGCA 949

RESULT 12
US-10-112-793-5
Sequence 5, Application US/10112793
Publication No. US20020192729A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A


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0y 121 GIVAlAlaLeuHtASrGHtStHrArLeuLeuCySerArRrArRgAsPThrAsPcYsGlyThr 140
Db 809 GGGGCCCTGCACCGCCACACAGGGCTACTCTGTTCCCGCAGATTAAGTACTGTGGGACC 868
0y 141 CysLeuProGlyPheYrYrGluHtISGLAsPc1YcYsValSerCyProThSerThrLeu 160
Db 869 TGCGCGCTGGCTCTTATGAAACATGGGAGTGGCGGTGCGGTCTGTCGCCACAGTAATTCCTA 928
0y 161 GlySerCySProGluArGcYsAlaAlaValAlcYsGlyTrpArgIn 175
Db 929 -----GCTGTGCTGGATGAGAGCA 949

RESULT 14
US-09-884-733-5
? Sequence 5, Application US/09884733
? Patent NO. US20020123116A1
? GENERAL INFORMATION:
? APPLICANT: Ashkenazi, Avi J.
? TITLE OF INVENTION: Apo-2 Ligand Inhibitor
? NUMBER OF SEQUENCES: 9
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: Genentech, Inc.
? STREET: 460 Point San Bruno Blvd
? CITY: South San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94080
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 Inch, 1.44 MB floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: WinPatIn (Genentech)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/884,733
? FILING DATE: 19-Jun-2001
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/304,003
? FILING DATE: 14-JUNE-2000
? ATTORNEY/AGENT INFORMATION:
? NAME: Marschang, Diane L.
? REGISTRATION NUMBER: 35,600
? REFERENCE/DOCKET NUMBER: P1007
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415/225-5416
? TELEFAX: 415/952-9881
? TELEX: 910/371-7168
? INFORMATION FOR SEQ ID NO: 5:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1438 base pairs
? TYPE: Nucleic Acid
? STRANDEDNESS: Single
? TOPOLOGY: Linear
? SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-884-733-5

Alignment Scores:
Pred. NO.: 8,98e-77 Length: 1438
Score: 952.00 Matches: 163
Percent Similarity: 93.71% Conservative: 1
Best Local Similarity: 93.14% Mismatches: 3
Query Match: 43.10% Indels: 8
DB: 10 Gaps: 1

US-09-993-234-6_COPY_25_417 (1-393) x US-09-884-733-5 (1-1438)
0y 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHtLysLysIleGly 20
Db 449 CAGGCGCGCACTCGTAGGCCCCAGAGTGTGACTGTGCGGTGACTTCACCAAGAGATTGGT 508
0y 21 LeuPheCySPsArGdGlyCySPsAlaGlyHtISrYrLeuLysAlaPcYsSPThrGluPro 40
Db 509 CTGTTTGTTCACAGAGGTGGCCACGCGGCGACTACCTGAAGGCCCTTCACAGGAGACC 568

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03  569  TCGGGCAACTCCACCTGCGCTTGCTGTGTGCCAAGACACTCTTGCGCTGGAGAACAC 628
04  Db
05  61  HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
06  Db
07  629  CATATTTCTGAATGATGCCCGCTGCCAGGCGTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 688
08  Oy
09  81  GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTTPheValGlu 1000
10  Db
11  669  GAGAACTTTGACGAGTGGCCGACACCGCGTGGCTGTAGCCAGGCTGGTTGTGGAG 748
12  Oy
13  101  CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
14  Db
15  749  TCCCGAGTCAGCCCAATGTGTGACGAGTTCACTTACCTTGCTACGCAACATGCTTAGACTGC 808
16  Oy
17  121  GlyAlaLeuHisArgHisThrArgLeuLeuGluCysSerArgArgAspThrAspCysGlyThr 1400
18  Db
19  809  GGGGGCGTCGACCGCCACACAGCGGTACTGTTCGCCGAGAGATGACTGAGCTGGGAGCC 866
20  Oy
21  141  CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 1600
22  Db
23  869  TCCCGCGCTGCGCTTGAAGAACATGGCGATGGCGCGTGTCTCCGCCACGATTAATTCCTA 928
24  Oy
25  161  GlySerCysProGluArgCysAlaAlaCysGlyTTPArgGln 175
26  Db
27  929  -----GCTGTCTCGTGGATGGAGGGA 949
28
29  RESULT 15
30  : Sequence 5, Application US/09993234
31  : Patent No. US20020146768A1
32
33  GENERAL INFORMATION:
34  APPLICANT: Ashkenazi, Avi J.
35  TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
36  NUMBER OF SEQUENCES: 11
37  CORRESPONDENCE ADDRESS:
38  ADDRESSEE: Genentech, Inc.
39  STREET: 460 Point San Bruno Blvd
40  CITY: South San Francisco
41  STATE: California
42  COUNTRY: USA
43  ZIP: 94080
44
45  COMPUTER READABLE FORM:
46  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
47  COMPUTER: IBM PC compatible
48  OPERATING SYSTEM: PC-DOS/MS-DOS
49  SOFTWARE: WinPatIn (Genentech)
50  CURRENT APPLICATION DATA:
51  APPLICATION NUMBER: US/09/993,234
52  FILING DATE: 19-No. US20020146768A1-2001
53  CLASSIFICATION: <Unknown>
54  PRIOR APPLICATION DATA:
55  APPLICATION NUMBER: 08/828,683
56  FILING DATE: <Unknown>
57  ATTORNEY/AGENT INFORMATION:
58  NAME: Maerschang, Diane L.
59  REGISTRATION NUMBER: 35,600
60  REFERENCE/DOCKET NUMBER: P1007P1
61  TELECOMMUNICATION INFORMATION:
62  TELEPHONE: 415/225-5416
63  TELEFAX: 415/952-9881
64  TELEX: 910/371-7168
65
66  INFORMATION FOR SEQ ID NO: 5:
67  SEQUENCE CHARACTERISTICS:
68  LENGTH: 1438 base pairs
69  TYPE: Nucleic Acid
70  STRANDEDNESS: Single
71  TOPOLOGY: Linear
72
73  SEQUENCE DESCRIPTION: SEQ ID NO: 5:
74  US-09-993-234-5

```

Alignment Scores:

Pred. No.:	8,98e-77	Length:	1438
Score:	952.00	Matches:	163
Percent Similarity:	93.71%	Conservative:	1
Best Local Similarity:	93.14%	Mismatches:	3
Query Match:	43.10%	Indels:	8
DB:	10	Gaps:	1

US-09-993-234-6_COPY_25_417 (1-393) x US-09-993-234-5 (1-1438)

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QY 1 GluGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
   |||||
Db 449 CAGGGCGGCACTGCTAGCCAGGCTGAGCTGCTCCGGTGACTCCACAGAAAGATTGCT 508
   |||||

QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
   |||||
Db 509 CTGTTTGTGGCAGAGGCTGCCCGCGGCGGCTGAGCTGAAAGCCCTTGACACGAGCC 568
   |||||

QY 41 CysGlyAsnSerThrCysLeuValCysProGluAspPheLeuAlaTrpGluAsnHis 60
   |||||
Db 569 TGGCGGCACTCCACTGCTGCTGCTGCTGCCAGACACCTTCTGGCTGGAGAACCC 628
   |||||

QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
   |||||
Db 629 CATAAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTGGCCTG 688
   |||||

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
   |||||
Db 689 GAGAACTGTTACAGCAGCGCCGACACCCGCTGTGGCTGAAGCCAGGCTGTGTGGAG 748
   |||||

QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
   |||||
Db 749 TGGCAGGTGAGCCATGTGTGACAGTTCACCTTCTACTGCAACCATGCTAGACTGC 808
   |||||

QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
   |||||
Db 809 GGGGCCCTGACGACGACACACGCGTACTGTTCCCGCAGAGTACTGACTGGGACC 868
   |||||

QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
   |||||
Db 869 TGCCTGCTGGCTTATGAAACATGGCGAGGCTGCTGCTGCCCGCCACGTAATTCCTA 928
   |||||

QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrPheGln 175
   |||||
Db 929 -----GCTGTGCTGGGATGAGGGA 949

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Search completed: April 7, 2003, 03:58:32
 Job time : 188.643 secs

GenCore version 5.1.4.p5.4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:19:54 ; Search time 2458.26 Seconds

(without alignments)

2589.161 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_417

Perfect score: 2209

Sequence: 1 GCGTSPRCDCAGDFHKKIG.....ERKGLDGCYEDLRLQKGP 393

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n model -DEV=xlh
-O=/cgn2.1/USPTO.spool/US09993234/runat_27032003_115456_15362/app_query.fasta.1.2346
-DB=EST -OPT=fastap -SUFFIX=1st -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blonsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptco -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09993234.cgn.1.1.4749.0runat.27032003.115456.15362 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-HARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database :

EST:*
1: em.estba:*
2: em.esthum:*
3: em.estlin:*
4: em.estnu:*
5: em.estlov:*
6: em.estpl:*
7: em.estro:*
8: em.htc:*
9: gb.est1:*
10: gb.est2:*
11: gb.htc:*
12: gb.est3:*
13: gb.est4:*
14: gb.est5:*
15: em.estfun:*
16: em.estom:*
17: gb.gss:*
18: em.gss.hum:*
19: em.gss.lnv:*
20: em.gss.pln:*
21: em.gss.vtc:*
22: em.gss.fun:*
23: em.gss.mam:*
24: em.gss.mus:*
25: em.gss.other:*
26: em.gss.pro:*
27: em.gss.rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1423	64.4	1010 14	B0068309
2	1211	54.8	698 9	A1807913
3	1179	53.4	681 10	BE563566
4	1166	52.8	767 13	B1909448
5	1090	49.3	632 10	AW268610
6	1082	49.0	651 13	BM009354
7	1065.5	48.3	647 14	BM794760
8	1026	46.4	648 9	A1424936
9	979	44.3	562 9	A1140043
10	968	43.8	539 12	BF726557
11	952	43.1	552 14	BM783972
12	952	43.1	585 10	AW517358
13	943	42.7	565 14	BM744307
14	937	42.4	514 14	BM756372
15	937	42.4	514 14	BM783979
16	932	42.2	492 14	BM741016
17	916	41.5	508 9	A1203624
18	893	40.4	488 14	BM770798
19	869.5	39.4	494 10	BE220347
20	839	38.0	673 13	BM251737
21	798.5	36.1	478 10	AW002222
22	781	35.4	427 12	BE696572
23	780.5	35.3	434 14	BM826048
24	698	31.6	439 14	BM824360
25	680	30.8	422 9	A1700459
26	666	30.1	433 14	H41522
27	654	29.6	687 10	BE670189
28	639	28.9	572 10	BE668836
29	597.5	27.0	500 9	AA476747
30	591	26.8	432 14	N71143
31	560.5	25.4	345 14	BM853061
32	537	24.3	623 9	A1811528
33	518.5	23.5	443 14	H46211
34	517	23.4	345 9	AA934992
35	486.5	22.0	372 14	W76376
36	479.5	21.7	435 10	AV664983
37	474.5	21.5	755 13	B1655045
38	472	21.4	587 9	A1380959
39	463	21.0	468 14	H46374
40	455	20.6	633 10	BB212432
41	446	20.2	618 10	AW074008
42	445.5	20.2	582 10	AW182875
43	436.5	19.8	775 12	BG867742
44	420.5	19.0	322 9	AA971249
45	416	18.8	274 12	BF552058

ALIGNMENTS

RESULT 1
B0068309
LOCUS B0068309
DEFINITION AGENCOURT_6794093 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5770562
5' mRNA sequence.
ACCESSION B0068309
VERSION B0068309.1 GI:19897355
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1010)
NIH-MGC http://mhc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LLM12833 row: n column: 03
 High quality sequence stop: 689.
 Location/Qualifiers
 1. 1010

FEATURES
 source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5770562"
 /clone_1lb="NHL_MGC_121"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
 fetal brains, female age 20 weeks, female age 24 weeks,
 and male age 26 weeks. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb. Insert size range
 0.7-3.5 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gardner
 (Invitrogen). Research Genetics tracking code 017. Note:
 this is a NHL_MGC Library."

BASE COUNT 179 a 353 c 287 g 191 t
 ORIGIN

Alignment Scores:
 Pred. No.: 3 45e-109 Length: 1010
 Score: 1423.00 Matches: 257
 Percent Similarity: 91.58% Conservative: 4
 Best Local Similarity: 90.18% Mismatches: 13
 Query Match: 64.42% Indels: 11
 DB: 14 Gaps: 3

US-09-993-234-6_COPY_25_417 (1-393) x B0068309 (1-1010)

QY 30 GYHISYTYRLEULYSLAIPROCYSYTHRGILUPROCYSGLYASNSERTHRCSYLEUVALYS 49
 DB 50 GGGCACTACTGAAAGCCCTTGSCAGAGACCCTGGGCACTCCACCTGCTGTGT 109
 QY 50 PROGLNAPTHPHELEUALATRGILUASNHSISASNSERTGLUCYSLAARGCYGLN 69
 DB 110 CCCCAAGACACCTTCTTGCCCTGGGAGAACACCATTAATTCGAATGTCGCCGCCAG 169
 QY 70 ALACYSASGLUGLALASERGLNALALALEUGLUAASCYSERALVALAASPTH 89
 DB 170 GCTGTGATGACAGAGCCCTCCAGGAGGCGCTGGAGAACTGTTCAGCACTGCCAGCAC 229
 QY 90 ARGCYSGLYCYSLYSPROGLYTRPHEVALGLUCYSGLNAVALSERGLNYSVALSER 109
 DB 230 CCTGTGGCTGTAAGCAGAGCTGTTGTGGAGTCCAGGTACCAATGTCTCAGCACT 289
 QY 110 SERPROPHETRYCYGLNIPROCYSLEUASPCYSGLYALALEUHSIARGHISTHARGLEU 129
 DB 290 TCACCTTCTACTGCCAACCATGCTAGACATGCGGGCCCTCCACGCCACAGCGCTA 349
 QY 130 LEUCYSERARGARASPTHARSPCYSGLYTHRCYSLEUAPROGLYPHETRYGLNLSGLY 149
 DB 350 CTCGTCTCCCGAGAGATACACTGTGGAGACTCCCTGCTGCTCTATGAAACATGCG 409
 QY 150 ASPLGYCYVALSERCYSPROTHSERTHREUGLYSERCYSPROGLIARGCYSLAALA 169
 DB 410 GATGGCTCGTGTCTGCCAGAGCACTGGGGAGACTGTCCAGAGCGCTGTCCCT 469
 QY 170 VALCYSGLYTPARGGLMETPHETRYPVALGLN-VALLEULEUALAGLYLEUVALVALPR 189
 DB 470 GTCTGTGGCTGGAGG-----CAGAGTCTCTGCTGGCTGGCTGTGGTCC 514

QY 189 OLEULEULEUGLYALATHRLEUTHRYTHRYTARYHISCYSTRPPOHISYSPROLE 209
 DB 515 CCTCTGCTGGGGCCACCTGACCTTACATATACCGGCACTGTGGCTCCACAGCCCT 574
 QY 209 VALATHRALASPGLUALAGYMETGLUALALEUTHPPOPROBOLATHRHSLEUSE 229
 DB 575 GGTTACTGACAGATGAACTGGATGAGGCTGTGACCCACACCGGCCACCAATCTGTC 634
 QY 229 RPROLEUASERLALHISHTHREULEUALAPROPROASPSERSEGLIULYSILECYTH 249
 DB 635 ACCCTTGACAGCGCCACACCTTCTAGACCTCTGACAGCAGTGAAGATCTGCAC 694
 QY 249 VALGLNLEUALGLYASNSERTPHRPHROGLYTRYPRROGLINTHGLNALALEUCY 269
 DB 695 CGTCCAGTTGTGGTGGTACAGCTGAGACCTCTGCTACCCACCAAGACCGAGGCGCTG 754
 QY 269 SPROGLNVALTHTRPSERTTPASGLINLEUPROSERARG---ALALEUGLYPROALAL 288
 DB 755 CCGCAAGTACATGATGCTGGGACCAATTCGCCAGCAAGCTCTGGCCCCCTGCGC 814
 QY 288 AALAPROTHLEUSERTPROGLISERTPROALAGLY-----SERPROALAMELME 304
 DB 815 TGGCCCCAAATCTTGCCAGAGATCCCGAGCCGCGCTCCGCCACCATTCATTCATGCC 874
 QY 304 LLEUGLNPROGLY 308
 DB 875 TTGCCAACCGGG 887

RESULT 2
 LOCUS A1807913 698 bp mRNA linear EST 19-DEC-1999
 DEFINITION w552c03.x1 Soares_NFL.T.GBC.S1 Homo sapiens cDNA clone
 IMAGE:2359204.3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
 PRECURSOR ;, mRNA sequence.
 ACCESSION A1807913 GI:5394479
 VERSION A1807913.1 GI:5394479
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert length: 1568 Std Error: 0.00
 Seq primer: -400P from Glibco
 High quality sequence stop: 459.
 Location/Qualifiers
 1. 698

FEATURES
 source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2359204"
 /clone_1lb="Soares_NFL.T.GBC.S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pRT73D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBHL19W, testis NHT, and B-cell
 NCI-CGAP-GCB1) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bernaldo."

BASE COUNT 111 a 218 c 214 g 155 t
ORIGIN

Alignment Scores:

Score: 1,226-91 Length: 698
Pred. No.: 1211.00 Matches: 210
Percent Similarity: 95.02% Conservative: 0
Best Local Similarity: 95.02% Mismatches: 11
Query Match: 54.82% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x A1807913 (1-698)

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QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
   |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 36 CAGGGGGGGGCTGATGCCAGAGTGTGACTGTGCTCCGCTGACTCCACAGAGATGTGT 95

QY 21 LeuPheCysAspArgGlyCysProAlaGlyHisLysLysAlaProCysThrGluPro 40
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 96 CTGTTTGTGTGACAGAGCTGCCAGCGGGGACACTGTAAGGCCCTTGCACGAGCC 155

QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 156 TGGGGACACTCCACCTGCTGTGTGTGTCCCAAGACACTTCTTGCTGGGAGAACAC 215

QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 216 CAAATATCTCAATGTGCCCTGCGAGGCTGTGATGAGCAGAGGCTCCAGGTGGCGCTG 275

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 276 GAAACCTGTCACAGTGGCGGACACCCGCTGTGCTGAAGCCAGGCTGTGTGTGAG 335

QY 101 CysGlnValSerGlnCysValSerSerProPheThrCysGlnProCysLeuAspCys 120
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 336 TGGCAGGTTCAGCCATGTGTGACAGATTCACCTTCTACCTCCACCATGCTTGAATCC 395

QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 396 GGGGGCCCTGCACGCCACACAGCGCTACTGTTCCCGCAGAGTACTGACTGTGGGACC 455

QY 141 CysLeuProGlyPheThrArgLysGlyAspGlyCysValSerCysProThrSerThrLeu 160
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 456 TGGCTGCTGCTGCTTATGACATGAGGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 515

QY 161 GlySerCysProGlnArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 516 TGGAGCTGTCCAGAGCCCTGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 575

QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTrpThrTyr 200
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 576 GTGCTGCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 635

QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 636 CTGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 695

QY 221 Thr 221
   |||
Db 696 ACT 698
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RESULT 3
BE563566 681 bp mRNA linear EST 15-AUG-2000
LOCUS 601334867F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688721 5',
DEFINITION mRNA sequence.
ACCESSION BE563566
VERSION BE563566.1 GI:9807286
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 681)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: LLCM382 row: f column: 18
High quality sequence stop: 681.
Location/Qualifiers
1. 681

FEATURES

source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3688721"
/clone_11b="NIH_MGC_39"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies)."

BASE COUNT 110 a 236 c 220 g 115 t
ORIGIN

Alignment Scores:

Score: 5,596-89 Length: 681
Pred. No.: 1179.00 Matches: 225
Percent Similarity: 99.12% Conservative: 0
Best Local Similarity: 99.12% Mismatches: 2
Query Match: 53.37% Indels: 2
DB: 10 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x BE563566 (1-681)

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QY 151 GlyCysValSerCysProThrSerThrLeuGlySerCysProGlnArgCysAlaAlaVal 170
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 3 GGTGCGGTGTCTCTCCACAGACACACCTGCGGAGCTGTCCAGAGCGCTGTGCGCTGTC 62

QY 171 CysGlyTrpArgGlnMetPheTrpValGlnValLeuLeuAlaGlyLeuValValProLeu 190
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 63 TGTGCTGAGAGGACAGATGTTCTGTGGTCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTG 122

QY 191 LeuLeuGlyAlaThrLeuThrTrpThrTrpArgHisCysTrpProHisLysProLeuVal 210
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 123 CTGCTTGGGGGACCCGTGACCATACATACCGCACATGCTGCTGCTGCTGCTGCTGCTG 182

QY 211 ThrAlaAspGluAlaGlyMetGluAlaLeuThrProProProAlaThrHisLeuSerPro 230
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 183 ACTGACATGAGCTGGATGAGAGGCTGTGACCCACACCGGCGCCACCATCTGTACCC 242

QY 231 LeuAspSerAlaHisThrLeuLeuAlaProProAspSerSerGlyLysIleCysThrVal 250
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 243 TTGGACAGCGCCACACACCTCTAGACACTCTGACAGCACTGAGAAGATGTGCACCGTC 302

QY 251 GlnLeuValGlyAsnSerTrpThrProGlyLysTrpProGlnThrGlnGluAlaLeuCysPro 270
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 303 CAGTTGTGTGTAACACTGTGACCCCTGTGCTACCCCGAGACCCAGAGAGCGCTGTGCGCG 362

QY 271 GlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaPro 290
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 363 CAGGTGACATGTCTCTGGAGACACTTGGCCGACAGAGAGTCTTGGCCCGCGCTGTGCGCG 422

QY 291 ThrLeuSerProGlnSerProAlaGlySerProAlaMetLeuGlnProGlyProGln 310
```

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|||||
Db 423 ACACCTCCGACAGATGCCAGCGGCTCGCCAGCCATGATGCTGACGCCGGCCGACG 482
Oy 311 LeuTyrAspValMetAspAlaValProAlaArgTyrIleuValArgThrIleu 330
Db 483 CTCCTAGACGCTGATGACCGCGGCCGCGCCGCTGGAAGAGTTCGCGCCACGCTG 542
Oy 331 GlyLeuArgGluAlaGluIleGluAlaValGluIleGlyArgPheArgAspGln 350
Db 543 GGGCTCGCGACGACAGATCGAAGCCCTGAGAGTGGAGATCGCGCTTCGAGACGAG 602
Oy 351 GlnTyrGluMetLeuLysArgTyrParGlnGlnGlnProAlaGlyLeuGlyAlaValTyr 370
Db 603 CAGTACGAGATGCTCAAGCGCTGCGCCAGCAGCAGCCGCG-GGCCCTGAGCGCTTTAC 661
Oy 371 AlaAlaGluAlaArgMetGly 377
Db 662 GCGGC-CTGGAGCGCATGGGG 681

RESULT 4
BI909448 767 bp mRNA linear EST 16-OCT-2001
LOCUS 603065172F1 NIH_MGC_118 Homo sapiens CDNA clone IMAGE:5214568 5',
DEFINITION mRNA sequence.
ACCESSION BI909448
VERSION BI909448.1 GI:16172666
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE NIH_MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLML1538 Row: O Column: 17
High quality sequence stop: 754.
FEATURES
source
1..767
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5214568"
/clone_lib="NIH_MGC_118"
/tissue_type="Leukocyte"
/lab_host="DH10B"
/note="Vector: PCMV-SPORE6; Site.1: NotI; Site.2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC library."
BASE COUNT 122 a 243 c 241 g 161 t
ORIGIN
Alignment Scores:
Pred. No.: 8,32e-88 Length: 767
Score: 1166.00 Matches: 213
Percent Similarity: 97.71% Conservative: 0
Best Local Similarity: 97.71% Mismatches: 3
Query Match: 52.78% Indels: 5
DB: 13 Gaps: 1

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US-09-993-234-6_COPY_25_417 (1-393) x BI909448 (1-767)
Oy 1 GlnGlyIleThrArgSerProArgCysAspGlyAlaAspPheHisLysIleGly 20
Db 109 CAGGGGGGACATCGTAGCCCGACGAGTGTGCTGCCGAGCTTCACAGAAAGATTGGT 168
Oy 21 LeuPheCysArgGlyCysProAla-GlyHisTyrLeuLysAlaProCysThrGluPr 40
Db 169 CAGTTTGTGGAGAGGCTGCCAGCTGGGCACTACCTGAAGGCCCTTGCACGAGACC 228
Oy 40 OCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnH 60
Db 229 CTGCGGCAACTCCACTGCTGCTGTGTCCTCCAAACACACTTCTTGCTGGGAACCA 288
Oy 60 sHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAla 80
Db 289 CCAATATTTGTGAATGTGCCCTGCCAGGCTGTGATGACGAGGCTCCAGAGTGGCT 348
Oy 80 uGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValG 100
Db 349 GGAAGAACTGTTACAGCAGTGGCCGACACCGCTGTGCTGTAAAGCAGGCTGGTTGTGA 408
Oy 100 uCysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCy 120
Db 409 GTGCCAGTCACCACTGCTGTCAGCATCCCTTACTGCAACCACTGCTAGACTG 468
Oy 120 sGlyAlaLeuHisArgHisTyrArgLeuLeuCysSerArgAspThrAspCysGlyTh 140
Db 469 CGGGGCCCTCGACACCGCCACACAGCGTACTCTGTGTTCCGCCACAGATACAGATGGGAC 528
Oy 140 rCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThr 160
Db 529 CTGCCCTGCTGGCTGTATGAACATGCGATGCGTGGCTGCTGCCACACAGACCT 588
Oy 160 uGlySerCysProGluArgCysAlaValCysGlyTyrParGlnMetPheTyrValG 180
Db 589 GGGGACCTGTCAGACGCTGTGCCCTGTCTGTGGCTGAGACATTTCTGGGTCA 648
Oy 180 nValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThr 200
Db 649 GTGCTCTCGGCGGCTGCTGCTCCCTCCCTGCTGGGGCCACCTG-ACCTACACATA 707
Oy 200 rArgHisCysTyrProHisLysProLeuValThrAlaAspGluAlaGlyMet 217
Db 708 CGC-CAGTGTGGCT-CACAAAGCCCTGCTACT---GATGAAGCTGGGATG 754

RESULT 5
AM268610 632 bp mRNA linear EST 03-JAN-2000
LOCUS xv41b12.x1 Soares.NFL.T.GBC.SI Homo sapiens CDNA clone
DEFINITION IMAGE:2815679 3, similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECUSOR ; mRNA sequence.
ACCESSION AM268610
VERSION AM268610.1 GI:6655640
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -400p from Glibco
High quality sequence stop: 455.

```


Db 183 CACTGCTGGCTTCACAGGCCCTGTTACTGCAGATGAAGCTGGATGAGGAGCTTGACC 242
QY 222 ProProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuAlaProPro 241
Db 243 CCACCAACGGC-ACCATCTGTACCTTGGACAGGCCACACCTTCTAGACCTCTCT 301
QY 242 AspSerSerGluIleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTyr 261
Db 302 GACAGAGTGAAGATGTGCACAGCTGCAGATTGGTGAACAGCTGAGCCCTGGCTAC 361
QY 262 ProGluThrGlnGlnAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSer 281
Db 362 CCCGAGACCCAGGAGGCGCTGCTCCGACAGTACATGCTCCGGAGACCACTTCCACAG 421
QY 282 ArgAlaLeuGlyProAlaAlaProThrLeuSerProGluSerProAlaGlySerPro 301
Db 422 AGAGCTCTTGCGCCCGCTGTGGCCACACCTCTCCGACAGTCCGACGCGGCTGGCCA 481
QY 302 AlaMetLeuGln-ProGlyProGlnLeuTyrAspValMetAspAlaValProAlaAr 321
Db 482 GCCATATGCTGCAGCCCGGCGCCGACGCTCTACGACGTGTAGACGCGGCTCCACGCG 541
QY 321 GAGGTTPyGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValG 341
Db 542 GCGCTGAAGAGTCTGTGCGACGCTGGGGCTGCGCGAGCAGATCGAAGCCGTGA 601
QY 341 uValGluIleGly-ArgPheArgAspGlnGlnTyrGluMet 354
Db 602 GGTGAGATGCGCCCGCTTCCGAGACGACGATGACGAGT 642
RESULT 7
BM794760 647 bp mRNA linear EST 05-MAR-2002
LOCUS K-EST0076219 S22SNUI6n1 Homo sapiens cDNA clone S22SNUI6n1-48-G11
DEFINITION 5', mRNA sequence.
ACCESSION BM794760
VERSION BM794760.1 GI:19142992
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 647)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsungemail.kr@ibb.re.kr
Place: 48 row: G column: 11
High quality sequence stop: 647.
Location/Qualifiers
1. 647
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S22SNUI6n1-48-G11"
/clone_lib="S22SNUI6n1"
/sex="F"
/tissue_type="Ascites"
/cell_line="Lymphoblast-like"
/cell_line="SNU-16"
/lab_host="DH10B"
/note="Organ: Stomach; Vector: pT73-Pac; Site: 1. EcoRI;
Site: 2. NotI; The S22SNUI6 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldio, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested

cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."

BASE COUNT 110 a 229 c 203 g 105 t
ORIGIN
Alignment Scores:
Pred. No.: 1.44e-79 Length: 647
Score: 1066.50 Matches: 201
Percent Similarity: 99.51% Conservative: 1
Best Local Similarity: 99.01% Mismatches: 0
Query Match: 48.28% Indels: 1
Gaps: 1
DB: 14
US-09-993-234-6_copy_25_417 (1-393) x BM794760 (1-647)
QY 176 MetPheTrpValGlnValLeuLeuAlaGlyLeuValProLeuLeuLeuGlyAlaThr 195
Db :
QY 40 GTGTTCTGGGTCCAGGTGCTCTGCTGGCTGTGGCTCCCTGCTGGGGCCACC 99
QY 196 LeuThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAla 215
Db 100 CTGACCTACACATACCGCCACATGCTGCTCCTCACAGCCCTGTACT---GATGAAGCT 156
QY 216 GlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHis 235
Db 157 GGGATGAGAGGCTCTGACCCACACCGGCGCCACCATCTGTACACCTTGGACAGCGCCAC 216
QY 236 ThrLeuLeuAlaProProAspSerSerGlyLysIleCysThrValGlnLeuValGlyAsn 255
Db 217 ACCCTTGTAGCACCTCTTCCAGACAGTGAAGATCTGCACGCTCCAGTTGGGTGAAC 276
QY 256 SerTrpThrProGlyTyrProGluThrGlnGlnAlaLeuCysProGlnValThrTrpSer 275
Db 277 AGCTGAGACCCCTGTGCTACCCCGAGACCGAGAGCGCTCTGCCCGAGGTGACATGTCTC 336
QY 276 TrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGlu 295
Db 337 TGGGACAGACTTGGCCGACGAGAGCTTGGCCCGCTGCTGCGCCACACTCTGCGCAGAG 396
QY 296 SerProAlaGlySerProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMet 315
Db 397 TCCCGACCGGCTCGCCAGCATGATGCTGACCGCGGCCGCTCTACACGCTGAGT 456
QY 316 AspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAla 335
Db 457 GACGCGGTCCACAGCGCGGCGCTGGAAGAGTTGCTGCGACGCTGGCGCGCGAGGCA 516
QY 336 GluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeu 355
Db 517 GAGATGGAAGCCCTGGAGGTGAGATCGCGCTTCCGAGACGACGATGAGATGCTC 576
QY 356 LysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValThrAlaLeuGluArg 375
Db 577 AACGCTGGGCGCCAGCAGCAGCCCGGCGCTGAGAGCCTTTACCGGCGCTGGAGCGC 636
QY 376 MetGlyLeu 378
Db 637 ATGGGCGTG 645
RESULT 8
A1424936 688 bp mRNA linear EST 30-MAR-1999
LOCUS t919b08.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2109207 3'
DEFINITION similar to TR:000276 000276 LYMPHOCYTE ASSOCIATED RECEPTOR OR DEATH
2. mRNA sequence.
ACCESSION A1424936
VERSION A1424936.1 GI:4270854
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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Db 65 CAGGGGCGACCTGTAGTCCAGCCAGTGTGACTGCGGCTGCTCCACAAGATTGCT 124
QY 21 LeuPhcCysArGlYcysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 125 CTTGTTTGTGCGAGAGCTGCGCCAGCGGGGCGACTTACCTTAAGGCCCTTGCAGGAGCC 184
QY 41 CysGlyAAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAAsnHis 60
Db 185 TGGGCACTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 244
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 245 CATTAATCTGAATGTGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 304
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 305 GAGAACTGTCAGAGTGGCGCCGACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 365 TGGCAGGTGACCAAGTGTGACAGTGTGACCTTCTACTGACCAACCATGCTAGACTGC 424
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 140
Db 425 GGGGCGCTGACCGCCACACAGCGCTACTGTTCCCGAGATGACTGACTGTGGAGCC 484
QY 141 CysLeuProGlyPheTyrGlnHisGlyAlaAspGlyCysValSerCysProThrSerThr 160
Db 485 TGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 544
QY 161 GlySerCysProGluArg 166
Db 545 NGAGCTGTGTCAGAGCGC 562

RESULT 10
LOCUS BF726557 539 bp mRNA linear EST 05-JAN-2001
DEFINITION sapiens cDNA clone by08d05 5', mRNA sequence.
ACCESSION BF726557
VERSION BF726557.1 GI:12042468
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 539)
AUTHORS Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
TITLE NESTBANK: EST analysis and bioinformatics for ocular
JOURNAL Invest. Ophthalmol. Vis. Sci. 41, (2000) In press
CONTACT: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: gtraeme@helix.nih.gov
Plate: 08 Row: d Column: 05
Seq primer: M13RP1 reverse primer (AB1).
FEATURES
SOURCE
1. 539
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_id="Human Lens cDNA (Un-normalized, unamplified):
By"
/tissue_type="Lens"
/dev_stage="Adult"
/lab_host="EMDH10B"
/note="Organ: Eye; Vector: pCMVSPORT6; Two human lenses
from different adults (both approximately 40 years old)
together yielded 20ug of total RNA and 150ug mRNA for cDNA
library synthesis. A directionally cloned cDNA library in

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BASE COUNT 97 a 192 c 167 g 83 t
ORIGIN
Alignment Scores:
Pred. No.: 2.02e-71 Length: 539
Score: 968.00 Matches: 179
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 43.82% Indels: 0
DB: 12 Gaps: 0

US-09-993-234-6_copy_25_417 (1-393) x BF726557 (1-539)
QY 192 LeuGlyAlaThrLeuThrTyrThrArgHisCysTrpProHisLysProLeuValThr 211
Db 2 CTTGGGGCCACCTGACCTACACATACCGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 61
QY 212 AlaAspGluAlaGlyMetGlnAlaLeuThrProProProAlaThrHisLeuSerProLeu 231
Db 62 GCAGATGAAAGCTGGAGTGGAGGCTGACCCACACACCGGCCACCACTGTGCACCTTG 121
QY 232 AspSerAlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCysThrValGln 251
Db 122 GACAGCGCCACACCCCTTGTACACCTCTGACAGCAGAGTGAAGAATGTGCACCTCAG 181
QY 252 LeuValGlyAAsnSerThrProGlyTyrProGlyThrGlnGlnAlaLeuCysProGln 271
Db 182 TTGGTGGGTACAGCTGGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 241
QY 272 ValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaProThr 291
Db 242 GTGACATGCTGCTGGAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 301
QY 292 LeuSerProGlnSerProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeu 311
Db 302 CTTCCCGCAGAGTCCCGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
QY 312 TyrAspValMetAspAlaValProAlaArgArgTyrGlyGluPheValArgThrLeuGly 331
Db 362 TACGAGCTGATGGACGCGGTCCAGCGCGGCTGGAAGAGTTCTGCGCACGCTGGGG 421
QY 332 LeuArgGluAlaGluIleGluAlaValGluValGluValArgPheArgAspGlnGln 351
Db 422 CTCGCGGAGGCAAGATCGAAGCCGTGGAGGTGGAATGGCGCTTCGAGACGACGAG 481
QY 352 TyrGluMetLeuLysArgTyrArgGlnGlnProAlaGlyLeuGlyAlaValTyr 370
Db 482 TAGCAGATGCTCAACCGCTGCGCCACGACGACCGCGCGCTGAGACCGCTTTAC 538

RESULT 11
LOCUS BM783972 552 bp mRNA linear EST 05-MAR-2002
DEFINITION K-EST0062019 S6SNU620 Homo sapiens cDNA clone S6SNU620-31-H06 5',
mRNA sequence.
ACCESSION BM783972
VERSION BM783972.1 GI:19132204
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 552)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

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the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the SuperScript plasmid system full details of which are contained in the manufacturer's instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer adapter [5'-pGACTTACTTGTAGTCCGCGCCGCGCC(7)15-3']. Not I blunt end inserts were cloned into the Not I/BclI V sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsungemail.kr@kribb.re.kr
Plate: 31, row: H column: 06
High quality sequence stop: 552.

FEATURES

source

1. 552
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SN620-31-H06"
/clone_1lb="S6SN620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="T1010P"
/note="Organ: Stomach; Vector: PCNS; Site: 1: EORI; Site: 2: Not; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deapped with tabacco acid pyrophosphatase (TAP). The deapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli T1010P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 92 a 172 c 173 g 115 t
ORIGIN

Alignment Scores:

Pred. No.: 4.6e-70 Length: 552
Score: 952.00 Matches: 163
Percent Similarity: 93.71% Conservative: 1
Best Local Similarity: 93.14% Mismatches: 3
Query Match: 43.10% Indels: 8
DB: 14 Gaps: 1

US-09-993-234-6_copy_25_417 (1-393) x BM783972 (1-552)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 38 CAGGCGCGACCTCTAGCCCGAGGTGACGTGCGGGTGACTCCACAAAGAGTTGGT 97
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 98 CTGTTTGTTCAGAGCTGCCAGCGGGGCACACTGGAAGGCCCTTGCACGGAGCCC 157
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 158 TGGCGCAACTCCACCTGCTGTGTCGCCAAGACACTCTTGGCTGGAGAACAC 217
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGluValAlaLeu 80
DB 218 CATATATCTGAAATGTCCTGCCAGGCTGTGATGAGCAGGCTCCACAGTGGCGCTG 277
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 278 GAGAACTGTTTCAGCAGTGGCCGACACCGCTGTGGCTTTAAGCCAGGCTGTTGTGGAG 337

QY 101 CysGlnValSerGlnCysValSerSerProPheTrpCysGlnProCysLeuAspCys 120
DB 338 TGGCAGGACGACCAATGTGTCAGGAGTTTACACCTTCTACTGCAACCAAGCTGAGACGC 397
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 140
DB 398 GGGGCGCTGCACCGCCACACAGCGGTACTGTTCCCGCAGAGATACGACTGTGGACC 457
QY 141 CysLeuProGlyPheThrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 458 TGGCTGCTGCTCTTATGAACATGCGCATGGCTCCGCTGCTGCCCCACGATTCCTA 517
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGln 175
DB 518 -----GCTGTCGCGGATGAGAGGAA 538

RESULT 12

AM517358 585 bp mRNA linear EST 03-MAR-2000
LOCUS xp93902.x1 Soares_NHCE_cervix Homo sapiens cDNA IMAGE:2747954
DEFINITION 3' similar to FR:000276 000276 LYMPHOCYTE ASSOCIATED RECEPTOR OF

DEATH 2. ; mRNA sequence.

ACCESSION

AM517358

VERSION

AM517358.1

KEYWORDS

GI:7155440

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 585)

ADDITIONAL

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapsb@nci.nih.gov

This clone is available royalty-free through LNC ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: similarity on wrong strand

Possible reversed clone: polyA not found

Seq primer: -400p from G1bco

High quality sequence stop: 489.

FEATURES

source

1. 585

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2747954"

/clone_1lb="Soares_NHCE_cervix"

/lab_host="DH10B (phage-resistant)"

/note="Organ: cervix; Vector: pTZ19-Pac (Pharmacia) with

a modified polylinker; Site: 1: Not I; Site: 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer (5'

TGTATCCATCTGTAAGTGGAGCGCGCGGCTTTTCTTTTCTTTTCTTTTCTTTT

T 3') ; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pTZ19 vector.

Library is normalized; constructed by Bento Soares and

M. Fatima Bonaldo."

BASE COUNT 94 a 181 c 193 g 117 t
ORIGIN

Alignment Scores:

Pred. No.: 5e-70 Length: 585
Score: 952.00 Matches: 163
Percent Similarity: 93.71% Conservative: 1
Best Local Similarity: 93.14% Mismatches: 3
Query Match: 43.10% Indels: 8
DB: 10 Gaps: 1

US-09-993-234-6_copy_25_417 (1-393) x AM517358 (1-585)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
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```

Db 65 CAGGGCGACATGTAAGCCCGAGTGTGACTGCGGTGACTTCCACAGAAGATTGTT 124
QY 21 LeuphCysysaraglyCysProAlaGlyHisTyrLeuYsAlaProCysThrGluPro 40
Db 125 CTGTGTTGTCAGAGGCTCCCGAGGGGCGGAGCTTGAAGGCCCTTTCACGAGAGCC 184
QY 41 CysGlyAsnSerThrcysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 185 TGGGGGACATCCACAGCTGCTGTGTGTGCCCAAGACACCTTCTGGCTGGGAGAACAC 244
QY 61 HisAsnSerGluCysAlaArGysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 245 CATTAATCTTAATGTGCCCCCTGAGGCTGTGATGAGAGGCTCCAGAGGGGCGCTG 304
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysTyrProGlyTrpPheValGlu 100
Db 305 GAGAACTGTTTCAGACAGTGGCGGACACCCGCTGTGCTGTAAAGCCAGGCTGTGTGGAG 364
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 365 TGGCAGGTTCAGCAATGTGTACAGAGTTCAACCTTCTACTGCAACCATGCTTAGACTGC 424
QY 121 G1YAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 425 GGGGCGCTGACCGCCACACAGGCTACTGTCTCCGCAAGATCTGACTGCTGGGAGCC 484
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 485 TGGCTGCTGCTGCTTCTATGAACATGGGATGGCTGCTGCTGCTGCTGCTGCTGCTGCT 544
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGln 175
Db 545 -----GCTGTGCTGGGATGAGGAGGA 565

RESULT 13
LOCUS BM744307 565 bp mRNA linear EST 01-MAR-2002
DEFINITION K-EST0017828 S6SN620 Homo sapiens cDNA clone S6SN620-17-C06 5',
mRNA sequence.
VERSION BM744307
XREF GI:19065636
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 565)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
            ZIC Frontier Korean EST Project 2001
TITLE Unpublished (2002)
JOURNAL Contact: Kim YS
COMMENT Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4409
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 17 row: C column: 06
            High quality sequence stop: 565.

FEATURES
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                /tissue_type="Ascites"
                /cell_type="Scattering floating"
                /cell_line="SNU-620"
                /lab_host="Top10F"
                /note="Organ: Stomach; Vector: pcNS; site_1: EcoRI;

```

```

site_2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
with tabacco acid pyrophosphatase (TAP). The deapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

BASE COUNT 95 a 175 c 178 g 117 t
ORIGIN

Alignment Scores:
Pred. No.: 2,7e-69 Length: 565
Score: 943.00 Matches: 162
Percent Similarity: 93.14% Conservative: 1
Best Local Similarity: 92.57% Mismatches: 4
Query Match: 42.69% Indels: 8
DB: 14 Gaps: 1

US-09-993-234-6_copy_25_417 (1-393) x BM744307 (1-565)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisTyrGly 20
Db 38 CAGTGGGCGACCTGTGAGCCCGAGGTGACTGTGCGGTGACTCCACAGAAGATTGTT 97
QY 21 LeuphCysysaraglyCysProAlaGlyHisTyrLeuYsAlaProCysThrGluPro 40
Db 98 CTGTGTTGTCAGAGGCTCCCGAGGGGCGGACTACTGAAGGCCCTTTCACGAGAGCC 157
QY 41 CysGlyAsnSerThrcysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 158 TGGGGCAACATCCACATGCTGTGTGTGCCCAAGACACCTTCTGGCTGGGAGAACAC 217
QY 61 HisAsnSerGluCysAlaArGysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 218 CATTAATCTTAATGTGCCCCCTGAGGCTGTGATGAGAGAGGCTCCAGATGGGCGT 277
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysTyrProGlyTrpPheValGlu 100
Db 278 GAGAACTGTTTCAGACAGTGGCGGACACCCGCTGTGCTGTAAAGCCAGGCTGTGTGGAG 337
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 338 TGGCAGGTTCAGCAATGTGTACAGAGTTCAACCTTCTACTGCCAACCATGCTTAGACTGC 397
QY 121 G1YAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 398 GGGGCGCTGACCGCCACACAGGCTACTGTCTCCGCAAGATACTGACTGTGGAGCC 457
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 458 TGGCTGCTGCTGCTTCTATGAACATGGGATGGCTGCTGCTGCTGCTGCTGCTGCTGCT 517
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGln 175
Db 518 -----GCTGTGCTGGGATGAGGAGGA 538

RESULT 14
LOCUS BM756372 514 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0034666 S6SN620 Homo sapiens cDNA clone S6SN620-27-G03 5',
mRNA sequence.
VERSION BM756372
XREF GI:19085987
KEYWORDS EST.
SOURCE human.

```


ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 514)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 27 row: G column: 03
 High quality sequence stop: 514.
 FEATURES
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 1. 514
 /organism="Homo sapiens"
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 /clone="S6SNU620-27-G03"
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 /cell_line="SNU-620"
 /lab_host="Top10F"
 /note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
 Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tabacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."
 BASE COUNT 86 a 166 c 153 g 109 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 7.52e-69 Length: 514
 Score: 937.00 Matches: 157
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 42.42% Indels: 0
 DB: 14 Gaps: 0
 US-09-993-234-6_COPY_25_417 (1-393) x BM756372 (1-514)
 QY 1 Glnclgylmrrarserrproarqcyasprcyslaaglyasrphenhlslyslleclg 20
 |||||||
 Db 38 CAGGGCGGCACTGTAGCCCAAGGTGACGTGTCCGGTGACTTCCACAAAGAAAGTTGT 97
 |||||||
 QY 21 Leuphecyscsaraglycysproalaglyhstlyrleuylsalaprocsythrclupro 40
 |||||||
 Db 98 CTGTTTGTTCACAGCGTGTCCAGCGGGGACACTACGGAAGGCCCTTCGACCGAGGCC 157
 |||||||
 QY 41 Cysglaysnserrthrcysleuvalcysproglinsprthelaulatrpcluasnhls 60
 |||||||
 Db 158 TGCAGCAACTCCACTGCTGTGTGTGCCCAAGACACTTCTGGCCTGGAGAACAC 217
 |||||||
 QY 61 Hisnsberglucysalaarqcygclnalacysasprgluglnalaserclnvalaleu 80
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 Db 218 CATAAATCTGAATGTGCCGCTGTCCAGGCGCTGTGATGAGAGGCGCTCCAGGTGCGCTG 277

QY 81 Gluanscyssseralalavalalaspthrargcysglycyslysproglytyrphvalcl 100
 |||||||
 Db 278 GAGAACTGTAGCAGTGGCGGACACCGCGTGTGCTGAAGCCAGCGTGTGTGAG 337
 |||||||
 QY 101 Cysglvalserglncysvalseraserprorherycysglinprocysleuapcys 120
 |||||||
 Db 338 TGCAGGTCCACCAATGTGTGACGAGTTCACCCCTTCTACTGCACCACTGTGACACGC 397
 |||||||
 QY 121 GlvalalauhlsarqhlsthrargleuencysseratargaspthrAspcysglythr 140
 |||||||
 Db 398 GGGGCGCTGCACCGGCACACAGGCTACTGTGTCCCGAGATACTGACTGTGGACC 457
 |||||||
 QY 141 Cysleuproglypherythrghlslaspglycysvalsercysprothr 157
 |||||||
 Db 458 TGCCTGCGCTGTCTATGAACATGCGCATGGCTCGTGTGCGCCACG 508
 |||||||
 RESULT 15
 BM783979 514 bp mRNA linear EST 05-MAR-2002
 LOCUS K-EST0062030 S6SNU620 Homo sapiens cDNA clone S6SNU620-32-A05 5'
 DEFINITION mRNA sequence.
 ACCESSION BM783979
 VERSION BM783979.1 GI:19132211
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 514)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 32 row: A column: 05
 High quality sequence stop: 514.
 FEATURES
 SOURCE
 1. 514
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="S6SNU620-32-A05"
 /clone_1lb="S6SNU620"
 /sex="F"
 /tissue_type="Ascites"
 /cell_type="Scattering floating"
 /cell_line="SNU-620"
 /lab_host="Top10F"
 /note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
 Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tabacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."
 BASE COUNT 86 a 166 c 153 g 109 t
 ORIGIN

Alignment Scores:

Pred. No.:	7.52e-69	Length:	514
Score:	937.00	Matches:	157
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	42.42%	Indels:	0
DB:	14	Gaps:	0

US-09-993-234-6_COPY_25_417 (1-393) x BM783979 (1-514)

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QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
   |||
DB 38 CAGGGGCGACCTGACGCCAGGTGACTGTCGGTGACTTCACAGAAAGATTGGT 97
   |||

QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
   |||
DB 98 CTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGAAGGCCCTTGACAGGAGACC 157
   |||

QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
   |||
DB 158 TCGGGCAACTCCACCTGCTTGTGTGCCAAGACACCTTCTGGCCCTGGAGAACCCAC 217
   |||

QY 61 HisAsnSerGlnCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
   |||
DB 218 CATTAATTCGTAATGTGCCCTGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTGGCGCTG 277
   |||

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTTPPheValGlu 100
   |||
DB 278 GAGAACTGTTACAGCAGCGCGACACCCGCTGTGGCTGTAAAGCCAGGCTGTTGTGGAG 337
   |||

QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
   |||
DB 338 TCCAGGTGAGCCAAATGTGTCCAGCAGTTCAACCTTCTACTGCCAACCATGCTAGACTGC 397
   |||

QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
   |||
DB 398 GGGGCCCTGACCGCCACACAGCGCTACTGTGTCCCGCAGAGATACTGACTGTGGGACC 457
   |||

QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThr 157
   |||
DB 458 TGCCTGCTGCTTCTATGAAACATGGGAGTGGTGGCTGCTGCCCCAGCAG 508
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Search completed: April 6, 2003, 23:25:13
Job time : 2464.26 secs


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FT FT /transl_except="(pos:481..482, aa:Asp)"
FT FT /note="this codon has an apparent 1 nucleotide
FT FT deletion which alters the reading frame"
FT FT /transl_except="(pos:558..559, aa:Cys)"
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FT FT deletion which alters the reading frame"
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FT FT /note="this codon has an apparent 1 nucleotide
FT FT deletion which alters the reading frame"
FT FT /transl_except="(pos:718..719, aa:Met)"
FT FT /note="this codon has an apparent 1 nucleotide
FT FT deletion which alters the reading frame"
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FT FT 1..72
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FT FT 73..1247
FT FT /*tag= c
FT FT mat_peptide
FT FT 73..1247
FT FT /*tag= c
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FT FT
FT FT 25-MAY-2001.
FT FT
FT FT 17-NOV-2000; 2000WO-US31692.
FT FT
FT FT 19-NOV-1999; 99US-0166583.
FT FT
FT FT (TITL/) TITLLE T V.
FT FT (WEGM/) WEGMANN K W.
FT FT
FT FT Tittle TV, Wegmann KW;
FT FT
FT FT MPI; 2001-343711/36.
FT FT P-PDSB; AAB84941.
FT FT
FT FT Composition for treatment of T-cell mediated disease e.g. arthritis,
FT FT cancer comprises a biologically active TR3-specific binding agent
FT FT especially a monoclonal antibody -
FT FT
FT FT Disclosure; Page 72; 77pp; English.
FT FT
FT FT The invention relates to a composition comprising a biologically active
FT FT TR3-specific binding agent (I) that binds to TR3 and inhibits the
FT FT proliferation of cells expressing TR3. (I) identified by the methods are
FT FT useful for treating a subject suspected of having a disease associated
FT FT with a proliferation of cells expressing TR3 especially leukemias or
FT FT lymphomas or a T-cell mediated disease especially autoimmune diseases
FT FT such as myasthenia gravis, systemic lupus erythematosus, rheumatoid
FT FT arthritis, diabetes, multiple sclerosis, sarcoidosis, myocarditis,
FT FT thyroiditis and tumours. (I) is also useful for treating a subject
FT FT suspected of having graft-versus-host disease, rejection of a
FT FT transplanted organ such as heart, liver, lung, kidney, pancreas, bowel,
FT FT skin or an appendage, or inflammatory diseases, allergies and contact
FT FT dermatitis. The present sequence represents the nucleotide sequence of
FT FT human TR3 gene.
FT FT
SQ Sequence 1250 BP; 201 A; 419 C; 406 G; 224 T; 0 other;

Alignment Scores:
Pred. NO.: 1.88e-44 Length: 1250
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x AAF83770 (1-1250)
OY 1 ValMetaspAlaValPrcAlaArgArGTrrPyScIunheValAryghrLeuglyLeuarq 20
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Db 1008 GTGATGGACCGCGGCACCAGCCGCCGTGGAAAGAGTTCTTCGTGGCACGCGTGCGCC 1067
|||||
OY 21 GIUnlaGIUleGIuaValaGlUnlaGIUnlleGIyArphArgrgAspgInGIrGIUn 40
|||||

```

Dd	1068	GAGGACGATTCGAAGCCGTGAGCTGAGATCGGCCGGCTTCCGACACGACGATNACG	1127
Oy	41	MettLeuysatgTTPAtpAgIngnIngnProAlaIgLyLeuSlyALaValTrAlaLaLeu	60
Dd	1128	ATGCCTCAAGCGCCTGCCCCCACACACCACCGCGGCGCTTGGAACCCCTTTACCGCGCCCTG	1187
Oy	61	GIuAtgMetGtLyLeuAspGlyCySValGluaSpLeuArgSerArqreLnslnArgGlyPro	80
Dd	1188	GAGCGCATGGGGCTGGACGCGCTGCTGGAAAGACTGCGGAGCGCGCTGCAGCGCGCGCCG	1247
RESULT 2.			
ID	AAT89427	standard; cDNA; 1254 bp.	
XX	AAT89427;		
AC	02-MAR-1998	(first entry)	
XX			
DE	Death domain containing receptor DR3 cDNA.		
XX			
KM	Death domain containing receptor; DR3; human; apoptosis;		
KW	Inflammation; NF-kappaB; ds.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	sig_peptide	1..72	
FT		/*tag= a	
FT	mat_peptide	73..1251	
XX		/*tag= b	
PN	WO9733904-A1.		
XX			
PD	18-SEP-1997.		
XX			
PF	17-OCT-1996;	96MO-US16849.	
XX			
PR	12-MAR-1996;	96US-0013285.	
PA	(HUMA-) HUMAN GENOME SCI INC.		
PA	(UNMI) UNIV MICHIGAN.		
XX			
PI	Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;		
XX			
DR	WPL; 1997-470812/43.		
DR	P-PSDB; AAW31517.		
PT	Death domain containing receptor polypeptide(s) DR3 and DR3-V1 -		
PT	to treat inflammatory diseases		
XX			
PS	Claim 6; Page 75-77; 108pp; English.		
XX			
CC	This cDNA clone codes for human death domain containing receptor		
CC	DR3 (see AAW31517), a novel member of the tumour necrosis factor		
CC	receptor family. It was isolated from a HOVEC cDNA library.		
CC	Related death domain containing receptor DR3-V1 cDNA (see AAT89426)		
CC	was isolated from a human testis tumour cDNA library. The genes		
CC	have also been identified in cDNA libraries of foetal liver,		
CC	foetal brain, tonsil and leukocyte. Nucleic acids encoding full-		
CC	length or mature DR3, or the extracellular, transmembrane,		
CC	intracellular or especially the death domain of DR3, can be		
CC	produce recombinant polypeptides in transformed host cells. These		
CC	polypeptides can be used to treat diseases and disorders associated		
CC	with the inhibition of apoptosis. Antagonists can be used to treat		
CC	diseases and disorders associated with increased apoptosis and for		
CC	treating inflammatory diseases and disorders.		
XX			
SQ	Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;		
Alignment Scores:			
Pred. No.:	1.89e-44	Length:	1254
Score:	413.00	Matches:	80

PS Example 2B; Fig 2; 273pp; English.

XX The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-V1. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischemia, aneurysms, arterial occlusive diseases, embolisms,
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune diseases such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.

SO Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:

Pred. No.:	1,89e-44	Length:	1254
Score:	413.00	Matches:	80
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-993-234-6_COPY_338_417 (1-80) x AAC68777 (1-1254)

QY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1012 GTGATGAGCGGCTCCAGCGCGCGCTGGAGAGACTTCCTGCCACGCTGGGGCTGGCG 1071

QY 21 GluAlaGluIleGluAlaValAlaGluValGluIleGlyArgPheArgAspGlnGlnTrpGlu 40
DB 1072 GAGGCGAGAGATCGAACCGCGGAGGTGGAGATGGCGCGCTCCGACACCGAGTACGAG 1131

QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTrpAlaAlaLeu 60
DB 1132 ATGCTCAACGCGCGCGCCAGCAGCAGCCCGCGCGCTCGGAGCCGTTACCGCGCCCTG 1191

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1192 GAGCGCATGGGCTGGACGCGCTGCGTGAAGACTTCGCGAGCCGCTCGCAGCGCGCCCG 1251

RESULT 5
AAT91180
ID AAT91180 standard; cDNA; 1634 BP.

AC AAT91180;
XX
XX 14-APR-1998 (first entry)
XX
XX Human apoptosis protein Apo-3 cDNA clone FH20.57.
DE
XX
XX Apo-3; apoptosis; human; therapy; drug screening; ss.
KM
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 89..1342
FT sig_peptide 89..160
FT /*tag= a
FT /*tag= b
FT /*note= "determined by hydrophathy analysis"
FT mat_peptide 161..1339
FT /*tag= c

W09737020-A1.
XX
XX
XX 09-OCT-1997.
XX
XX
XX 31-MAR-1997; 97WO-US05230.
XX
XX
XX 23-SEP-1996; 96US-0710802.
XX
XX 01-APR-1996; 96US-0625328.
XX
XX
XX (GENE) GENENTECH INC.

XX Ashkenazi AJ;
PI WPI; 1997-503105/46.
DR
XX
XX Polypeptide(s) Apo-3 and Apo-2L1 - useful for regulating apoptosis
PT in mammalian cells
PS Example 1; Page 45-46; 70pp; English.

CC cDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see
CC W26709), designated Apo-3, that stimulates or induces apoptotic
CC activity in mammalian cells. It was isolated from a human foetal
CC heart cDNA library by screening with probes (see T91183-84) based
CC on an EST sequence (Genbank locus W71984) that showed homology to
CC the intracellular domain of human TNFR1 and CD95. Amino acid
CC residues 1-181 of Apo-3 are identical to another novel apoptosis
CC polypeptide, Apo-2L1 (see W26708). Nucleic acids encoding Apo-3
CC can be used diagnostically for tissue-specific typing and to
CC produce recombinant Apo-3 polypeptides, especially the
CC extracellular domain (amino acids 1-198) or death domain (amino
CC acids 338-417). Apo-3 can be used to induce apoptosis or
CC NF-kappa-N- or JNK-mediated gene expression for therapeutic
CC purposes. Non-human transgenic animals containing cells that
CC express Apo-3 nucleic acid, and knockout animals containing
CC cells that have an altered Apo-3 gene, can be used in drug
CC screening and development.

SO Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:

Pred. No.:	2.61e-44	Length:	1634
Score:	413.00	Matches:	80
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	18	Gaps:	0

US-09-993-234-6_COPY_338_417 (1-80) x AAT91180 (1-1634)

QY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1100 GTGATGAGCGGCTCCAGCGCGCGCTGGAGAGACTTCCTGCCACGCTGGGGCTGGCG 1159

QY 21 GluAlaGluIleGluAlaValAlaGluValGluIleGlyArgPheArgAspGlnGlnTrpGlu 40
DB 1160 GAGGCGAGAGATCGAACCGCGGAGGTGGAGATGGCGCGCTCCGACACCGAGTACGAG 1219

QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTrpAlaAlaLeu 60
DB 1220 ATGCTCAACGCGCGCGCCAGCAGCAGCCCGCGCGCTCGGAGCCGTTACCGCGCCCTG 1279

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1280 GAGCGCATGGGCTGGACGCGCTGCGTGAAGACTTCGCGAGCCGCTCGCAGCGCGCCCG 1339

RESULT 6
AAH27782
ID AAH27782 standard; DNA; 1634 BP.

AC AAH27782;
XX
XX 15-AUG-2001 (first entry)
XX
XX Human genomic DNA encoding a rheumatoid arthritis associated protein.
DE
XX
XX Rheumatoid arthritis; transmembrane protein; human; ds.
KM
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 89..1342
FT /*tag= a

/product- "rheumatoid arthritis associated protein"

FT XX WO200132921-A2.
PN XX
XX
PD 10-MAY-2001.
XX
PF 01-NOV-2000; 2000WO-JP07690.
XX
PR 01-NOV-1999; 99JP-0310805.
XX
PA (SHIO/) SHIOZAWA S.
XX
PI Shiozawa S, Konishi Y;
XX
DR WPI: 2001-308750/32.
DR P-PSDB; AAB97370.
XX
PT Diagnosing rheumatoid arthritis by probing digested human genomic DNA
PT or comparing expression of mRNA or polypeptide of a region of
PT transmembrane protein
XX
PS Claim 1; Page 14-18; 21pp; Japanese.
XX
CC This invention relates to a method of diagnosing chronic rheumatoid
CC arthritis by digesting human genomic DNA with EcoRI and hybridizing it
CC with a probe containing a fragment of the present sequence which
CC represents DNA encoding a transmembrane protein. The method is used for
CC the diagnosis of chronic rheumatoid arthritis, and for developing new
CC treatments.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:
Pred. No.: 2, 61e-44 Length: 1634
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x AAL47186 (1-1634)

QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1100 GTGATGAGCGCGGTCCAGCGCGGCTGGAGAGAGTTGTCGCGCAGCTGGGGCTGCGC 1159
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTrpGlu 40
DB 1160 GAGCGAGAGATCGAACCGGTGGAGGTGAGATGCGCGCTTCGAGACGACAGTACGAG 1219
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
DB 1220 ATGCTCAAGCGCTGGCGCCAGCAGACCGCGGCTTCGAGACCGTTCGCGGCTG 1279
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1280 GAGCGCATGGGCTGGAGCGCTGCGTGGAGAGACTGCGCAGCGCTGCGGCGCGC 1339

RESULT 7
AAL47186
ID AAL47186 standard; cDNA; 1634 BP.
XX
AC AAL47186;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human rheumatoid arthritis associated DR3 gene related cDNA #1.
XX
KW Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
XX gene therapy; gene; ss.
OS Homo sapiens.
XX

PH Key Location/Qualifiers
FT CDS 89..1342
FT /tag- a
FT /product- "AAL17879"
XX
PN WO200234912-A1.
XX
PD 02-MAY-2002.
XX
PF 24-OCT-2001; 2001WO-JP09313.
XX
PR 24-OCT-2000; 2000JP-0324296.
PR 27-MAR-2001; 2001JP-0090546.
PR 30-MAR-2001; 2001JP-0099990.
XX
PA (NEW-) NEW IND RES ORG.
PA (SHIO/) SHIOZAWA S.
XX
PI Shiozawa S, Konishi Y;
XX
DR WPI: 2002-417132/44.
DR P-PSDB; AAO17879.
XX
XX
PT Genomes, particularly DR3 genomic DNA, participating in rheumatoid
PT arthritis via mutation, useful in evaluating disease onset and its
PT possibility and providing therapy and remedies -
XX
PS Example 1; Page 66-69; 84pp; Japanese.
XX
CC The present invention relates to the human DR3 gene, which is associated
CC with rheumatoid arthritis. Certain mutations in the gene can be linked to
CC the disease. The sequences can be used to evaluate disease onset and its
CC possibility and to provide therapy and remedies. The present sequence is
CC a coding sequence described in the exemplification of the invention.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:
Pred. No.: 2, 61e-44 Length: 1634
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x AAL47186 (1-1634)

QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1100 GTGATGAGCGCGGTCCAGCGCGGCTGGAGAGAGTTGTCGCGCAGCTGGGGCTGCGC 1159
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTrpGlu 40
DB 1160 GAGCGAGAGATCGAACCGGTGGAGGTGAGATGCGCGCTTCGAGACGACAGTACGAG 1219
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
DB 1220 ATGCTCAAGCGCTGGCGCCAGCAGACCGCGGCTTCGAGACCGTTCGCGGCTG 1279
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1280 GAGCGCATGGGCTGGAGCGCTGCGTGGAGAGACTGCGCAGCGCTGCGGCGCGC 1339

RESULT 8
AAC91477
ID AAC91477 standard; cDNA; 1662 BP.
XX
AC AAC91477;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO779 cDNA.
XX

Human; PRO; antiinflammatory; dermatological; antiarthritic;
antrihumatic; cardiant; antianaemic; immunosuppressive; antihydroid;
antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
antiallergic; antiasthmatic; immune related disorder;
hepatobiliary disease; autoimmune disease; allergy; ss.
Homo sapiens.
WO200073452-A2.
07-DEC-2000.
02-JUN-2000; 2000WO-US15264.
02-JUN-1999; 99WO-US12252.
20-JUL-1999; 99US-0144732.
20-JUL-1999; 99US-0144758.
28-JUL-1999; 99US-0146222.
01-SEP-1999; 99WO-US20111.
15-SEP-1999; 99WO-US21090.
15-SEP-1999; 99WO-US21547.
29-OCT-1999; 99US-0162506.
30-NOV-1999; 99WO-US28313.
01-DEC-1999; 99WO-US28634.
09-DEC-1999; 99US-0170262.
20-DEC-1999; 99WO-US30911.
05-JAN-2000; 2000WO-US00219.
06-JAN-2000; 2000WO-US00376.
11-FEB-2000; 2000WO-US03565.
18-FEB-2000; 2000WO-US04341.
18-FEB-2000; 2000WO-US04342.
22-FEB-2000; 2000WO-US04414.
24-FEB-2000; 2000WO-US04914.
15-MAR-2000; 2000WO-US06884.
20-MAR-2000; 2000WO-US07377.
21-MAR-2000; 2000WO-US07532.
30-MAR-2000; 2000WO-US08439.
17-MAY-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US14042.
(GENTH) GENENTECH INC.
Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AJ,
Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK,
Wood WJ;
WPI; 2001-025253/03.
P-PSDB; AAB50918.
Thirty three nucleic acids encoding PRO polypeptides which are useful
in the diagnosis and treatment of immune related disorders, e.g.,
thyroiditis and diabetes mellitus -
Claim 48; Fig 33; 218pp: English.
The present sequence is one of thirty three nucleic acids encoding PRO
polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
antagonists are useful for treating and diagnosing immune related
disorders such as systemic lupus erythematosus, rheumatoid arthritis,
osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
immune-mediated renal disease, demyelinating diseases of the central
and peripheral nervous systems (such as multiple sclerosis, idiopathic
demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
inflammatory demyelinating polyneuropathy), hepatobiliary diseases
(such as infectious, autoimmune chronic active hepatitis, primary
biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
disease, autoimmune or immune-mediated skin diseases (such as bullous
skin diseases, erythema multiforme, contact dermatitis, psoriasis),

allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
food hypersensitivity and urticaria), immunological diseases of the
lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
and hypersensitivity pneumonitis), transplantation associated diseases
including graft rejection and graft-versus-host diseases.
Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 2,67e-44 Length: 1662
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 22
US-09-993-234-6_COPY_338_417 (1-80) x AAC91477 (1-1662)
QY 1 ValMetAspAlaValProAlaArgArgTyrPlysgluPheValArgThrLeuGlyLeuArg 20
DB 1114 GTGATGAGACGGCTGCCACGCGCGCTGGAAGAGATTGTCGACGCTGGGCTGCC 1173
QY 21 GluAlaGluIleGluAlaValAlaGluIleGlyArgPheArgAspGlnIleTyrGlu 40
DB 1114 GAGGAGAGATCGAAGCCGCTGGAGATCGGCCCTCCGAGACGACGATACGAG 1233
QY 41 MetLeuLysArgTyrArgGlnGlnInpProAlaGlyLeuGlyAlaValTyrAlaLeu 60
DB 1234 ATGCTCAAGCGCTGGCGCCACGACGACGCCGCGGCTCGGAGCGGTTACCGGCCCTG 1293
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1294 GAGCGCATGGGCGCTGAGCGGCTGCGTGAAGACTTGGCAGACGCGCTGAGCGGCCG 1353
RESULT 9
ID ABR40265 standard; cDNA; 1662 BP.
XX
AC ABR40265;
XX
DT 15-JUL-2002 (first entry)
XX
DE cDNA encoding human PRO779 polypeptide.
XX
KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder;
KW gene therapy; cytostatic; neuroprotective; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200153486-A1.
XX
PD 26-JUL-2001.
XX
PE 11-FEB-2000; 2000WO-US03565.
XX
PF 08-MAR-1999; 99WO-US05028.
XX 11-MAR-1999; 99US-123972P.
XX 11-MAY-1999; 99US-133459P.
XX 02-JUN-1999; 99WO-US12252.
XX 22-JUN-1999; 99US-140650P.
XX 20-JUL-1999; 99US-140653P.
XX 26-JUL-1999; 99US-144758P.
XX 28-JUL-1999; 99US-145698P.
XX 17-AUG-1999; 99US-146222P.
XX 31-AUG-1999; 99US-149395P.
XX 01-SEP-1999; 99WO-US20111.
XX 15-SEP-1999; 99WO-US21090.
XX 30-NOV-1999; 99WO-US28313.
XX 01-DEC-1999; 99WO-US28634.
XX 01-DEC-1999; 99WO-US28634.

PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0234984.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.

PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

PA (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-565190/63.
XX
XX Nucleic acid encoding novel connective tissue associated polypeptides,
XX used in diagnosing, preventing, treating or ameliorating a disorder
XX such as cancer or rheumatoid arthritis -
XX
XX Disclosure; SEQ ID No 1577; 673bp; English.
XX
XX The present invention relates to the isolation of novel human connective
XX tissue related polypeptides (AAU86435-AAU86922) and the polynucleotide
XX (cDNA and genomic) sequences encoding them. The sequences of the
XX invention are useful in the diagnosis, treatment, prevention and/or
XX prognosis of diseases associated with connective tissue(s), including
XX cancer. The polynucleotide sequences of the invention are also useful
XX in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding
XX the novel human connective tissue related polypeptides.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 10797 BP; 2003 A; 3215 C; 3378 G; 2201 T; 0 other;

Alignment Scores:
Pred. No.: 2.67e-43 Length: 10797
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 23 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x ABK42690 (1-10797)

QY 1 ValMetAspAlaValAlaProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db 9119 GTGATGGAGCGGCTCCAGCGCGGCTGGAGGAGTTCGTGCGACCTGGGGCTGGCG 9178

QY 21 GluAlaGluIleGluAlaValAlaGluIleGluArgPheArgAspGlnGlyTrpGlu 40
Db 9179 GAGCGAGAGTCGAAGCGCTGGAGTGGAGATCGGCCCTTCGAGACACAGACAGACAG 9238

QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
Db 9239 ATGCTCAAGCGCTGGCGCCAGCAGACGCCCGGCGCTCGAGAGCGCTTACGCGCGCTG 9298

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
Db 9299 GAGCGATGGAGCTGGAGCGCTGGAGAGACTTGGCCAGCGCGCTCGAGCGCGCGCG 9358

Mon Apr 7 09:25:00 2003

us-09-993-234-6_copy_338_417.rng

Page 12

Search completed: April 6, 2003, 16:52:44
Job time : 81.489 secs

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:35:34 ; Search time 929.72 Seconds

(without alignments)
2504.221 Million cell updates/sec

Title: US-09-993-234-6_COPY_338_417

Perfect score: 413
Sequence: 1 VMDAVPARRWKEFVRTLGLR.....ERMGIDGVEEDLSRLQNGP 80

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPRO.spool/US09993234/runat_27032003_115455_15349/app_query.fasta_1.2346
-DB=GenBml -OPMT=fastap -SUFFIX=rge -MINMATCH=0.1 -DOOPCL=0 -DOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human4.0.cdi -LIST=45
-DOCCALIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09993234.@cgn2.1.8534.0runat_27032003_115455_15349 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEOMETRY -NEG_SCORES=0 -WAIT -LONGLOG -DEVTIMEOUT=120
-NARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenBml:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_com:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrl:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	413	100.0	HSU94508	U94508 Human lymph
2	413	100.0	HSU94507	U94507 Human lymph
3	413	100.0	HSU94506	U94506 Human lymph
4	413	100.0	HSU94505	U94505 Human lymph
5	413	100.0	HSU94509	U94509 Human lymph
6	413	100.0	HSU94510	U94510 Human lymph
7	413	100.0	HSU94504	U94504 Human lymph
8	413	100.0	AX150176	AX150176 Sequence
9	413	100.0	AR119657	AR119657 Sequence
10	413	100.0	HSU72763	U72763 Human death
11	413	100.0	HSU78029	U78029 Human death
12	413	100.0	HSU94501	U94501 Human lymph
13	413	100.0	HSU94502	U94502 Human lymph
14	413	100.0	HSU94503	U94503 Human lymph
15	413	100.0	HSU83597	U83597 Human death
16	413	100.0	HSU75380	U75380 Human apopt
17	413	100.0	AK094463	AK094463 Homo sapi
18	413	100.0	HSU74611	U74611 Human Apo-3
19	413	100.0	AX055442	AX055442 Sequence
20	413	100.0	AX201344	AX201344 Sequence
21	413	100.0	AR119656	AR119656 Sequence
22	413	100.0	AK094488	AK094488 Homo sapi
23	413	100.0	AB051851	AB051851 Homo sapi
24	413	100.0	AB051850	AB051850 Homo sapi
25	413	100.0	AL158217	AL158217 Homo sapi
26	401	97.1	AF026070	AF026070 Homo sapi
27	401	97.1	AX331947	AX331947 Sequence
28	401	97.1	HSWSL1	Y09392 H. sapiens m
29	401	97.1	AF026071	AF026071 Homo sapi
30	395	95.6	BC017526	BC017526 Mus muscu
31	395	95.6	AC118359	AC118359 Rattus no
32	395	95.6	AL772240	AL772240 Mus muscu
33	389	94.2	AF329969	AF329969 Mus muscu
34	354	85.7	AF134858	AF134858 Mus muscu
35	300	72.6	G37503	G37503 SHGC-57889
36	175.5	2004	SSU19994	U19994 Sus scrofa
37	171	2115	AF329976	AF329976 Rattus no
38	171	2115	AF329977	AF329977 Rattus no
39	171	2115	AF329978	AF329978 Rattus no
40	171	2115	AF329979	AF329979 Rattus no
41	171	2115	AF329980	AF329980 Rattus no
42	171	2115	AF329981	AF329981 Rattus no
43	171	2130	AX401925	AX401925 Sequence
44	171	2130	RAT1NFR	M63122 Rat tumor n
45	171	41.4	AC125909	AC125909 Rattus no

RESULT 1

ALIGNMENTS

HSU94508
LOCUS HSU94508 705 bp mRNA linear PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 7 mRNA, alternatively
spliced, complete cds.
ACCESSION U94508
VERSION U94508.1 GI:2071962
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 705)
Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J., and Bell,J.I.
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL 97272273
MEDLINE 9114039
PUBMED 2 (bases 1 to 705)
REFERENCE Screation,G.R.
AUTHORS Direct Submission
TITLE Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
JOURNAL Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source 1. .705 Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1. .705
/function="mediates apoptosis"
/note="similar to Fas and TNF-R1; lacks transmembrane
domain; possibly soluble; LARD-6; LARD-7; NGR family
member"
/codon_start=1
/product="lymphocyte associated receptor of death 7"
/protein_id="AAC51313.1"
/db_xref="GI:2071963"
/translation="MEORPRGCAVVAALILVILGARGGTRSPRCDAGDFHKKIG
LFCRCGPADAGGAGALTPPATHTSPIDSAHTLAPDSSEKICTYVLYVNSMTPIG
PETDPAICPQYTWNSMDLPSPALGPAAFTSPSPASGPAAMLOPGQLDVMADVP
ARKNKEFRITGLNEATEAVEIGERFDQOYELTKRWROQOPAGLAVYAALERMG
LDGVEDLRSRLQNGP"
misc_feature 160. .161
/note="deletion compared to LARD 1a, deposited in Genbank
Accession Number U94501, probable skipping of putative
exons 3, 4, 5, 6 and 7"
BASE COUNT 112 a 236 c 248 g 109 t
ORIGIN
Alignment Scores:
Pred. No.: 1.3e-35 Length: 705
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_338_417 (1-80) x HSU94508 (1-705)
QY 1 ValMetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
|||||
Db 463 GTGATGGACGGGTCCAGCGCGCGGTGGAAGAGTTCGTCCGACGCTGGGGCTGCC 522
QY 21 GluAlaGluIleGluAlaValAlaGluIleGlyArgPheArgAspGlnGlyTyrGlu 40
|||||
Db 523 GAGCGAGAGATCGAAGCCGTGAGGTGAGATCGCGCCCTCCGACACGACGATACGAG 582
QY 41 MetLeuysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
Db 583 ATGCTCAAGCGGTGGCGCCAGCAGACGCCGCGGCTCTCGAGCCGTTTACGCGGCCCTG 642

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
Db 643 GAGCGCATGTGGGTGGACGCGGTGCGGTGGAAGACTTCGCGACGCCGCTGCAGCGGCCGCCG 702
RESULT 2
HSU94507
LOCUS HSU94507 838 bp mRNA linear PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 6 mRNA, alternatively
spliced, complete cds.
ACCESSION U94507
VERSION U94507.1 GI:2071960
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 838)
Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J., and Bell,J.I.
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL 97272273
MEDLINE 9114039
PUBMED 2 (bases 1 to 838)
REFERENCE Screation,G.R.
AUTHORS Direct Submission
TITLE Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
JOURNAL Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source 1. .838 Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1. .838
/function="mediates apoptosis"
/note="similar to Fas and TNF-R1; truncated before the
transmembrane domain; possibly soluble; LARD-6"
/codon_start=1
/product="lymphocyte associated receptor of death 6"
/protein_id="AAC51312.1"
/db_xref="GI:2071961"
/translation="MEORPRGCAVVAALILVILGARGGTRSPRCDAGDFHKKIG
LFCRCGPAAQVALENCSAYADTRCGCKPFWYECOVSGCVSSPFCQPLDQAL
HRHTRLDCHPSVTTLGQRHPSSTs"
misc_feature 160. .161
/note="deletion compared to LARD 1a, deposited in Genbank
Accession Number U94501, probable skipping of putative
exon 3"
misc_feature 328. .329
/note="deletion compared to LARD-1a, deposited in Genbank
Accession Number U94501, probably due to skipping of
putative exons 5, 6 and 7, leading to premature
transcriptional termination"
BASE COUNT 134 a 281 c 285 g 138 t
ORIGIN
Alignment Scores:
Pred. No.: 1.56e-35 Length: 838
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_338_417 (1-80) x HSU94507 (1-838)
QY 1 ValMetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
|||||
Db 596 GTGATGGACGGGTCCAGCGCGCGGTGGAAGAGTTCGTCCGACGCTGGGGCTGGCGC 655

OY		21	GUAUAGUUUGGUAUAAValaGluaGUUUGUAYARphEARASGLmTyrGu	40
D8	656	GAGCGACGATCAAGCCCTGGAGGTGGAGTCGCCCGCTTCGAGACCAGCAGTAGAG	715	
OY	41	MettLeuYSatgTrPARgInglnglnInProAlagIleuAlaValTyraLaalaleu	60	
D8	716	ATGCTACAAGCGCTGCAGCACAGACGCCGGGCGCTCGAGCGCTTTAACGGCCCCTG	775	
OY	61	GIUAUGmetGIyLeuAspGIcysValGIuaspleuArgrserArgLeuglNlyPro	80	
D8	776	GAGCGCATggggGCTGGAGCGCTGCCTGGAGAAGACTTCGACAGCGCGCGCCG	835	
RESULT 3				
LOCUS	HSU94506	952 bp	mRNA	linear PRI 15-MAY-1997
DEFINITION	Human lymphocyte associated receptor of death 5 mRNA, alternatively spliced, complete cds.			
ACCESSION	U94506			
VERSION	U94506.1	GI:2071958		
KEYWORDS	.			
SOURCE	Homo sapiens.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (bases 1 to 952)			
JOURNAL	McMichael,A.J., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,			
MEDLINE	LARD: a new lymphoid-specific death domain containing receptor			
PUBMED	regulated by alternative pre-mRNA splicing			
REFERENCE	Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)			
AUTHORS	9114039			
TITLE	2 (bases 1 to 952)			
JOURNAL	Screaton,G.R.			
PUBMED	Direct Submission			
REFERENCE	Submitted (19-MAR-1997) Molecular Immunology Group, Institute of			
AUTHORS	Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3			
TITLE	9DU, UK			
FEATURES				
CDS	location/qualifiers			
misc_feature	1..952			
misc_count	/organism="Homo sapiens"			
misc_origin	/db_xref="taxon:9606"			
	/cell_line="HeLa"			
	/cell_type="lymphocyte"			
	1..411			
	/function-"mediates apoptosis"			
	/note-"LARD-5; similar to Fas and TNF-R1; possibly soluble; truncated before the transmembrane domain"			
	/codon_start=1			
	/product-"lymphocyte associated receptor of death 5"			
	/protein_id="AACSl311.1"			
	/db_xref="GI:2071952"			
	/translation-"MEORPRCAAVALALLVLGARAOGTRSPRCADGFHKIGT			
	LFECRGCPAASOVALENCASVADRRCGRCKRGEVCQVSVPYCQPCLDCCAL			
	HRHRLCSRDPTDCGTCLPGFYEHGSGCVSCP"			
	160..161			
	/note-"deletion compared to LARD 1a, deposited in GenBank			
	Accession Number U94501, probable skipping of putative			
	exon 3"			
	407..408			
	/note-"deletion compared to LARD-1a, deposited in GenBank			
	Accession Number U94501, probably due to skipping of			
	putative exons 6 and 7, leading to premature			
	transcriptional termination"			
	BASE COUNT 154 a 317 c 319 g 162 t			
	ALIGNMENT SCORES:			
	Pred. No.: 1.79e-35 Length: 952			
	Score: 413.00 Matches: 80			
	Percent Similarity: 100.00% Conserves: 0			
	Best Local Similarity: 100.00% Mismatch: 0			

Query Match	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-993-234-6_COPY_338_417 (1-80) x HSU94506 (1-952)

OY 1 ValMetAspAlaValProIlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 710 GRGATGGACCGCGCTCCAGCAGCGCGGCTTGGAAGAGTTGTGCACAGCTGGGGCTGGC 769
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 21 GluaIaGluiLegIuaLaVaIgluVaIgluiLegIyaRpheArgAspGlnInTyrgLu 40
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 770 GAGGCAgAATCGAAAGCCGTGGAGGTGGAGATCGGCCCTTCCGAGACAGCAGTAGAG 829
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 41 MetLeuLyAsyTrpArgGlnGlnInProAlaGlyLeuGlyAlaValTyTAALaLeu 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 830 ATGCCTCAACCGCTGGCGCCAGCAGCAGCCGCGGCGCTTCGAGCCGTTACGCGCGCC 889
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 61 GluArGmetGlyLeuAspGlyCytyValGIuaBapLeuAgsSerArgLeuGlnArgIyPro 80
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 890 GAGCGCATGGGCTGGACGCGTGCCTGGAAAGACTTGCGCACGCCCTGCACGCGCGCCG 949
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
LOCUS HSU94505
DEFINITION Homo sapiens 1087 bp mRNA linear PRI 15-MAY-1997
ACCSSION U94505 Human lymphocyte associated receptor of death 4 mRNA, alternatively
VERSION spliced, complete cds.
KEYWORDS U94505.1 GI:2071956
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1087)
AUTHORS Screation,G.R., Xu,X.N., Olsen,A.L., Comper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.T.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PubMed 9114039
REFERENCE 2 (bases 1 to 1087)
AUTHORS Screation,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

FEATURES
source Location/Qualifiers
1..1087
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HeLa"
/cell_type="lymphocyte"
1..546
/function="mediates apoptosis"
/note="LARD-4: similar to Fas and TNF-R1; possibly
soluble; truncated before the transmembrane domain"
/codon_start=1
/product="lymphocyte associated receptor of death 4"
/protein_id="AAC51310.1"
/db_xref="GI:2071957"
/translation="MEORPRGCAVAANAALLVLIGARGNGTSPPRCDAAGDHHKRG
LFQCRDPAGHYLKAPCMPEPCNSTICVCPDPTLAENHNHNSCARCAQCADQASGY
ALENCSAVDTRCCCKPMWRYECOVSCVSSPYCPCLDCGALNHRRLILCSRRDT
DCGICLDFEYEHGGCVSCSP"
542..543
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exons 6 and 7 leading to premature transcriptional
termination"

misc_feature
BASE COUNT 180 a 363 c 355 g 189 t
ORIGIN

Alignment Scores:

Pred. No.: 2,06e-35 Length: 1087
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x HSU94505 (1-1087)

QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20

DB 845 GTGATGAGACGGGTCCAGCGCGCGCTGGAGAGAGTTGTCGGACGCGTGGGGCTCGC 904

QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIleTyrGlu 40

DB 905 GAGGCGAGAGTCGACGCCGTGGAGTGGAGATCGCCGCTCCGAGACGACGAGTACGAG 964

QY 41 MetLeuLysArgTrpArgGlnGlnInProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60

DB 965 ATGCTCAAGCGGTGGCGCCAGCAGACGCCGCGCTCGAGCCGTTTACGGCGCCCTG 1024

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80

DB 1025 GAGCGATGGGGCTGAGCGGCTGCTGGAAGACTTGGCGCGCCCTCGACGCCGCCCG 1084

RESULT 5 HSU94509 1119 bp mRNA linear PRI 15-MAY-1997

LOCUS Human lymphocyte associated receptor of death 8 mRNA, alternatively

ACCESSION U94509

VERSION U94509.1 GI:2071964

KEYWORDS

SOURCE

ORGANISM

Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 1119)

Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,

McMichael,A.J., and Bell,J.I.
LARD: a new lymphoid-specific death domain containing receptorregulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3

9DU, UK

FEATURES

source

misc.feature

160..161
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exon 3"
BASE COUNT 175 a 374 C 371 G 199 T
ORIGIN

Alignment Scores:

Pred. No.: 2.13e-35 Length: 1119
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x HSU94509 (1-1119)

QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20

DB 877 GTGATGAGACGGGTCCAGCGCGCGCTGGAGAGAGTTGTCGGACGCGTGGGGCTCGC 936

QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIleTyrGlu 40

DB 937 GAGGCGAGATCGAGCGCGGTGGAGTGGAGATCGCCGCTCCGAGACGACGAGTACGAG 996

QY 41 MetLeuLysArgTrpArgGlnGlnInProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60

DB 997 ATGCTCAAGCGGTGGCGCCAGCAGACGCCGCGCTCGAGCCGTTTACGGCGCCCTG 1056

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80

DB 1057 GAGCGATGGGGCTGAGCGGCTGCTGGAAGACTTGGCGCGCCCTCGACGCCGCCCG 1116

RESULT 6 HSU94510 1143 bp mRNA linear PRI 15-MAY-1997

LOCUS Human lymphocyte associated receptor of death 9 mRNA, alternatively

ACCESSION U94510

VERSION U94510.1 GI:2071966

KEYWORDS

SOURCE

ORGANISM

Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 1143)

Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,

McMichael,A.J., and Bell,J.I.
LARD: a new lymphoid-specific death domain containing receptorregulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3

9DU, UK

FEATURES

source

misc.feature

160..161
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exon 3"
BASE COUNT 175 a 374 C 371 G 199 T
ORIGIN

Alignment Scores:

Pred. No.: 2.13e-35 Length: 1119
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x HSU94509 (1-1119)

QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20

DB 877 GTGATGAGACGGGTCCAGCGCGCGCTGGAGAGAGTTGTCGGACGCGTGGGGCTCGC 936

QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIleTyrGlu 40

DB 937 GAGGCGAGATCGAGCGCGGTGGAGTGGAGATCGCCGCTCCGAGACGACGAGTACGAG 996

QY 41 MetLeuLysArgTrpArgGlnGlnInProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60

DB 997 ATGCTCAAGCGGTGGCGCCAGCAGACGCCGCGCTCGAGCCGTTTACGGCGCCCTG 1056

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80

DB 1057 GAGCGATGGGGCTGAGCGGCTGCTGGAAGACTTGGCGCGCCCTCGACGCCGCCCG 1116

RESULT 6 HSU94510 1143 bp mRNA linear PRI 15-MAY-1997

LOCUS Human lymphocyte associated receptor of death 9 mRNA, alternatively

ACCESSION U94510

VERSION U94510.1 GI:2071966

KEYWORDS

SOURCE

ORGANISM

Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 1143)

Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,

McMichael,A.J., and Bell,J.I.
LARD: a new lymphoid-specific death domain containing receptorregulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3

9DU, UK

FEATURES

source

misc.feature
/note="deletion compared to LARD 1a, deposited in Genbank
Accession Number U94501, probable skipping of putative
exon 7 encoding the transmembrane domain"

BASE COUNT 188 a 378 c 378 g 199 t

ORIGIN

Alignment Scores:
Pred. No.: 2.18e-35 Length: 1143
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x HSU94510 (1-1143)

QY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db 901 GTGATGACCGCGGCGCCGAGGAGGAGTTCGTCGCGACGCGGCGCTCGC 960

QY 21 GluAlaGluIleGluAlaValGluIleGlyArgPheArgAspGlnGlyTyrGlu 40
Db 961 GAGCAGAGATCGAAGCGGAGGTGAGATCGCGCTTCGAGACGACGATACGAG 1020

QY 41 MetLeuysArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaLeu 60
Db 1021 ATGCTCAAGCGCTGGCGCGACGACCGCGGCGCTCGGAGCGCTTACGCGCCTG 1080

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
Db 1081 GAGCGCATGGGCGTGGAGCGCTGCGAGACTTGGCGACGCGCTGACGCGCGCG 1140

RESULT 7
HSU94504 1198 bp mRNA linear PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 3 mRNA, alternatively
DEFINITION spliced, complete cds.
ACCESSION U94504
VERSION U94504.1 GI:2071954
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1198)
AUTHORS Secretan,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMinn,A.J., and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 9114039
PUBMED 2 (bases 1 to 1198)
REFERENCE Secretan,G.R.
TITLE Direct Submision
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford, OX3
9DU, UK

FEATURES
source Location/Qualifiers
1..1198
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
1..657
/cell_type="lymphocyte"

CDS

/function="mediates apoptosis"
/note="LARD-3; similar to Fas and TNF-R1; possibly
soluble; truncated before the transmembrane domain"
/codon_start=1
/product="lymphocyte associated receptor of death 3"
/protein_id="AAC51309.1"
/db_xref="GI:2071954"
/translation="MEQPRGCAVAALALLVLGARAAGGTRSPRCDCAGDFHKKIG
LFCCRCGPAGHTLAKAPCTEPGNSSTLCVCPDFFLAMEHHNSCARCAQCDQASQV
ALENCSAVADTRCGCKRGMFVEQVSCVSSPFYCPCLDCGALHRTLCSSRDT
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misc.feature
542..543
/note="deletion compared to LARD 1a, deposited in Genbank
Accession Number U94501, probable skipping of putative
exon 6 leading to premature transcriptional termination"

BASE COUNT 193 a 405 c 384 g 216 t

ORIGIN

Alignment Scores:
Pred. No.: 2.29e-35 Length: 1198
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x HSU94504 (1-1198)

QY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db 956 GTGATGACCGCGGCGCCGAGGAGGAGTTCGTCGCGACGCGGCGCTCGC 1015

QY 21 GluAlaGluIleGluAlaValGluIleGlyArgPheArgAspGlnGlyTyrGlu 40
Db 1016 GAGCAGAGATCGAAGCGGAGGTGAGATCGCGCTTCGAGACGACGATACGAG 1075

QY 41 MetLeuysArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaLeu 60
Db 1076 ATGCTCAAGCGCTGGCGCGACGACCGCGGCGCTCGGAGCGCTTACGCGCCTG 1135

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
Db 1136 GAGCGCATGGGCGTGGAGCGCTGCGAGACTTGGCGACGCGCTGACGCGCGCG 1195

RESULT 8
AX150176 1250 bp DNA linear PAT 08-JUN-2001
LOCUS Sequence 1 from Patent WO0135995.
ACCESSION AX150176
VERSION AX150176.1 GI:14348204
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1250)
AUTHORS Titile,T.V. and Wegmann,K.W.
TITLE T13-specific binding agents and methods for their use
JOURNAL Patent: WO 0135995-A 1 25-MAY-2001;
Patent: Thomas V. (US); Wegmann, Keith W. (US)
FEATURES
source Location/Qualifiers
1..1250
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 201 a 420 c 406 g 223 t

ORIGIN

Alignment Scores:
Pred. No.: 2.4e-35 Length: 1250
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-09-993-234-6_COPY_338_417 (1-80) x AX150176 (1-1250)			
QY	1 ValMetAspAlaValProAlaIarGArGTrrPLySGluPheValArGThrLeuGlyLeuArG	20	
DB	1008 GIGATGGAGCGGGTCCACAGCGGGCGCTGGAGAGAGATTGCTGCACGCTGGGGCGTCCGCC	1067	
QY	21 GluAlaGluIleGluAlaValGluValGluIleGlyArGpHeArGAspGlnGlyGlu	40	
DB	1068 GAGGACAGAAATCGAAGCCCTGGAGGTGGAGATCGGGCCCTCCGAGACAGACAGTACAG	1127	
QY	41 MetLeuLYsArGTrrPArGlnGlnGlnInProAlaGlyLeuGlyAlaValTyrAlaIleLeu	60	
DB	1128 ATGCTCAAGCGCTGGCGCCACAGACAGACCGCGGGGCTTGAGAGCGCTTACCGGCGCTTG	1187	
QY	61 GluArGMetGlyLeuAspGlyCySValGluAspLeuArGSerArGLeuGlnArGglyPro	80	
DB	1188 GAGCGCATGGGGCTGGAGCGGTGCTGGAGAACTTGCGACAGCGCGCTCGACGCGGCCG	1247	
RESULT 9			
LOCUS	AR119657	1254 bp	DNA
DEFINITION	Sequence 3 from patent US 6153402.	linear	PAT 16-MAY-2001
ACCESSION	AR119657		
VERSION	AR119657.1	GI:14102356	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1254)		
TITLE	Yu, G., 'L.', Ni, J., Gentz, R.L. and Dillon, P.J.		
JOURNAL	Death domain containing receptors		
FEATURES	Patent: US 6153402-A 3 28-NOV-2000;		
Source	Location/Qualifiers		
	1..1254		
	/organism="unknown"		
BASE COUNT	201 a 420 c 407 g 226 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	2.4e-35	Length:	1254
Score:	413.00	Matches:	80
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-09-993-234-6_COPY_338_417 (1-80) x AR119657 (1-1254)			
QY	1 ValMetAspAlaValProAlaIarGArGTrrPLySGluPheValArGThrLeuGlyLeuArG	20	
DB	1012 GIGATGGAGCGGGTCCACAGCGGGCGCTGGAGAGATTGCTGCACGCTGGGGCGTCCGCC	1071	
QY	21 GluAlaGluIleGluAlaValGluValGluIleGlyArGpHeArGAspGlnGlyGlu	40	
DB	1072 GAGGACAGAAATCGAAGCCCTGGAGGTGGAGATCGGGCCCTCCGAGACAGACAGTACAG	1131	
QY	41 MetLeuLYsArGTrrPArGlnGlnGlnInProAlaGlyLeuGlyAlaValTyrAlaIleLeu	60	
DB	1132 ATGCTCAAGCGCTGGCGCCACAGACAGACCGCGGGGCTTGAGAGCGCTTACCGGCGCTTG	1191	
QY	61 GluArGMetGlyLeuAspGlyCySValGluAspLeuArGSerArGLeuGlnArGglyPro	80	
DB	1192 GAGCGCATGGGGCTGGAGCGGTGCTGGAGAACTTGCGACAGCGCGCTCGACGCGGCCG	1251	
RESULT 10			
LOCUS	HSU72763	1254 bp	mrna
DEFINITION	Human death receptor 3 (DR3) mRNA, complete cds.	linear	PRI 15-NOV-1996
ACCESSION	U72763		
VERSION	U72763.1	GI:1669511	

KEYWORDS	ORGANISM	TITLE	JOURNAL	REFERENCE	AUTHORS	FEATURES	source	gene	CDS	BASE COUNT	ORIGIN	Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best local Similarity:	Query Match:	DB:	US-09-993-234-6_COPY_338-417 (1-80) x HSUT2763 (1-1254)	OY	Db	OY	Db	OY	Db	OY	Db	RESULT 11	LOCUS	DEFINITION	ACCESSION																				
Homo sapiens.	Homo sapiens	1 (bases 1 to 1254)	Chinnaiyan, A.M., O'Rourke, K., Yu, G.L., Lyons, R.H., Garg, M., Duan, P.R., Xing, L., Gentz, R., Ni, J., and Dixit, V.M.	Signal transduction by DR3, a death domain-containing receptor related to TNFR-1 and CD95	Science 274 (5289), 990-992 (1996)	97081063	8875942	2 (bases 1 to 1254)	Chinnaiyan, A.M., O'Rourke, K., Yu, G.-L., Lyons, R.H., Garg, M., Duan, R., Xing, L., Gentz, R., Ni, J., and Dixit, V.M.	Submitted (29-SEP-1996) Pathology, University of Michigan Medical School, 1301 Catherine St., Box 0602, Ann Arbor, MI 48109, USA	Location/Qualifiers	1. .1254	/organism="Homo sapiens"	1. .1254	/db_xref="taxon:9606"	1. .1254	/gene="DR3"	1. .1254	/gene="DR3"	1. .1254	/codon_start=1	/product="death receptor 3"	/protein_id="AAC50819.1"	/db_xref="GI:1669512"	/translation="MEORPRGCAVAALLLVILGARAQGTSPRCDCAGDFHKKIGLEFCRGCPAGHYTLAKPTPCGNSCTLCVCPDPTLAMEHNHNSCARQACDEQASQVYALFENCSAVADHTRCGCKPGMEFECVSCVSPYCPCLDCGALHRTLLGSRDPCDGLPEFYEHGGVGCSCPTSLGSCPERCAAGCGRMVQVVLGAVLPVLLIGTLVTVHCHWPKRPLVYADAEAGMETALPPRPAHTLSPDLATLAPDSSKICTTVGNSTWGTGYPETQALCPQVYVMSDQLPSRALGPAAPPTLSPSPAGSPAMVLPGLVYDMADVAPARKMEFYRTTGLREALELVAEVEITGRFRDDOYMLKRWRRDQAPAGLGVYALALERNGDGCEVEDLSRLQRP"	201 a	420 c	407 g	226 t	2.4e-35	Length: 1254	Matches: 80	Conservative: 100.00%	Mismatches: 0	Indels: 0	Gaps: 0	1 ValMetAspAlaValAlaProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20	1012 GTGATGGACGGGCTCCACGGCGCTGGAGAGGCTTCGTGCGACGCTGGGCTGGCG 1071	21 GluAlaGluIleGluAlaValAlaGluValGluIleGlyArgPheArgAspGlnIleTrpGlu 40	1072 GAGGACGAGATCGAAGCCGCTGGAGGTGAGATGCGGCCCTTCCGAGACACAGTACAG 1131	41 MetLeuLysArgTTPAPAGTGlNGlNGlNGlNGlNGlNGlNGlNGlNGlNGlNGlNGlNGl 60	1132 ATGCTCAAGCGCTGGCGCCACACAGACGCGCGGCGCTCGGAGCGCTTACGCGGCGCTG 1191	61 GluLysArgMetGlyLeuAspGlyCysValGluLysPheLeuArgSerArgLeuGlnArgGlyPro 80	1192 GAGCGCATGGGGCTGGAGAGCGCTGCTGGAAAGACTTGGCCACCGCGCTTCACGCGCGCG 1251	HSUT8029	1254 bp	mRNA	linear	PRI 15-JAN-1997	Human apoptosis inducing receptor AIR mRNA, complete cds.	U78029

KEYWORDS U78029.1 GI:1778763
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
TITLE Degli-Esposti, M.A., Din, W.S., Cosman, D., Smith, C.A. and Goodwin, R.G.
JOURNAL AIR, A Novel Member of the TNF Receptor Family, is a Strong Inducer of Apoptosis
REFERENCE 2 (bases 1 to 1254)
AUTHORS Degli-Esposti, M.A. and Goodwin, R.G.
JOURNAL Direct Submission
TITLE Submitted (12-NOV-1996) Biochemistry, Immunex Corporation, 51 University St., Seattle, WA 98101, USA
FEATURES
source
1..1254
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1pter"
/cell_type="peripheral blood T-cells"
1..1254
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/product="apoptosis inducing receptor AIR"
/protein_id="AAB40918.1"
/db_xref="GI:1778764"
/translation="MEGRPRGCAVAAALLVLGARGGSTRSPDCADDEHKKIG
LFCRGCPAGHYLAKPCTEPCGNSLVCPODFTFLAENHNSECARQACDEQASV
ALENCASVADTRCGCKPGWVECVSOVSSSPYCPQCDGALHRTILCSRBT
DCGTCLPGFEGHDGCVSCPTSLGSCPERCAAVCGWROMFWVLLAGLVPLLAGA
TLVTYTRHCHPHKPLVTADAGMEALTPPATLHSPDLSAHTLLAPDSSKICTVOL
VGNSTGPGYPTGEOALCPQVWWSMDOLPSRALGPAAVPTLSPSPASPMMLQPGPO
LYDMAVAPARBRKEFYRTGLRAEIEAVEVEIGRRDQYEMLKRRROQPAIGLCA
VYALEMKGIDCGVEDLRSLQKRP"
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN
Alignment Scores:
Pred. No.: 2.4e-35 Length: 1254
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-993-234-6_COPY_338_417 (1-80) x HSU78029 (1-1254)
QY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db 1012 GTGATGAGCGGGGTCCAGCGCGCGCGTGGAGAGTTCGTCGCCACGCTGGCGTGGC 1071
QY 21 GluAlaGluIleGluAlaValGluValIleGlyArgPheArgAspGlnGlyTyrGlu 40
Db 1072 GAGCAGAGATCGAAGCGGTGGAGATCGCGCTCCAGACACACAGATACAGAG 1131
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
Db 1132 ATGCTCAAGCGCTGGCGCCAGCAGCGCGCGCTGGAGCGCTTACGCGGCGCTG 1191
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
Db 1192 GAGCGCATGGGGCTGGAGCGGTGGTGAAGACTTGGCGACCGCGCTGCGCGCGCG 1251
RESULT 12
HSU94501 1254 bp mRNA linear PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 1a mRNA, complete
DEFINITION cds.
ACCESSION U94501 GI:2071948
VERSION

KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
TITLE MCMichael, A.J., Xu, X.N., Olsen, A.L., Cowper, A.E., Tan, R., LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
REFERENCE 97272273
AUTHORS Screation, G.R.
JOURNAL Screation, G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK
FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..1254
/function="mediates apoptosis"
/note="LARD-1a; membrane protein; similar to Fas and TNF-RI; contains a death domain"
/codon_start=1
/product="lymphocyte associated receptor of death 1a"
/protein_id="AAC51306.1"
/db_xref="GI:2071949"
/translation="MEGRPRGCAVAAALLVLGARGGSTRSPDCADDEHKKIG
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ALENCASVADTRCGCKPGWVECVSOVSSSPYCPQCDGALHRTILCSRBT
DCGTCLPGFEGHDGCVSCPTSLGSCPERCAAVCGWROMFWVLLAGLVPLLAGA
TLVTYTRHCHPHKPLVTADAGMEALTPPATLHSPDLSAHTLLAPDSSKICTVOL
VGNSTGPGYPTGEOALCPQVWWSMDOLPSRALGPAAVPTLSPSPASPMMLQPGPO
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VYALEMKGIDCGVEDLRSLQKRP"
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN
Alignment Scores:
Pred. No.: 2.4e-35 Length: 1254
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-993-234-6_COPY_338_417 (1-80) x HSU94501 (1-1254)
QY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db 1012 GTGATGAGCGGGGTCCAGCGCGCGCGTGGAGAGTTCGTCGCCACGCTGGCGTGGC 1071
QY 21 GluAlaGluIleGluAlaValGluValIleGlyArgPheArgAspGlnGlyTyrGlu 40
Db 1072 GAGCAGAGATCGAAGCGGTGGAGATCGCGCTCCAGACACAGATACAGAG 1131
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
Db 1132 ATGCTCAAGCGCTGGCGCCAGCAGCGCGCGCTGGAGCGCTTACGCGGCGCTG 1191
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
Db 1192 GAGCGCATGGGGCTGGAGCGGTGGTGAAGACTTGGCGACCGCGCTGCGCGCGCG 1251
RESULT 13
HSU94502 1257 bp mRNA linear PRI 15-MAY-1997
LOCUS

DEFINITION Human lymphocyte associated receptor of death 1b mRNA,
alternatively spliced, complete cds.
ACCESSION U94502
VERSION U94502.1 GI:2071950
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1257)
Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL
MEDLINE 97272273
PUBMED 9114039
REFERENCE
AUTHORS 2 (bases 1 to 1257)
Screation,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="Lymphocyte"
1..1257
/function="mediates apoptosis"
/note="LARD-1b: membrane protein, similar to Fas and
TNF-R1; contains a death domain"
/codon_start=1
/product="Lymphocyte associated receptor of death 1b"
/protein_id="AAC51307.1"
/db_xref="GI:2071951"
/translation="MEORRGCAGAAVAAALLVLLGARAAGCTRRPCDCAADPFHKKIG
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DCGCLPGFYEHDGCVSCPTSLGSCPCRAACVGMROMFWOYLALGLVPLLGA
TLTYVRRHCPMPKPLVTADDEAGMEALPPRPATHLSPIDSAHTLLAPDSSKICTVO
LVNSMTPTGVPETOLALCPVOYVWMDOLPSRALGPAAPTLSPESPAGSPAMILDPP
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misc_feature
708..711
/note="insertion compared to LARD-1a, deposited in Genbank
Accession Number U94501, probably represents alternative
3' splice site"
BASE COUNT 202 a 421 c 408 g 226 t
ORIGIN
Alignment Scores:
Pred. No.: 2,41e-35 Length: 1257
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-993-234-6_COPY_338_417 (1-80) x HSU94502 (1-1257)
QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1015 GTGATGAGAGCGGCTCCACCGCGCGCTGGAAGAGTTCGTGGCGCGCTGGCGCGC 1074
QY 21 GtualaGluIleGluAlaValaGluValaGluIleGlyArgPheArgAspGlnGlnArg 40
DB 1075 GAGGAGAGATGAGAGCGCTGGAGGTGAGATCGCGCTTCGAGACGACGAGTACGAG 1134
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyValaValaTyrAlaAlaLeu 60
DB 1135 ATGCTCAAGCGCTGGCGCGACGACGACCGCGCGCGCTTACCGCGCGCTTG 1194

QY 61 GluArgMetGlyLeuAspGlyCysValaGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1195 GAGCGATGGGCGCTGGACGCGCTGGTGAAGACTGGCGACGCGCTTCGAGCGCGCGC 1254
RESULT 14
HSU94503
LOCUS 1355 bp mRNA linear PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 2 mRNA, alternatively
spliced, complete cds.
ACCESSION U94503
VERSION U94503.1 GI:2071952
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1355)
Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL
MEDLINE 97272273
PUBMED 9114039
REFERENCE
AUTHORS 2 (bases 1 to 1355)
Screation,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source Location/Qualifiers
1..1355
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="Lymphocyte"
1..762
/function="mediates apoptosis"
/note="LARD-2: similar to Fas and TNF-R1; possibly
soluble; truncated before the transmembrane domain"
/codon_start=1
/product="Lymphocyte associated receptor of death 2"
/protein_id="AAC51308.1"
/db_xref="GI:2071953"
/translation="MEORRGCAGAAVAAALLVLLGARAAGCTRRPCDCAADPFHKKIG
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DCGCLPGFYEHDGCVSCPTSLGSCPCRAACVGMROMFWOYLALGLVPLLGA
TLTYVRRHCPMPKPLVTADDEAGMEALPPRPATHLSPIDSAHTLLAPDSSKICTVO
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misc_feature
599..700
/note="insertion compared to LARD 1a, deposited in Genbank
Accession Number U94501, probable retained intron leading
to premature transcriptional termination"
BASE COUNT 223 a 441 c 451 g 240 t
ORIGIN
Alignment Scores:
Pred. No.: 2,61e-35 Length: 1355
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-993-234-6_COPY_338_417 (1-80) x HSU94503 (1-1355)
QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1113 GTGATGAGAGCGGCTCCACCGCGCGCTGGAAGAGTTCGTGGCGCGCTGGCGCGC 1172
QY 21 GtualaGluIleGluAlaValaGluValaGluIleGlyArgPheArgAspGlnGlnArg 40

Db 1173 GAGGACAGATCGAACCCGCTGGAGGTGGAGATTCGGCCGCTCCGAGACCAGCATACGAG 1232

Qy 41 MetLeuLysArgTTPArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
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Db 1233 ATGCTCAAGCCGCTGGCGCCAGCAGCAACCCGCGGCGCTCGAGAGCGCTTACGCGGCGCTG 1292

Qy 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
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RESULT 15
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LOCUS
DEFINITION Human death domain receptor 3 (DDR3) mRNA, partial cds.
ACCESSION U83597
VERSION U83597.1 GI:1800292
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Chaudhary, P.M. and Hood, L.E.
TITLE 1 (bases 1 to 1528)
JOURNAL Direct Submission
Submitted (03-JAN-1997) Molecular Biotechnology, University of
Washington, 1705 NE Pacific Street, HSB-K360, Seattle, WA 98195,
USA

FEATURES
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Location/Qualifiers
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/function="mediates apoptosis when cross-linked"
/note="A TNFR1-related death-domain containing receptor;
DR3, WSL-LR, Apo-3, TRAMP; transmembrane form; similar to
human EST clone 298913, GenBank accession Number N71143"
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BASE COUNT 280 a 496 c 470 g 282 t
ORIGIN

Alignment Scores:
Pred. No.: 2.97e-35 Length: 1528
Score: 413.00 Matches: 80
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US-09-993-234-6_COPY_338_417 (1-80) x HS083597 (1-1528)

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Qy 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
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Db 1056 GAGGACAGATCGAACCCGCTGGAGGTGGAGATTCGGCCGCTCCGAGACCAGCATACGAG 1115

Search completed: April 6, 2003, 21:08:02
Job time : 933.72 secs

Qy 41 MetLeuLysArgTTPArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
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Db 1116 ATGCTCAAGCCGCTGGCGCCAGCAGCAACCCGCGGCGCTCGAGAGCGCTTACGCGGCGCTG 1175

Qy 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
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Db 1176 GAGGCAATGGGGCTGGAGCGCTGCTGGAGAACTTGCAGCCGCTGACGCGGCGCGC 1235

121

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GenCore version 5.1.4.p5.4578
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Run on: April 6, 2003, 16:28:24 ; Search time 13.5049 Seconds
(without alignments)
1816.682 Million cell updates/sec

Title: US-09-993-234-6_COPY_338_417

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Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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4	413	100.0	1783	3	US-08-815-469-1
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6	163	39.5	2440	4	US-09-513-007-1
7	158	38.3	427	4	US-09-397-787-236
8	158	38.3	2062	1	US-08-050-3198-24
9	158	38.3	2062	2	US-08-465-982-24
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ALIGNMENTS

RESULT 1
US-08-815-469-3
Sequence 3, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: YU, Guo-Liang
APPLICANT: NI, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HERewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285


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1      REFERENCE/DOCKET NUMBER: P1007P1
2      TELECOMMUNICATION INFORMATION:
3      TELEPHONE: 650/225-5416
4      TELEFAX: 650/952-9881
5      INFORMATION FOR SEQ ID NO: 9:
6      SEQUENCE CHARACTERISTICS:
7      LENGTH: 1634 base pairs
8      TYPE: Nucleic Acid
9      STRANDEDNESS: Single
10     TOPOLOGY: Linear
11     SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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34     Oy      61  GluArgMetGlyLeuAspGlyCysValAlaAspLeuArgSerArgLeuGlnArgGlyPro 80
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38     US-08-815-469-1
39     Sequence 1, Application US/08015469
40     Patent No. 6153402
41     GENERAL INFORMATION:
42     APPLICANT: Yu, Guo-Liang
43     APPLICANT: Ni, Jian
44     APPLICANT: Dixit, Vishva
45     APPLICANT: Dillon, Patrick J.
46     TITLE OF INVENTION: Death Domain Containing Receptors
47     NUMBER OF SEQUENCES: 17
48     CORRESPONDENCE ADDRESS:
49     ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
50     STREET: 1100 New York Ave., NW, Suite 600
51     CITY: Washington
52     STATE: DC
53     COUNTRY: USA
54     ZIP: 20005-3934
55     COMPUTER READABLE FORM:
56     MEDIUM TYPE: Floppy disk
57     COMPUTER: IBM PC compatible
58     OPERATING SYSTEM: PC-DOS/MS-DOS
59     SOFTWARE: PatentIn Release #1.0, Version #1.30
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62     FILING DATE: HEREWITH
63     CLASSIFICATION: 435
64     PRIOR APPLICATION DATA:
65     APPLICATION NUMBER: No. 6153402 yet Assigned
66     FILING DATE: 06-FEB-1997
67     PRIOR APPLICATION DATA:
68     APPLICATION NUMBER: US 60/028,711
69     FILING DATE: 17-OCT-1996

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PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 60/013,285
  FILING DATE: 12-MAR-1996
  ATTORNEY/AGENT INFORMATION:
    NAME: Steffe, Eric K.
    REGISTRATION NUMBER: 36,688
    REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 202-371-2600
      TELEFAX: 202-371-2540
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 1783 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: both
    MOLECULE TYPE: CDNA
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 198..1481
      US-08-815-469-1

US-08-815-469-1

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QY 61 GluArgMetGlyLeuAspGlyCysValAlaGluAspLeuArgSerArgLeuGlnArgGlyPro 80
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RESULT 5
US-08-762-308-10
: Sequence 10, Application US/08762308
: Patent No. 5925548
: GENERAL INFORMATION:
: APPLICANT: Beutler, Bruce A.
: APPLICANT: Bazzoni, Flavia M.
: TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY
: TITLE OF INVENTION: SIGNAL
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/762,308
: FILING DATE: 09-DEC-1996

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; LOCATION: (294)...(1706)
US-09-513-007-1

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Db 1545 AGCATGTGGCGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 1604
OY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
Db 1605 GCGCGCGTGCCTGACGAGACATGAGACCTGCTGCTGCTGCGAAACATAGAGAGCGCTG 1664

RESULT 7
US-09-397-787-236
; Sequence 236, Application US/09397787
; Patent No. 6468758
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
; FILE REFERENCE: 210121.46662
; CURRENT APPLICATION NUMBER: US/09/397,787
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 236
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-397-787-236

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Score: 158.00 Matches: 36
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Best Local Similarity: 45.00% Mismatches: 27
Query Match: 38.26% Indels: 4
DB: 4 Gaps: 2

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Db 113 GACCACGAGATCGATCGCTGGAGCTGCGAGAACGGGCGCTGCTGCTGCGGAGCGGATAC 172
OY 40 GluMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
Db 173 AGCATGTGGCGACCTGGAGGCGCGCGCACGCGCGCGCGCGCGCGCGCGCGCGCGCTG 232

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QY 57 TyralalaleuGluaArgMetGlyLeuaspGlyCysValaGluaPleuArgSerArgLeu 76
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RESULT 8
US-08-050-319B-24
Sequence 24, Application US/08050319B
Patent No. 5633145
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2062 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 155..1519
US-08-050-319B-24

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Pred. No.: 4.62e-12 Length: 2062
Score: 158.00 Matches: 36
Percent Similarity: 61.25% Conservative: 13
Best Local Similarity: 45.00% Mismatches: 27
Query Match: 38.26% Indels: 4
Gaps: 2

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QY 21 GluaIaGluIleGluAlaValaGluValaGluIleGlyArg---PheArgSPGInGlnTyr 39
Db 1298 GACCACAGAGATCGATCGCGTCGAGAGCTGCAAGAGCGGCGCTGCCCGCGAGCGCAATAC 1357

QY 40 GluMetLeuLysArgTrpArgGlnGlnPro-----AlaGlyLeuGlyAlaVala 56
Db 1358 AGCATGCTGGCGACCTGGAAGCGGCGACCGCGCGAGCGCACGCTGAGACCTGCTG 1417

QY 57 TyralalaleuGluaArgMetGlyLeuaspGlyCysValaGluaPleuArgSerArgLeu 76

Db 1418 GGACGGCTGCTCCGACATGAGACCTGCTGGGCTGCGAGGACATCGAGAGCGCCTT 1477

RESULT 9
US-08-465-982-24
Sequence 24, Application US/08465982
Patent No. 5863786
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,982
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319
FILING DATE: 10-May-1993
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2062 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 155..1519
US-08-465-982-24

Alignment Scores:
Pred. No.: 4.62e-12 Length: 2062
Score: 158.00 Matches: 36
Percent Similarity: 61.25% Conservative: 13
Best Local Similarity: 45.00% Mismatches: 27
Query Match: 38.26% Indels: 4
Gaps: 2

US-09-993-234-6_COPY_338_417 (1-80) x US-08-465-982-24 (1-2062)

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Db 1238 GTGGTGGAGAACGTCGCCCGCTGGAGGAATTCGTGGCGCCCTGAGGCTGAGC 1297

QY 21 GluaIaGluIleGluAlaValaGluValaGluIleGlyArg---PheArgSPGInGlnTyr 39
Db 1298 GACCACAGAGATCGATCGCGTCGAGAGCTGCAAGAGCGGCGCTGCCCGCGAGCGCAATAC 1357

QY 40 GluMetLeuLysArgTrpArgGlnGlnPro-----AlaGlyLeuGlyAlaVala 56
Db 1358 AGCATGCTGGCGACCTGGAAGCGGCGACCGCGCGAGCGCACGCTGAGACCTGCTG 1417

QY 57 TyralalaleuGluaArgMetGlyLeuaspGlyCysValaGluaPleuArgSerArgLeu 76

Db 1418 GGACGCGTCTCCGGACATGAGCCTGCTGCTGAGAGACATCGAGAGCGCTT 1477
RESULT 10
US-09-106-038A-1
Sequence 1, Application US/09106038A
Patent No. 6007995
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker and Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Isis Pharmaceuticals, Inc.
STREET: 2292 Faraday Avenue
CITY: Carlsbad
STATE: CA
COUNTRY: U.S.A.
ZIP: 92008
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,038A
FILING DATE: June 26, 1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Laurel Spear Bernstein
REGISTRATION NUMBER: 37,280
REFERENCE/DOCKET NUMBER: RFS-0004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (760) 931-9200
TELEFAX: (760) 603-3820
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2161
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-106-038A-1
Alignment Scores:
Pred. No.: 4.91e-12 Length: 2161
Score: 158.00 Matches: 36
Percent Similarity: 61.25% Conservative: 13
Best Local Similarity: 45.00% Mismatches: 27
Query Match: 38.26% Indels: 4
Gaps: 2
US-09-993-234-6_COPY_338_417 (1-80) x US-09-106-038A-1 (1-2161)
QY 1 ValmetaspAlaValProAlaArgTrpIlyGluPheValArgThrLeuGlyLeuArg 20
Db 1339 GTGGTGAGAGACGTCCTCCCGCTGGAGAGAAATTCGTGGCGCTGAGCGCTGAGC 1398
QY 21 GluAlaGluIleGluAlaValAlaGluIleGlyArg---PheArgSpGlnGlnTyr 39
Db 1399 GACCAAGAGATGATGCTGAGCTGAGCGGAGAGAGGCGCTGCTGCGCAGCGCAATTC 1458
QY 40 GluMetLeuLysArgTrpArgGlnGlnInPro-----AlaGlyLeuGlyAlaVal 56
Db 1459 AGCATGCTGGCGACCTGGAGGGGCGCAGCGCGGAGAGCCACGCTGAGCTGCTG 1518
QY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
Db 1519 GGACCGCTGCTCCGGACATGAGCCTGCTGCTGAGAGACATCGAGAGCGCTT 1578
RESULT 11
US-09-505-250-3
Sequence 3, Application US/09505250A
Patent No. 6329148

GENERAL INFORMATION:
APPLICANT: Rosen, Glenn
APPLICANT: Kao, Peter
TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
Triptolides and Death Domain Ligands
FILE REFERENCE: SUN-109PRV2
CURRENT APPLICATION NUMBER: US/09/505,250A
CURRENT FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 3
LENGTH: 2161
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (256)...(1623)
US-09-505-250-3
Alignment Scores:
Pred. No.: 4.91e-12 Length: 2161
Score: 158.00 Matches: 36
Percent Similarity: 61.25% Conservative: 13
Best Local Similarity: 45.00% Mismatches: 27
Query Match: 38.26% Indels: 4
Gaps: 2
US-09-993-234-6_COPY_338_417 (1-80) x US-09-505-250-3 (1-2161)
QY 1 ValmetaspAlaValProAlaArgTrpIlyGluPheValArgThrLeuGlyLeuArg 20
Db 1339 GTGGTGAGAGACGTCCTCCCGCTGGAGAGAAATTCGTGGCGCTGAGCGCTGAGC 1398
QY 21 GluAlaGluIleGluAlaValAlaGluIleGlyArg---PheArgSpGlnGlnTyr 39
Db 1399 GACCAAGAGATGATGCTGAGCTGAGCGGAGAGAGGCGCTGCTGCGCAGCGCAATTC 1458
QY 40 GluMetLeuLysArgTrpArgGlnGlnInPro-----AlaGlyLeuGlyAlaVal 56
Db 1459 AGCATGCTGGCGACCTGGAGGGGCGCAGCGCGGAGAGCCACGCTGAGCTGCTG 1518
QY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
Db 1519 GGACCGCTGCTCCGGACATGAGCCTGCTGCTGAGAGACATCGAGAGCGCTT 1578
RESULT 12
US-08-321-668-1
Sequence 1, Application US/08321668
Patent No. 5665859
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSH, Cord
APPLICANT: VARELOMEY, Eugene
APPLICANT: BARKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWNE AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,668
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435

STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,016
FILING DATE: 24-SEP-1993
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/625668
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1620
NAME/KEY: mat_peptide
LOCATION: 319..1620
US-08-126-016-1

Alignment Scores:
Pred. No.: 4,95e-12 Length: 2175
Score: 158.00 Matches: 36
Percent Similarity: 61.25% Conservative: 13
Best Local Similarity: 45.00% Mismatches: 27
Query Match: 38.26% Indels: 4
DB: 1 Gaps: 2

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QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39
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Db 1399 GACCAAGAGATGATCGGCTGAGAGCTGCAGAACGGGGCTGCGCGCGAGGGCGCAATAC 1458
QY 40 GluMetLeuLysArgTrpArgGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
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Db 1459 AGCATGCTGGCGAGCTGAGGGCGGCGACGCGCGCGAGCGCCAGCTGAGAGCTGCTG 1518
QY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
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Db 1519 GGACGCGTCTCGCGACATGAGCTGCTGCGCTGCGAGGACATCGAGAGGCGCTT 1578

RESULT 15
US-08-054-970-1
Sequence 1, Application US/08054970
Patent No. 6395267
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/054,970
FILING DATE: 03-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1620
US-08-054-970-1

Alignment Scores:
Pred. No.: 4,95e-12 Length: 2175
Score: 158.00 Matches: 36
Percent Similarity: 61.25% Conservative: 13
Best Local Similarity: 45.00% Mismatches: 27
Query Match: 38.26% Indels: 4
DB: 1 Gaps: 2

US-09-993-234-6_COPY_338_417 (1-80) x US-08-054-970-1 (1-2175)

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Db 1339 GTGGTGAAGAACGTGCCCCGCTGCGCTGAAGAAATTCGTGCGCGCTAGGGCTGAGC 1398
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39
|||||
Db 1399 GACCAAGAGATGATCGGCTGAGAGCTGCAGAACGGGGCTGCGCGCGAGGGCGCAATAC 1458
QY 40 GluMetLeuLysArgTrpArgGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
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Db 1459 AGCATGCTGGCGAGCTGAGGGCGGCGACGCGCGCGAGCGCCAGCTGAGAGCTGCTG 1518
QY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
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Db 1519 GGACGCGTCTCGCGACATGAGCTGCTGCGCTGCGAGGACATCGAGAGGCGCTT 1578

Search completed: April 6, 2003, 23:29:52
Job time: 19.5049 secs

GenCore version 5.1.4-p5.4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 21:08:18 ; Search time 30.4618 Seconds

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Perfect score: 413
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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
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Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

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12: /cg2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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14: /cg2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match Length	DB ID	Description
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2	413 100.0	1634 9	US-10-081-780-9 Sequence 9, Appl1
3	413 100.0	1634 9	US-10-112-793-9 Sequence 9, Appl1
4	413 100.0	1634 9	US-10-112-193-11 Sequence 11, Appl1

5	413 100.0	1634 10	US-09-993-234-9 Sequence 9, Appl1
6	413 100.0	1783 10	US-09-333-966-1 Sequence 1, Appl1
7	413 100.0	10797 9	US-10-092-154-1577 Sequence 1577, Ap
8	413 100.0	10797 10	US-09-764-847-1577 Sequence 1577, Ap
9	401 97.1	1743 9	US-09-954-531-1389 Sequence 1389, Ap
10	171 41.4	2130 10	US-09-917-800A-1601 Sequence 1601, Ap
11	171 41.4	2173 9	US-09-898-234-14 Sequence 14, Appl
12	171 41.4	2173 9	US-09-898-429A-24 Sequence 24, Appl
13	171 41.4	2173 10	US-09-792-356-14 Sequence 14, Appl
14	171 41.4	2173 10	US-09-899-422-14 Sequence 14, Appl
15	163 39.5	2440 10	US-09-970-532-1 Sequence 1, Appl1
16	158 38.3	427 10	US-09-876-889-236 Sequence 236, App
17	158 38.3	479 9	US-10-043-487-100 Sequence 100, App
18	158 38.3	1368 9	US-09-898-234-1 Sequence 1, Appl1
19	158 38.3	1368 9	US-09-899-429A-1 Sequence 1, Appl1
20	158 38.3	1368 9	US-09-792-356-1 Sequence 1, Appl1
21	158 38.3	1368 10	US-09-899-422-1 Sequence 1, Appl1
22	158 38.3	2111 10	US-09-880-107-2360 Sequence 2360, Ap
23	158 38.3	2141 9	US-09-898-234-16 Sequence 24, Appl
24	158 38.3	2141 9	US-09-899-429A-26 Sequence 26, Appl
25	158 38.3	2141 9	US-09-792-356-16 Sequence 16, Appl
26	158 38.3	2141 10	US-09-899-422-16 Sequence 16, Appl
27	158 38.3	2175 12	US-10-120-397-1 Sequence 1, Appl1
28	94 22.8	1062 8	US-08-916-625B-3 Sequence 3, Appl1
29	94 22.8	1236 9	US-10-076-754-1 Sequence 1, Appl1
30	94 22.8	1236 9	US-10-076-754-1 Sequence 1, Appl1
31	94 22.8	1236 12	US-10-067-615-1 Sequence 1, Appl1
32	94 22.8	1600 10	US-09-874-138-1 Sequence 1, Appl1
33	94 22.8	1600 12	US-10-005-842-1 Sequence 1, Appl1
34	94 22.8	1799 9	US-09-992-964-10 Sequence 10, Appl1
35	94 22.8	1799 10	US-09-828-739-1 Sequence 10, Appl1
36	94 22.8	1799 10	US-09-887-879-10 Sequence 10, Appl1
37	94 22.8	1799 12	US-10-052-798-2 Sequence 2, Appl1
38	94 22.8	3881 8	US-08-916-625B-1 Sequence 1, Appl1
39	94 22.8	3964 9	US-09-811-088-5 Sequence 5, Appl1
40	94 22.8	3964 10	US-09-757-421-3 Sequence 3, Appl1
41	94 22.8	4051 9	US-09-811-088-3 Sequence 3, Appl1
42	94 22.8	4051 10	US-09-757-421-1 Sequence 1, Appl1
43	77 18.6	2040 9	US-09-991-496-5 Sequence 5, Appl1
44	77 18.6	2040 10	US-09-874-923-5 Sequence 5, Appl1
45	77 18.6	4233 9	US-09-991-496-99 Sequence 99, Appl1

ALIGNMENTS

RESULT 1
US-09-333-966-3
Sequence 3, Application US/093333966
Patent No. US20020009773A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Retner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
APPLICATION NUMBER: NO. US2002009773A1 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-09-333-966-3

Alignment Scores:
Pred. No.: 7,46e-50 Length: 1254
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x US-09-333-966-3 (1-1254)

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DB 1012 GTGATGAGCGCGGTCCACGCGCGCGCTGGAGAGATTGTGTGCGACGCTGGGCGTGGC 1071
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlyGlu 40
|||||
DB 1072 GAGCGAGATCGAACCGCTGGAGGTGGAGATCGCGCTTCGAGACACGAGTACGAG 1131
QY 41 MetLeuLysArgTrpArgGlnGlnInpProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
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DB 1132 ATGCTCAAGCGGTGGCGCAGCAGACGCCGCGGCTCGGAGCCGTTTACGCGGCCCTG 1191
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
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DB 1192 GAGCGCATGGGCTGGACGCGCTGCGAAGACTTCGACGCCGCTGACGCGGCCCGC 1251

RESULT 2
US-10-081-280-9
Sequence 9, Application US/10081280
Patent No. US2002016517A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-081-280-9

Alignment Scores:
Pred. No.: 1.02e-49 Length: 1634
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x US-10-081-280-9 (1-1634)

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DB 1100 GTGATGAGCGCGGTCCACGCGCGCGCTGGAGAGATTGTGTGCGACGCTGGGCGTGGC 1159
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlyGlu 40
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DB 1160 GAGCGAGATCGAACCGCTGGAGGTGGAGATCGCGCTTCGAGACACGAGTACGAG 1219
QY 41 MetLeuLysArgTrpArgGlnGlnInpProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
DB 1220 ATGCTCAAGCGGTGGCGCAGCAGACGCCGCGGCTCGGAGCCGTTTACGCGGCCCTG 1279
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
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DB 1280 GAGCGCATGGGCTGGACGCGCTGCGAAGACTTCGACGCCGCTGACGCGGCCCGC 1339

RESULT 3
US-10-112-793-9
Sequence 9, Application US/10112793
Publication No. US20020192729A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-112-793-9

Alignment Scores:
Pred. No.: 1,02e-49 Length: 1634
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x US-10-112-793-9 (1-1634)
QY 1 ValmetaspalaValProAlaArGArGTTrpLysGluPheValArGThrLeuGlyLeuArg 20
DB 1100 GTGATGAGCGCGGTCCAGCGCGCGCTGGAGAGATTCTGCGCGCAGCGTGGCGTGC 1159
QY 21 GluAlaGluIleGluAlaValAlGluValGluIleGlyArgPheArgAspGlnGlyTyrGlu 40
DB 1160 GAGCAGAGATCGAAGCCGTGGAGGTGAGATCGCGCTTCCAGACACAGCATACGAG 1219
QY 41 MetLeuysArGTTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
DB 1220 ATGCTCAAGCGCTGGCCGACGACAGCCCGCGGCTCGAGCCGTTTACGCGGCCCTG 1279
QY 61 GluArgMetGlyLeuAspGlyCysValAlGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1280 GAGCGCATGGGCGTGGAGCGGTGCGTGGAGACTTGGCGACGCCGCTGACGCGGCCG 1339

RESULT 4
US-10-112-193-11
Sequence 11, Application US/10112193
Publication No. US20030004313A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,193
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,069
FILING DATE: 11-Sep-1997
APPLICATION NUMBER: 60/026943
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-112-193-11

Alignment Scores:
Pred. No.: 1,02e-49 Length: 1634
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x US-10-112-193-11 (1-1634)
QY 1 ValmetaspalaValProAlaArGArGTTrpLysGluPheValArGThrLeuGlyLeuArg 20
DB 1100 GTGATGAGCGCGGTCCAGCGCGCGCTGGAGAGATTCTGCGCGCAGCGTGGCGTGC 1159
QY 21 GluAlaGluIleGluAlaValAlGluValGluIleGlyArgPheArgAspGlnGlyTyrGlu 40
DB 1160 GAGCAGAGATCGAAGCCGTGGAGGTGAGATCGCGCTTCCAGACACAGCATACGAG 1219
QY 41 MetLeuysArGTTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
DB 1220 ATGCTCAAGCGCTGGCCGACGACAGCCCGCGGCTCGAGCCGTTTACGCGGCCCTG 1279
QY 61 GluArgMetGlyLeuAspGlyCysValAlGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1280 GAGCGCATGGGCGTGGAGCGGTGCGTGGAGACTTGGCGACGCCGCTGACGCGGCCG 1339

RESULT 5
US-09-993-234-9
Sequence 9, Application US/09993234
Patent No. US20020146768A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/993,234

```

FILING DATE: 19-NOV-2001 US20020146768A1-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,683
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-993-234-9

Alignment Scores:
Pred. No.: 1,028-49 Length: 1634
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 10

US-09-993-234-6_COPY_338_417 (1-80) x US-09-993-234-9 (1-1634)
QY 1 ValMetaspalaValProlaaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1100 GTGATGAGGAGCGGCTCCACGCGGCGCTGGAAGAGATTGTCGCGACGCTGGGGCGCGCC 1159
QY 21 GUUAGUUGUUGUUAUAGUUAUAGUUAUAGUUAUAGUUAUAGUUAUAGUUAUAGUUAUAG 40
DB 1160 GAGGAGAGATCGAAGCGCTGAGGAGATCGGCGCTCCGAGACCGACGAGTACGAG 1219
QY 41 MetLeuValArgTrpArgGlnGlnProAlaGlyLeuGlyValAlaValTyrAlaAlaLeu 60
DB 1220 ATGCTCAAGCGCTGGGCGGAGCGACGCGGCGCTCGAGCGCTTTACCGGCGCTG 1279
QY 61 GUATGMeGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1280 GAGCGATGGGCTGAGCGGCTGCGTGGAGAACTTGGCGACGCGCTGACGCGGCGCCG 1339

RESULT 6
US-09-333-966-1
Sequence 1, Application US/09333966
Patent No. US20020009773A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
SEQ ID NO 1577

APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
APPLICATION NUMBER: No. US20020009773A1 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 198..1481
US-09-333-966-1

Alignment Scores:
Pred. No.: 1,148-49 Length: 1783
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 10

US-09-993-234-6_COPY_338_417 (1-80) x US-09-333-966-1 (1-1783)
QY 1 ValMetaspalaValProlaaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1242 GTGATGAGGAGCGGCTCCACGCGGCGCTGGAAGAGATTGTCGCGACGCTGGGGCGCGCC 1301
QY 21 GUUAGUUGUUGUUAUAGUUAUAGUUAUAGUUAUAGUUAUAGUUAUAGUUAUAGUUAUAG 40
DB 1302 GAGGAGAGATCGAAGCGCTGAGGAGATCGGCGCTCCGAGACCGACGAGTACGAG 1361
QY 41 MetLeuValArgTrpArgGlnGlnProAlaGlyLeuGlyValAlaValTyrAlaAlaLeu 60
DB 1362 ATGCTCAAGCGCTGGGCGGAGCGACGCGGCGCTCGAGCGCTTTACCGGCGCTG 1421
QY 61 GUATGMeGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1422 GAGCGATGGGCTGAGCGGCTGCGTGGAGAACTTGGCGACGCGCTGACGCGGCGCCG 1481

RESULT 7
US-10-092-154-1577
Sequence 1577, Application US/10092154
Publication No. US20030054375A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC00901
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1577

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; LENGTH: 10797
;
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1577

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Alignment Scores:	
Pred. No.:	9.88e-49
Score:	413.00
Percent Similarity:	100.00%
Best local Similarity:	100.00%
Query Match:	100.00%
DB:	9
Length:	1079
Matches:	80
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-993-234-6_COPY_338_417 (1-80) x US-10-092-154-1577 (1-10797)

Qy	1	ValMetSerPheValAlaProAlaLeuGArgTrpLysGluPheValArgThrLeuLysLeuArg	20
Db	9119	GTATGTGACCGCGGTCCACGCGCGCGCTGGAGAGATTGTGTGCACCTGGGGCTGGCC	9178
Qy	21	GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTrpGlu	40
Db	9179	GAGCAGAGATCCAGAACGGCTGTGAGGTGGAGATCGCGCTTCGAGACAGCAGTAGACAG	9238
Qy	41	MetLeuLysArgTrpArgGlnGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu	60
Db	9239	ATGCTCAAGCGCTGGCGCCACGACGACCCCGGGGCGTCTGGAGCCGTTACCGCGCCCTG	9298
Qy	61	GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyTrp	80
Db	9299	GAGCGCATGGGGCTGCAGCGCTCTCGTGGAGACTTTCGACGCGCGCTGCAGCGCGCCG	9358

RESULT 8
US-09-764-847-1577
; Sequence 1577, Application US/09764847

Alignment Scores:	
Pred. No.:	9.88e-49
Score:	413.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	10
Length:	1079
Matches:	80
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-993-234-6_COPY_338_417 (1-80) x US-09-764-847-1577 (1-10797)

QY	1	ValMetSerAspIaValProAlaArGArGTTPlysGluPheValArgThrLeuGlyLeuArg	20
Db	9119	GTGTGGAGCCGGGTCCCGAGGGGGCCCTGAAAGAGATTCTGCGACCGTGGGGCTGGGC	9178
QY	21	GluAlaGluIleGluIaValGluValGluIleGlyArgPheArgAspGlnIleArgGlu	40
Db	9179	GAGGCACAGATCCAGACCCGGTGGAGGTGGAGATCGCCGCTTCGAGACCAGCAGTACAG	9238
QY	41	MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrIleAlaIleu	60
Db	9239	ATGCTCAAGCGGTGGGGCCAGCAGCAGCCGGGGGGCTCTGGAGCGGTTCACGGGGCCCTG	9298
QY	61	GluArgMetIleuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro	80

D**b** 9299 GAGCGCATGGGCTGTGCACGCTCTGTGGAAAGATTTCGCCAGCCGCGCCTTGACAGCGGGCCCCG 9356
 |||||

RESU**L**T 9
US-09-954-531-1389
; Sequence 1389 Application US/09954531
; Patent No. US20020165180A1

Alignment Scores:	
Pred. No.:	5.72e-48
Score:	401.00
Percent Similarity:	97.508
Best Local Similarity:	97.508
Query Match:	97.098
DB:	9
Length:	1743
Matches:	78
Conservative:	0
Mismatches:	2
Indels:	0
Gaps:	0

US-09-993-234-6_COPY_338_417 (1-80) x US-09-954-531-1389 (1-1743)

OY	1	ValMetAspAlaValProAlaAlaGATGATGTPPLysGluPheValArgThrIleuGlyLeuArg	20
Db	1181	GTAATGAGACCGCGTCCACGCGCGCGCTGAGMAGATTCTGTGGCACGCTGGGGCTGGCC	1240
OY	21	GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIleuArgIu	40
Db	1241	GAGCAGACAGATCGAAGCGCGTGGAGGTGGAGATCGTCTCTCCGAGACACGACAGATRCAG	1300
OY	41	MetLeuLysArgTTPParGlnGlnGlnIleProAlaGlyLeuGlyValAlaValIrrAlaAlaLeu	60
Db	1301	ATGCTCAAGACACTGGCGCCACGACAGACGCCGCGCGGCTCGAGACCGATTACCGCGGCTCG	1360
OY	61	GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgIleuGlnIleArgIlePro	80
Db	1361	GAGGCCATGGGGCTGGACCGGCTCGTGGAGAACTTTCGACGCCGCTCGAGGTGGCCCG	1420

RESULT 10
US-09-917-800A-1601
Sequence 1601, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1601
LENGTH: 2130
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_013091
US-09-917-800A-1601

Alignment Scores:
Pred. No.: 5,02e-15 Length: 2130
Score: 171.00 Matches: 38
Percent Similarity: 62.96% Conservative: 13
Best Local Similarity: 46.91% Mismatches: 26
Query Match: 41.40% Indels: 4
Gaps: 2

US-09-993-234-6_COPY_338_417 (1-80) x US-09-917-800A-1601 (1-2130)

QY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1342 GTGGTGAGAGCGGTGCGTCCGACAGCGCTGGAAGAGTTTCATCGCTCGGGGTGAGC 1401
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTrp 39
DB 1402 GAGCGACAGATGAGCGCTGAGCTGCGAAGCGGCGTTCCTCGCGAGGCTCATTTAC 1461
QY 40 GluMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
DB 1462 ACCATGCTGGAAGCCTGGGCGCGCGACACCGCGACAGAGCGCGCTGAGCTAGTG 1521
QY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
DB 1522 GCCCGCGCTTTGGACATGAACCTGCGTGCCTGAGAGAACATCCGCGAGACTCTTA 1581
QY 77 Gln 77
DB 1582 GAA 1584

RESULT 11
US-09-898-234-14
Sequence 14, Application US/09898234
Patent No. US20020155112A1
GENERAL INFORMATION:
APPLICANT: Hauptmann, Rudolph
APPLICANT: Himmler, Adolf
APPLICANT: Maurer-Fogy, Ingrid
APPLICANT: Stralow, Christian
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
FILE REFERENCE: 98,385-I
CURRENT APPLICATION NUMBER: US/09/898,234
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 09/525,998

PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 08/383,676
PRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR FILING DATE: 1992-01-02
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 2173
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (245)..(1630)
OTHER INFORMATION: Description of Artificial Sequence: ratNF-R8
US-09-898-234-14

Alignment Scores:
Pred. No.: 5,14e-15 Length: 2173
Score: 171.00 Matches: 38
Percent Similarity: 62.96% Conservative: 13
Best Local Similarity: 46.91% Mismatches: 26
Query Match: 41.40% Indels: 4
Gaps: 2

US-09-993-234-6_COPY_338_417 (1-80) x US-09-898-234-14 (1-2173)

QY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1349 GTGGTGAGAGCGGTGCGTCCGACAGCGCTGGAAGAGTTTCATCGCTCGGGGTGAGC 1408
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTrp 39
DB 1409 GAGCAGAGATGAGCGGTGAGCTGCGAAGCGGCGTTCCTCGCGAGGCTCATTTAC 1468
QY 40 GluMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
DB 1469 ACCATGCTGGAAGCCTGGGCGCGCGACACCGCGACAGAGCGCGCTGAGCTAGTG 1528
QY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
DB 1529 GCCCGCGCTTTGGACATGAACCTGCGTGCCTGAGAGAACATCCGCGAGACTCTTA 1588
QY 77 Gln 77
DB 1589 GAA 1591

RESULT 12
US-09-899-429A-24
Sequence 24, Application US/09899429A
Patent No. US20020169118A1
GENERAL INFORMATION:
APPLICANT: Hauptmann, Rudolph
APPLICANT: Himmler, Adolf
APPLICANT: Maurer-Fogy, Ingrid
APPLICANT: Stralow, Christian
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
FILE REFERENCE: 98-385-J
CURRENT APPLICATION NUMBER: US/09/899,429A
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 09/792,356
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 08/477,639
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/383,676
PRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17

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; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 24
; LENGTH: 2173
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ratTNF-R8
; NAME/KEY: CDS
; LOCATION: (245)..(1627)
; US-09-899-429A-24

Alignment Scores:
Pred. No.: 5,14e-15 Length: 2173
Score: 171.00 Matches: 38
Percent Similarity: 62.96% Conservative: 13
Best Local Similarity: 46.91% Mismatches: 26
Query Match: 41.40% Indels: 4
Caps: 2

US-09-993-234-6_COPY_338_417 (1-80) x US-09-899-429A-24 (1-2173)
OY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db 1349 GTGGTGGATGCGCGCTCCGACACACCGCTGGAGAGATTCAATCGCGCTCGGCTGAGC 1408
OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39
Db 1409 GAGCAGCAGATCGAGCGCTGGAGCTGCAGAACGGCGCTGCTCCCGCAGAGCTCATTTAC 1468
OY 40 GluMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
Db 1469 AGCATGCTGGAGAGCTGGCGGCGCGCACACCGCGACACGAGCGCTGAGCTAGTGTG 1528
OY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
Db 1529 GCCCGCGCTGCTTGGCAGATGAACTGCGTGGCTGCTGGAGAACATCCGCGAGACTCTA 1588
OY 77 Gln 77
Db 1589 GAA 1591

RESULT 13
US-09-792-356-14
; Sequence 14, Application US/09792356
; Publication No. US20020183485A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stralow, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE OF INVENTION: Them
; FILE REFERENCE: 98,385-G
; CURRENT APPLICATION NUMBER: US/09/792,356
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
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; LENGTH: 2173
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (245)..(1630)
; OTHER INFORMATION: Description of Artificial Sequence: ratTNF-R8
; US-09-792-356-14

Alignment Scores:
Pred. No.: 5,14e-15 Length: 2173
Score: 171.00 Matches: 38
Percent Similarity: 62.96% Conservative: 13
Best Local Similarity: 46.91% Mismatches: 26
Query Match: 41.40% Indels: 4
Caps: 2

US-09-993-234-6_COPY_338_417 (1-80) x US-09-792-356-14 (1-2173)
OY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db 1349 GTGGTGGATGCGCGCTCCGACACACCGCTGGAGAGATTCAATCGCGCTCGGCTGAGC 1408
OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39
Db 1409 GAGCAGCAGATCGAGCGCTGGAGCTGCAGAACGGCGCTGCTCCCGCAGAGCTCATTTAC 1468
OY 40 GluMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
Db 1469 AGCATGCTGGAGAGCTGGCGGCGCGCACACCGCGACACGAGCGCTGAGCTAGTGTG 1528
OY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
Db 1529 GCCCGCGCTGCTTGGCAGATGAACTGCGTGGCTGCTGGAGAACATCCGCGAGACTCTA 1588
OY 77 Gln 77
Db 1589 GAA 1591

RESULT 14
US-09-899-422-14
; Sequence 14, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stralow, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE OF INVENTION: Them
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 2173
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (245)..(1630)
; OTHER INFORMATION: Description of Artificial Sequence: ratTNF-R8
```

US-09-899-422-14

Alignment Scores:

Pred. No.: 5,14e-15 Length: 2173

Score: 171.00 Matches: 38

Percent Similarity: 62.968 Conservative: 13

Best Local Similarity: 46.918 Mismatches: 26

Query Match: 41.404 Indels: 4

DB: 10 Gaps: 2

US-09-993-234-6_COPY_338_417 (1-80) x US-09-899-422-14 (1-2173)

QY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20

DB 1349 GTGGTGAATGGCTGCTCGACATGACGCGCGCCGACACGCGCGCTGCTCGCGGAGCTCATTTAC 1408

QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39

DB 1409 GAGCAGACGAGTGCAGGCTGGAGCTGCAGACGAGGCGGTTCCTCCGCGAGGCTCATTTAC 1468

QY 40 GluMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56

DB 1469 AGCATGCTGGAACCTCGCGCGCGCGCCGACACCGCGACAGCGCCACGCTGAGAGTAGTG 1528

QY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76

DB 1529 GCGCGGCTGCTTGCAGATGACATGACCTGCGGTGCTGCTGAGAAACATCCGAGACTCTA 1588

QY 77 Gln 77

DB 1589 GAA 1591

RESULT 15

US-09-970-532-1

; Sequence 1, Application US/0970532

; Patent No. US20020076765A1

; GENERAL INFORMATION:

; APPLICANT: Taylor, J. Michael

; APPLICANT: Kehrl, Jr., Marcus

; APPLICANT: Lee, Eun-Kyung

; APPLICANT: Mwangi, Simon

; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1

; FILE REFERENCE: 08411-018001

; CURRENT APPLICATION NUMBER: US/09/970,532

; PRIOR FILING DATE: 2001-10-03

; PRIOR APPLICATION NUMBER: 09/513,007

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2440

; TYPE: DNA

; ORGANISM: Bos taurus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (294)..(1706)

US-09-970-532-1

Alignment Scores:

Pred. No.: 8.2e-14 Length: 2440

Score: 163.00 Matches: 38

Percent Similarity: 60.00% Conservative: 10

Best Local Similarity: 47.50% Mismatches: 28

Query Match: 39.47% Indels: 4

DB: 10 Gaps: 2

US-09-993-234-6_COPY_338_417 (1-80) x US-09-970-532-1 (1-2440)

QY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20

DB 1425 GTGGTGAATGGCTGCTCGACATGACGCGCGCCGACACGCGCCACGCTGAGAGTAGTG 1484

QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39

DB 1485 GAGCAGACGAGTGCAGGCTGGAGCTGCAGAACGCGCGCCACCTCGCGAGCGGAGTAGTG 1544

QY 40 GluMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56

DB 1545 AGCATGCTGAGCGCTGCGCGCGCGCCGACACCGCGCGGAGGCGCGCTGAGAGTAGTG 1604

QY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76

DB 1605 GCGCGGCTGCTCGAGGACATGACCTGCTGCTGAGAAACATPAGAGAGGCGCTG 1664

Search completed: April 7, 2003, 03:58:57
Job time: 41.4618 secs

GenCore version 5.1.4.p5-4578
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 6, 2003, 16:19:54 ; Search time 500.409 Seconds
(without alignments)
2589.161 Million cell updates/sec

Title: US-09-993-234-6_COPY_338_417
Perfect score: 413
Sequence: 1 YMDAVPARMKKEFVRTIGLR.....ERMGIDGVEDLSRLQSGP 80

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+pn.model
-O/cgn2.1/USPFO-SPOL/US0999234/runat_27032003_115456_15362/app_query.fasta_1.2346
-DB=EST-QFMT-fslap-SOFFIX=1st-MINMATCH=0.1-LOOPCL=0-LOOPEXT=0
-UBITS=bits-START=1-END=1-MATRIX=bloms62-TRANS=human40.cdl-LIST=45
-DOCA=IGN=200-THR_SCORE=pc-THR_MAX=100-THR_MIN=0-ALIGN=15-MODE=LOCAL
-OUTFMT=ptc-NORM=ext-HEAPSIZE=500-MINLEN=0-MAXLEN=2000000000
-USER=US0999234.cgn2.1.4749.crunat_27032003_115456_15362-NCPU=6-ICPU=3
-NO_XLPHY-NO_MMAP-LARGEQUERY-NEG_SCORES=0-WAIT-LONGLOG-DEV_TIMEOUT=120
-WARN_TIMEOUT=30-THREADS=1-XGAPOP=10-XGAPEXT=0.5-FGAPOP=6-FGAPEXT=7
-YAPOP=10-YGAPEXT=0.5-DELOP=6-DELEXT=7

Database : EST: *
1: em_estba: *
2: em_esthum: *
3: em_estlin: *
4: em_estlun: *
5: em_estlov: *
6: em_estlpl: *
7: em_estro: *
8: em_hc: *
9: gb_estl: *
10: gb_estl2: *
11: gb_hc: *
12: gb_estl3: *
13: gb_estl4: *
14: gb_estl5: *
15: em_estlun: *
16: em_estlun: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_luv: *
20: em_gss_pin: *
21: em_gss_vit: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rtd: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413	100.0	510	14	BM695193
2	413	100.0	550	13	BM666370
3	413	100.0	687	10	BE670189
4	406	98.3	618	10	AM074008
5	399	96.6	587	9	AI380959
6	399	95.9	623	9	AI811528
7	396	95.9	289	12	BF655336
8	390	94.4	582	10	AM182875
9	370	89.6	544	9	AI380900
10	365	88.4	439	14	BM824360
11	346	83.8	459	14	BQ027499
12	345	83.5	507	10	AM964958
13	333	80.6	537	9	AI266746
14	332	80.4	647	14	BM794760
15	328	79.4	633	10	BB212432
16	320	77.5	523	12	BF552058
17	300	72.6	523	14	W71984
18	295	71.4	539	12	BF726557
19	276	66.8	681	10	BE563566
20	259.5	62.8	739	9	AA524052
21	254	61.5	433	10	AW134494
22	246.5	59.7	605	9	AI913906
23	242	58.6	292	9	AA088350
24	232	56.2	437	10	AA92480
25	210	50.8	348	9	AI703436
26	191	46.2	651	13	BM009354
27	175.5	42.5	530	10	BE014705
28	175	42.4	556	9	AA887388
29	167.5	40.6	619	10	BE334962
30	167.5	40.6	789	12	BF138948
31	167.5	40.6	853	13	BI525375
32	160.5	38.9	506	12	BF118096
33	160	38.7	378	9	AA631757
34	159	38.7	582	10	AA555430
35	159	38.5	414	9	AA088232
36	158	38.3	504	13	BI468367
37	158	38.3	591	14	BM694442
38	158	38.3	620	14	BM676536
39	158	38.3	636	12	BG035257
40	158	38.3	669	14	BM742388
41	158	38.3	889	9	AU117362
42	158	38.3	894	14	BO880824
43	158	38.3	923	14	BQ228387
44	158	38.3	1055	13	BM555065
45	158	38.3	1076	14	BM923204

ALIGNMENTS

RESULT 1
LOCUS BM695193 510 bp mRNA linear EST 28-FEB-2002
DEFINITION UT-E-COI-aey-1-03-0-UT-rl UT-E-COI Homo sapiens cDNA clone
ACCESSION BM695193
VERSION BM695193.1 GI:19008451
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 510)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL
MEDLINE
COMMENT

discovery
Genome Res. 6 (9), 791-806 (1996)
9704447
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@iue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.

FEATURES
SOURCE

Location/Qualifiers
1..510
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-COI-aev-1-03-0-UI"
/clone_lib="UI-E-COI"
/tissue_type="optic nerve"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-COI is a normalized cDNA library containing the following tissue(s): optic nerve. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCATTAGTG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 100 a 152 c 170 g 88 t

ORIGIN

Alignment Scores:

Pred. No.: 4.75e-43 Length: 510
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x BM695193 (1-510)

QY 1 ValMetAspAlaValProAlaArgArgTrpPheValArgThrLeuGlyLeuArg 20
Db 1 GGTATGGAGCGGGCTCCAGCGCGGTGGAGGAGTTCGTCCGACCGCTGGCGTGC 60
QY 21 GUAAGAGUUGGUAUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 40
Db 61 GAGGAGAGATGAGAGCGGTGGAGATGAGATGAGATGAGATGAGATGAGATGAG 120
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaLeu 60
Db 121 ATGCTCAAGCGCTGGCGCAGACAGACCGCGGCGCTGGAGCGCTTACCGCGCTG 180
QY 61 GUAAGAGUUGGUAUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 80
Db 181 GAGGAGAGATGAGAGCGGTGGAGATGAGATGAGATGAGATGAGATGAGATGAG 240

RESULT 2
BM66370/c

LOCUS BM66370 550 bp mRNA linear EST 27-FEB-2002
DEFINITION UI-E-COI-aev-1-03-0-UI-s1 UI-E-COI Homo sapiens cDNA clone
ACCESSION UI-E-COI-aev-1-03-0-UI 3', mRNA sequence.
VERSION BM66370
KEYWORDS BM66370.1 GI:18974007
SOURCE EST.
ORGANISM human.

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 550)
TITLE Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalizaton and subtracction: two approaches to facilitate gene
discovery

JOURNAL
MEDLINE
COMMENT

Genome Res. 6 (9), 791-806 (1996)
9704447
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@iue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-37, >POLY_A\$Simple_repeat (matched complement)
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
SOURCE

Location/Qualifiers
1..550
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-COI-aev-1-03-0-UI"
/clone_lib="UI-E-COI"
/tissue_type="optic nerve"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-COI is a normalized cDNA library containing the following tissue(s): optic nerve. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCATTAGTG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
TAG_LIB=UI-E-COI
TAG_TISSUE=human optic nerve
TAG_SEQ=CCATTAGTG"

BASE COUNT 90 a 175 c 156 g 129 t

ORIGIN

Alignment Scores:
Pred. No.: 5.3e-43 Length: 550
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x BM66370 (1-550)

QY 1 ValmetaspalaValProalAargArgrTprlysgluPheValargThrleuglyLeuarg 20
 DB 539 GTGATGACGCGGTCCAGCGCGGTGGAGAGATTCCGCGACAGCTGGGCTGGCG 480
 QY 21 GluaIaIuIleGluAlaValaGluValaGluIleGlyArgrPheargAspGlnGlnTyrGlu 40
 DB 479 GAGCAGACAGTCCAGACCGCTGGAGGTGAGATCGCCGCTTCGAGACACAGCAGTACGAG 420
 QY 41 MetleuysArgrTprArgrGlnGlnGlnProalAglLeuglyAlaValaTyrAlaAlaLeu 60
 DB 419 ATGCTCAAGCGCTGGCGCCAGCAGACCGCGGCTCGAGCGCTTTACGCGGCCCTG 360
 QY 61 GluarTmetGlyLeuAspGlyCysValaGluAspLeuArgrSerArgrLeuGlnArgGlyPro 80
 DB 359 GAGCGCATGGGGCTGACGCGCTGCTGGAGACTTCGCGACCGCGCTGACGCGGCCG 300
 RESULT 3
 BE670189/c 687 bp mRNA linear EST 08-SEP-2000
 LOCUS 7e31c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284086 3'
 DEFINITION similar to SW:MSL1_HUMAN Q93038 MSL-1 PROTEIN PRECURSOR ;, mRNA
 ACCESSION BE670189 GI:10030730
 VERSION BE670189.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 687)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
 info@imgc.llnl.gov
 Seq primer: -400P from Gibco
 High quality sequence stop: 466.
 FEATURES
 source location/Qualifiers
 1. 687
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3284086"
 /clone_1lb="NCI_CGAP_Lu24"
 /tissue_type="carcinoid"
 /lab_host="DH108"
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; Plasmid DNA from the normalized
 library NCI_CGAP_Lu5 was prepared, and ss circles were
 made in vitro. Following HAP purification, this DNA was
 used as tracer in a subtractive hybridization reaction.
 The driver was PCR-amplified cDNAs from a pool of 5,000
 clones made from the same library (cloneids
 1414920-1417991 and 1520904-1522439). Subtraction by Bento
 Soares and M. Fatima Bonaldo."
 BASE COUNT 111 a 215 c 225 g 134 t 2 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 7.36e-43 Length: 687
 Score: 413.00 Matches: 80
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0
 US-09-993-234-6_copy_338_417 (1-80) x BE670189 (1-687)
 QY 1 ValmetaspalaValProalAargArgrTprlysgluPheValargThrleuglyLeuarg 20
 DB 519 GTGATGACGCGGTCCAGCGCGGTGGAGAGATTCCGCGACAGCTGGGCTGGCG 460
 QY 21 GluaIaIuIleGluAlaValaGluValaGluIleGlyArgrPheargAspGlnGlnTyrGlu 40
 DB 459 GAGCAGACAGTCCAGACCGCTGGAGGTGAGATCGCCGCTTCGAGACACAGCAGTACGAG 400
 QY 41 MetleuysArgrTprArgrGlnGlnGlnProalAglLeuglyAlaValaTyrAlaAlaLeu 60
 DB 399 ATGCTCAAGCGCTGGCGCCAGCAGACCGCGGCTCGAGCGCTTTACGCGGCCCTG 340
 QY 61 GluarTmetGlyLeuAspGlyCysValaGluAspLeuArgrSerArgrLeuGlnArgGlyPro 80
 DB 339 GAGCGCATGGGGCTGACGCGCTGCTGGAGACTTCGCGACCGCGCTGACGCGGCCG 280
 RESULT 4
 AM074008/c 618 bp mRNA linear EST 13-OCT-1999
 LOCUS xb06c09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575504 3'
 DEFINITION similar to TR:000278 000278 LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH
 7. [2] TR:000279 ;, mRNA sequence.
 ACCESSION AM074008 GI:6029006
 VERSION AM074008.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 618)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Chris Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
 Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bdrp/image/image.html
 Seq primer: -400P from Gibco
 High quality sequence stop: 383.
 FEATURES
 source location/Qualifiers
 1. 618
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2575504"
 /clone_1lb="NCI_CGAP_GU1"
 /tissue_type="2 pooled high-grade transitional cell
 tumors"
 /lab_host="DH108"
 /note="Organ: genitourinary tract; Vector: pCMV-SPORE6;
 Site_1: SalI; Site_2: NotI; Cloned unidirectionally.
 Primer: Oligo dT. Library constructed by Life
 Technologies."
 BASE COUNT 110 a 204 c 182 g 120 t 2 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 4.99e-42 Length: 618
 Score: 406.00 Matches: 79
 Percent Similarity: 98.75% Conservative: 0
 Best Local Similarity: 98.75% Mismatches: 1
 Query Match: 98.31% Indels: 0
 DB: 10 Gaps: 0

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OY 1 ValMetaspAlaValProAlaArgTrpLysGluPhValArgThrLeuGlyLeuArg 20
    |||||
DB 516 GTGATGACGCGGCTCCACGCGGCGCTGGAGAGATTGTGCGACGCTGGGCGCGC 457
OY 21 GUUAGUAGUUGUUAUAGUUAUAGUUAUAGUUAUAGUUAUAGUUAUAGUUAUAGU 40
    |||||
DB 456 GAGGACAGATCGAAGCCCTGGAGATCGCGCGCTCCGAGACAGACAGTACGAG 397
OY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValArgAlaLeu 60
    |||||
DB 396 ATGCTCAACGCTGGCGCAGCAGCAGCCGCGGCTGGAGCCCTTACCGCGGCGCTG 337
OY 61 GUATGMeGlyLeuAspLysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
    |||||
DB 336 GAGCGATGGGCTGGAGCGCTGCGGAGAACTTCCGACGCCGCTGCAGCGGCGCCG 277

RESULT 5
AL380959/c 587 bp mRNA linear EST 30-MAR-1999
LOCUS tg18c01.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2109120 3'
DEFINITION similar to TR:000278 000278 LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH
7. [2] TR:000279 ;, mRNA sequence.
ACCESSION AL380959
VERSION AL380959.1 GI:4190801
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 587)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/dbp/image/image.html
Insert length: 1237 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 325.
FEATURES
Source
Location/Qualifiers
1..587
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2109120"
/clone_lib="NCI-CGAP-CLL1"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH10B"
/note="Vector: pRT7D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACATCTGAGTGGAGCGCGCCATGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 99 a 192 c 176 g 120 t
ORIGIN
Alignment Scores: 3.67e-41 Length: 587
Pred. No.: 399.00 Matches: 78
Score:

```

```

Percent Similarity: 97.50% Conservative: 0
Best Local Similarity: 97.50% Mismatches: 2
Query Match: 96.61% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x AI380959 (1-587)
OY 1 ValMetaspAlaValProAlaArgTrpLysGluPhValArgThrLeuGlyLeuArg 20
    |||||
DB 518 GTGATGACGCGCTCCACGCGGCGCTGGAGAGATTGTGCGACGCTGGGCGCTCCG 459
OY 21 GUUAGUAGUUGUUAUAGUUAUAGUUAUAGUUAUAGUUAUAGUUAUAGUUAUAGU 40
    |||||
DB 458 GAGGACAGATCGAAGCCCTGGAGATCGCGCGCTCCGAGACAGACAGTACGAG 399
OY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValArgAlaLeu 60
    |||||
DB 398 ATGCTCAACGCTGGCGCAGCAGCAGCCGCGGCTGGAGCCCTTACCGCGGCGCTG 339
OY 61 GUATGMeGlyLeuAspLysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
    |||||
DB 338 GAGCGATGGGCTGGAGCGCTGCGGAGAACTTCCGACGCCGCTGCAGCGGCGCCG 279

RESULT 6
AI811528/c 623 bp mRNA linear EST 15-DEC-1999
LOCUS tw43h06.x1 NCI CGAP Utl1 Homo sapiens cDNA clone IMAGE:2262491 3'
DEFINITION similar to TR:000278 000278 LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH
7. [2] TR:000279 ;, mRNA sequence.
ACCESSION AI811528
VERSION AI811528.1 GI:5398094
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 623)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/dbp/image/image.html
Insert length: 2337 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 392.
FEATURES
Source
Location/Qualifiers
1..623
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2262491"
/clone_lib="NCI-CGAP-Utl1"
/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"
BASE COUNT 105 a 188 c 199 g 128 t 3 others
ORIGIN
Alignment Scores: 4e-41 Length: 623
Pred. No.: 399.00 Matches: 78
Score:

```

Percent Similarity:	97.50%	Conservative:	0
Best Local Similarity:	97.50%	Mismatches:	2
Query Match:	96.61%	Indels:	0
DB:	9	Gaps:	0

Percent Similarity:	96.25%	Conservative:	1
Best local Similarity:	95.00%	Mismatches:	0
Query Match:	94.43%	Indels:	0
DB:	10	Gaps:	0

BASE COUNT (1990), Cancer Res 50: 2773-2780.
 76 a 148 c 150 g 65 t

Alignment Scores:

Pred. No.: 5,56e-37 Length: 439
 Score: 365.00 Matches: 70
 Percent Similarity: 91.25% Conservative: 3
 Best Local Similarity: 87.50% Mismatches: 7
 Query Match: 88.38% Indels: 0
 DB: 14 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x BM824360 (1-439)

QY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
 DB 191 GTGATGAGACCGCGTCCCAACGCCGCGCTGAGAGAGTATTGCGCACGCTGGCGCC 250
 QY 21 GluAlaGluIleGluAlaValGluIleGlyArgPheArgAspGlnGlyTrpGlu 40
 DB 251 GAGGCAATTAATCGAACGCCGCGAGTGTGATCGCGCGCTTACGAGACAGACATACGAG 310
 QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
 DB 311 ATGCTCAAGGCTGGCGCCGACAGATCCCGCGCTCGAGCGCTTACGCGCGCCCTG 370
 QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
 DB 371 GACGCGATGGGCGCTGACGCGCTGCTGGAAGACTTGGCGCAACCGTCTGCAACGCGGACCG 430

RESULT 11 BQ027499 499 bp mRNA linear EST 27-MAR-2002
 LOCUS UI-H-COO-tag9-a-09-0-UI-s1 NCI CGAP_Sub9 Homo sapiens cDNA clone
 DEFINITION IMAGE:3104895 3', mRNA sequence.

ACCESSION BQ027499
 VERSION BQ027499.1 GI:19762778
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 499)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapds-remail.nih.gov

CDNA Library Preparation: Dr. Jose Mercuende
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/HLN at: http://image.llnl.gov
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source location/Qualifiers
 1..499
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3104895"
 /clone_1ib="NCI CGAP_Sub9"
 /tissue_type="mixed"
 /dev_stage="mixed"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73-Pac (Pharmacia) with a modified.
 polylinker. Site 1: EcoR I; Site 2: Not I; tissues:
 choleonic mucosa with Crohns disease, choleonic mucosa with
 ulcerative colitis, fetal thymus, Cervix, Cervical
 adenosquamous carcinoma, ligament cells, Prostate
 carcinoma, Bladder carcinoma, Brain oligodendrocyte ;
 NCI CGAP_Sub9 is a subtracted cDNA library constructed

according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tags for this library are CTCG, AACG, GGGCC,
 GGAAG, TAGC, TAAGC, ATGC, AGACA, ATCAC. For additional
 information, contact: Bento Soares, bento-soares@uiowa.edu
 TAG-UI-H-COO
 TAG-TISSUE-Bladder Carcinoma
 TAG-SEO-AGACA"

BASE COUNT 85 a 155 c 145 g 113 t 1 others

Alignment Scores:

Pred. No.: 1.85e-34 Length: 499
 Score: 346.00 Matches: 68
 Percent Similarity: 97.14% Conservative: 0
 Best Local Similarity: 97.14% Mismatches: 2
 Query Match: 83.78% Indels: 0
 DB: 14 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x BQ027499 (1-499)

QY 11 LysGluPheValArgThrLeuGlyLeuArgGluAlaValGluValGlu 30
 DB 499 AAGGAGTTCGCGCCACGCTGGGCTGGCGAGGAGATCGAACCCGTGAGCTGAG 440
 QY 31 IleGlyArgPheArgAspGlnGlnGlnGlnMetLeuLysArgTrpArgGlnGlnGlnPro 50
 DB 439 ATGNCGCGCTCGAGACAGACACTAGAGATGCTCAAGCGCTGGCGCACAGACGCC 380
 QY 51 AlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGlu 70
 DB 379 GCGGCGCTCGGAGCGCTTACGCGCGCTGAGGCGCATGAGCGGCTGAGCGGTGGAA 320
 QY 71 AspLeuArgSerArgLeuGlnArgGlyPro 80
 DB 319 GACTTGGCAGCGCGCTGACAGCGCGCGC 290

RESULT 12 AW964958 507 bp mRNA linear EST 01-JUN-2000
 LOCUS EST376926 MAGC resequences, MAGC Homo sapiens cDNA, mRNA sequence.

ACCESSION AW964958
 VERSION AW964958.1 GI:8154689
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 507)
 Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspar,R., Gay,C., Holt
 I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
 Quackenbush,J.

Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element cDNA microarray

TITLE

Unpublished (2000)
 Contact: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: john@tigr.org
 Plate: 207

JOURNAL COMMENT The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: john@tigr.org
 Plate: 207

Seq primer: Forward.

FEATURES

source location/Qualifiers
 1..507
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

```

/clone.lib="MAGE resequences, MAGE
/note="Vector: pBluescriptSm"
BASE COUNT      85 a      155 c      156 g      111 t
ORIGIN

```

Alignment scores:	
Pred. No.:	2.54e-34
Score:	345.00
Percent Similarity:	94.67%
Best local Similarity:	90.67%
Query Match:	83.54%
DB:	10
Length:	507
Matches:	68
Conservative:	3
Mismatches:	4
Indels:	0
Gaps:	0

US-09-993-234-6_COPY_338_417 (1-80) X AW964958 (1-507)

[illegible]

LOCUS	A1266746	537 bp	mRNA	linear	EST 03-FEB-1999
DEFINITION	gq1ic06.x1 Soares_NhmMu.S1 Homo sapiens cDNA clone IMAGE:1932202				
	3' similar to TR:000278 000278 LIMPICCYTE ASSOCIATED RECEPTOR OF				
	DEATH 7. [2] TR:000280 ;, mRNA sequence.				
ACCESSION	A1266746				

VERSION AI266746.1 GI:3884904

SOURCE	human
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5	5
6	6
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99	99
100	100

ORGANISM	Homo sapiens
...	...

REFERENCE

AUTHORS	TITLE
---------	-------

ТОПНАТ

COMMENT

This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 837 Std Error: 0.00
 Seq primer: -40up from Gibco
 High quality sequence stop: 331.
 Location/Qualifiers
 1. .537
 FEATURES
 source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="1932202"
/clone_lib="Scars_NbHMPu.S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_post="DH108"
/note="Organ: mixed (see below): Vector: pRTT3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHm, pregnant uterus
NbHpu, and fetal heart NbH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of

```

5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G. clones 260232-265223, 340488-345479, and 484488-489479."

Alignment Scores:	
Pred. No.:	9.62e-33
Score:	333.00
Percent Similarity:	85.00%
Best Local Similarity:	85.75%
Query Match:	80.63%
DG:	9
Gaps:	0
Length:	537
Matches:	67
Conservative:	1
Mismatches:	12
Indels:	0
Gaps:	0

US-09-993-234-6_COPY_338_417 (1-80) x AI266746 (1-537)

[illegible]

BM794760					
LOCUS					
DEFINITION	647 bp	mrna	linear	EST 05-MAR-2002	
	K-EST0076219	S22SN16n1	Homo sapiens	CDNA clone S22SN16n1-48-c11	
	5', mRNA sequence.				

REVISION	2017-04-08	
VERSION	BM794760.1	GI:19142992

KEYWORDS
SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong, Yuseong-gu, Daejeon 305-333, South Korea
Tel.: +82-42-860-4470
Tel.: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@email.kribb.re.kr
Plate: 48 row: G column: 11
High quality sequence stop: 647.
Location/Qualifiers

```

source
1. 647
/organism="Homo sapiens"
/ab_xref="taxon:9606"
/clone="S225NU16n1-48-G11"
/clone_11b="S225NU16n1"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/cell_line="SNO-16"
/lab_host="DH10B"
/note="Organ: Stomach; Vector: p7T73-Pac; Site:1; EcoRI:
Site:2; Note: The S225NU16 library was contributed by the
Soares laboratory and it was constructed as described by

```


Db 252 ATGCTCAGCGCTGGCGTCAGCAGCAGCCTGCAGGCTCGGTGCCATCTATCG-GCTCTG 310
 QY 61 GIuArgMetGlyLeuAspGlyCysValGIuAspLeuArgSerArgLeuGlnArgGlyPro 80
 Db 311 GAGCGCATGGCTGTGGAGAGCTGTGCCGAGAGACCTGNC-AGCCGCCT-CAGCGTGCCCG 368

Search completed: April 6, 2003, 23:25:25
 Job time : 507.409 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:35:34 ; Search time 2161.6 Seconds

(without alignments)
2504.221 Million cell updates/sec

Title: US-09-993-234-6_COPY_19_204

Perfect score: 1101
Sequence: 1 LIGARAGGCTRSPDCACD.....GSCPERCAAVCGMROMFWQ 186

Scoring table:
BLOSUM62:
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODE=frame-p2n.model -DEV=xlh
-O/cgn2.1/USPTO.spool/US09993234/runat.27032003.115455.15349/app.query.fasta.1.2346
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human40.cdl -LIST=45
-DOCCALIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcr -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09993234.@CEN.1.1.8534.@runat.27032003.115455.15349 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MAP -LARGEDEV -NMG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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2: gb_hlg:*
3: gb_in:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pal:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rtd:*
36: em_hlg_mam:*
37: em_hlg_vrt:*
38: em_sy:*
39: em_hlgo_hum:*
40: em_hlgo_mus:*
41: em_hlgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1101	100.0	1254	6 AR119657	AR119657 Sequence
2	1101	100.0	1254	9 HSU72763	U72763 Human death
3	1101	100.0	1254	9 HSU78029	U78029 Human aopto
4	1101	100.0	1254	9 HSU94501	U94501 Human lymph
5	1101	100.0	1257	9 HSU94502	U94502 Human lymph
6	1101	100.0	1634	9 HSU74611	U74611 Human Apo-3
7	1101	100.0	1662	6 AX055442	AX055442 Sequence
8	1101	100.0	1662	6 AX201344	AX201344 Sequence
9	1101	100.0	1783	6 AR119656	AR119656 Sequence
10	1091	99.1	1528	9 HSU83597	U83597 Human death
11	1091	99.1	1557	9 HSU75380	U75380 Human aopto
12	1077	97.8	1355	9 HSU94503	U94503 Human lymph
13	1077	97.8	1743	6 AX331947	AX331947 Sequence
14	1077	97.8	1743	6 HSWS11	Y09392 H.sapiens m
15	1070	97.2	1143	9 HSU94510	U94510 Human lymph
16	1041	94.6	1250	6 AX150176	AX150176 Sequence
17	1041	94.6	1763	9 AF026071	AF026071 Homo sapi
18	1037	94.2	1669	9 AF026070	AF026070 Homo sapi
19	979	88.9	808	9 HSU75381	U75381 Human aopto
20	979	88.9	809	9 HSU94512	U94512 Human lymph
21	979	88.9	816	6 AX335086	AX335086 Sequence
22	979	88.9	816	9 HSU83598	U83598 Human death
23	965.5	87.7	1198	9 HSU94504	U94504 Human lymph
24	964	87.6	1087	9 HSU94505	U94505 Human lymph
25	794.5	72.2	1119	9 HSU94509	U94509 Human lymph
26	767	69.7	4825	9 AB051850	AB051850 Homo sapi
27	767	69.7	53982	9 AL158217	AL158217 Human DNA
28	760	69.0	4811	9 AB051851	AB051851 Homo sapi
29	657.5	59.7	952	9 HSU94506	U94506 Human lymph
30	636	57.8	651	9 HSU83599	U83599 Human alter
31	613	55.7	1665	10 AF329969	AF329969 Mus muscu
32	501	42.9	838	9 HSU94507	U94507 Human lymph
33	472	42.9	1619	10 BC017526	BC017526 Mus muscu
34	437	39.7	196368	2 AL772240	AL772240 Mus muscu
35	374.5	34.0	665	9 HSU83600	U83600 Human death
36	330.5	30.0	97483	2 AC118359	AC118359 Rattus no
37	231.5	21.0	2600	4 SSJ001202	U94508 Human lymph
38	216	19.6	705	9 HSU94508	U94508 Human lymph
39	216	19.6	2115	10 AF329976	AF329976 Rattus no
40	216	19.6	2115	10 AF329977	AF329977 Rattus no
41	216	19.6	2115	10 AF329978	AF329978 Rattus no
42	216	19.6	2115	10 AF329979	AF329979 Rattus no
43	216	19.6	2115	10 AF329980	AF329980 Rattus no
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45	216	19.6	2130	6 AX401925	AX401925 Sequence

ALIGNMENTS

RESULT 1

ARI19657
LOCUS ARI19657 1254 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 3 from patent US 6153402.
ACCESSION ARI19657
VERSION ARI19657.1 GI:14102356
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1254)
AUTHORS Yu, G.-L., Ni, J., Gentz, R.L. and Dillon, P.J.
TITLE Death domain containing receptors
JOURNAL Patent: US 6153402-A 3/28-NOV-2000;
FEATURES
Location/Qualifiers
1..1254
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN
Alignment Scores:
Pred. No.: 2.08e-68 Length: 1254
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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DB:
US-09-993-234-6_COPY_19_204 (1-186) x ARI19657 (1-1254)
OY 1 LeuLeuGLyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 55 CTGGCTGGGGCCCCGGGCCCAAGGGGCGGACTCGTAGCCCAAGGTGACTGTGCCGGTGC 114
OY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 115 TTCACAAAGAAATGTGTCTGTTTGTGCAGAGGCTGCCAGCGGGGCGACTACCTGAAG 174
OY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 175 GCCCCTGCACGGAGCGCCGCGCAACTCCACCTGCTGTGTCCCAAGACACCTTC 234
OY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 235 TTGGCCTGGGAGAACACCATTAATCTGAAATGTGCCCGCTGCTGTGATGAGCAG 294
OY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 295 GCCTCCAGAGTGGCGCTGGAGAACTGTCAGAGTGGCGGACACCGCGTGGCTGTAG 354
OY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerSerProPheTyrCys 120
DB 355 CAGGCGTGTGTGGAGTGCAGAGTCCAGCAATGTGTGAGAGTTCACCCCTTCACTGC 414
OY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 415 CAACATGCGCTAGACTGGGGGGCCCTGCACGCCACACAGGCTACTCTGCCCAAA 474
OY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspIlyCysValSer 160
DB 475 GATACTGACTGTGGAGCCCTGCTGCTCTGTGAACATGGCGATGGCTGCGGTGC 534
OY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaValAlaCysGlyTyrArg 180
DB 535 TGGCCACAGAGACCGCTGGGAGAGTGTCCAGAGCGCTGTGCGCTGTGTGGCTGAGG 594
OY 181 GlnMetPheTrpValGln 186
DB 595 CAGATGTCTGGGTCCAG 612
RESULT 2
LOCUS HSU72763 1254 bp mRNA linear PRI 15-NOV-1996
DEFINITION Human death receptor 3 (DR3) mRNA, complete cds.

ACCESSION U72763
VERSION U72763.1 GI:1669511
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
1 (bases 1 to 1254)
AUTHORS Chinaiyan, A.M., O'Rourke, K., Yu, G.-L., Lyons, R.H., Garg, M.,
Duan, R., Xing, L., Gentz, R., Ni, J. and Dixit, V.M.
TITLE Signal transduction by DR3, a death domain-containing receptor
JOURNAL Science 274 (5289), 990-992 (1996)
MEDLINE 97081063
PUBMED 8875942
REFERENCE 2 (bases 1 to 1254)
AUTHORS Chinaiyan, A.M., O'Rourke, K., Yu, G.-L., Lyons, R.H., Garg, M.,
Duan, R., Xing, L., Gentz, R., Ni, J. and Dixit, V.M.
TITLE Direct Submission
Submitted (29-SEP-1996) Pathology, University of Michigan Medical
School, 1301 Catherine St., Box 0602, Ann Arbor, MI 48109, USA
FEATURES
Location/Qualifiers
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TLTYTRICWPKPLVTADAEAMALTPPPATHLPLDSAHILAPPSSEKICVOL
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LYDVADVARMKKEFVTRIGLREAEIEAVEIEIGRPDQYEMLRNQDPAGIGA
YVALERMGIDGCEVDLRSRLQRP"
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN
Alignment Scores:
Pred. No.: 2.08e-68 Length: 1254
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB:
US-09-993-234-6_COPY_19_204 (1-186) x HSU72763 (1-1254)
OY 1 LeuLeuGLyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 55 CTGGCTGGGGCCCCGGGCCCAAGGGGCGGACTCGTAGCCCAAGGTGACTGTGCCGGTGC 114
OY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 115 TTCACAAAGAAATGTGTCTGTTTGTGCAGAGGCTGCCAGCGGGGCGACTACCTGAAG 174
OY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 175 GCCCCTGCACGGAGCGCCGCGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTC 234
OY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 235 TTGGCCTGGGAGAACACCATTAATCTGAAATGTGCCCGCTGCTGTGATGAGCAG 294
OY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 295 GCCTCCAGAGTGGCGCTGGAGAACTGTCAGAGTGGCGGACACCGCGTGTGGCTGTAG 354

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Db	55	CTGGTGGGGGCCCGGGCCACGGCGGCACGTGTGAAGCCACCAGTGTTGACTGGCGGTGAC	114		
OY	21	PheHlsLysLysIleGlyLeuPheCysGysArgGlyCysProAlaGlnHisTyrlLeuLys	40		
Db	115	TTCACAAGAAGATGGGTCTGTGTTGTGCAGAGGCTGCCACGGGGGCACTACTTAAG	174		
OY	41	AlAProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe	60		
Db	175	GCCCTTCACAGGAGCCCTGGCGCACTCACACTCCCTTGCTGTCCCCAACAACTTC	234		
OY	61	LeuAlArTrgLuAsnHIsAsnSergLucysAlaArgCysGlnAlaCysAspGluGln	80		
Db	235	TTCGGCTGGGAGAACCAACCATATTCTGAATGTGCCCGCTCCAGGCTGTGATGAGAG	294		
OY	81	AlAserrGlnValAlaLeuGluAsnCysSerArgAlaValAlaAspThrArgCysGlyCysLys	100		
Db	295	GCCCTCCAGGGGGGGCTGGAGAACTGTTCACAGTGGCGGACACCCTGTGGCTGTAAAG	354		
OY	101	ProGlyTrpPheValGluCysGlnValSerrGlnCysValSerrSerSerProPheTryCys	120		
Db	355	CCAGGCTGGTTGTGGAGATGCCAGSTCAAGCCAAATGTGTACAGATTCACTTTACTGCC	414		
OY	121	GlnProCysLeuAspCysGlyAlaLeuHIsArgHIsThrArgLeuLeuCysSerArgArg	140		
Db	415	CAACCATCTCTAAGACTGGGGGGCTGCACCGCCACACACGCGTACTGTGTCCCGAGA	474		
OY	141	AspThrAspCysGlyThrCysLeuProGlyPheArgGlnHisGlyAspGlyCysValSer	160		
Db	475	GATACTGACTGTGGAGACTGCCTGCCTGTCTATGAACTGGCGAGTGGCTGGCTGCC	534		
OY	161	CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg	180		
Db	535	TGCCCCACAGACACACCTGGGAGGCTGCACAGAGCGCTGCGCGTCTGTGGCTGGAGG	594		
OY	181	GlnMetPheTrpValGln	186		
Db	595	CAGATGTTCTGTGGTCCAG	612		
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RESULT 4					
LOCUS	HSU94501	1254 bp	mRNA	linear	PRI 15-MAY-1997
DEFINITION	Human lymphocyte associated receptor of death Ia mRNA, complete cds.				
ACCESSION	U94501				
VERSION	U94501.1	GI:2071948			
KEYWORDS					
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1254) McMichael,A.J., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R., Sreeratan,G.R.,				
TITLE	LMBD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)				
REFERENCE	9114039				
AUTHORS	2 (bases 1 to 1254) Sreeratan,G.R.				
TITLE	Direct Submission				
JOURNAL	Submitted (19-MAR-1997) Molecular Immunology Group, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK				
FEATURES	location/Qualifiers				
SOURCE	1..1254				
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	/db_xref="taxon:9606"				

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/cell_type="lymphocyte"
1..1254
/function="mediates apoptosis"
/Note="LARD-1a; membrane protein; similar to Fas and
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TLTYTRHCWPKPLVTADAGMELATPPPAHLPLSDASHLAPDSSERICTVO
LVNSWTGPEYDEALCPQVITWMDLPSPALGPAAPLSPSPAGSPAMMLOPPO
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BASE COUNT      201 a      420 c      407 g      226 t
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Alignment Scores:
Pred. No.:      2,08e-68      Length:      1254
Score:          1101.00      Matches:      186
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             9      Gaps:      0
US-09-993-234-6_COPY_19_204 (1-186) x HSU94501 (1-1254)
OY      1 LeuLeuGLyAlAaRgAlAGInGLyGlyThrArGSeRProArGcYsAspCySaLaGLyAsp 20
      55 CTGCTGGGGGGCCCGGGCCAGGGGGGCGGCGACTCGAGCCCGAGGTGACTGTGCCGGTGC 114
OY      21 PheHisLysLysIleGlyLeuPheCysArGgLYCysProAlaGlyHisTyrLeuLys 40
      115 TTCCACAAGAGATGCTGTGTTTGTTCAGAGCGCTGCCACGGGGCGACACTCTGAAG 174
OY      41 AlaProCysThnGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
      175 GCCCTCTGCAGGAGCGCCGCGGCAACTCCACTGCTGTGTGTCCTCCACAGACACTTC 234
OY      61 LeuAlaTrpGlnAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnGln 80
      235 TTGGCTGGGAGAACACCATATATCTGTAATGTGCCGCTGCCAGGCTGTGATGAGCAG 294
OY      81 AlaSerGlnValAlaLeuGlnuAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
      295 GCCTCCAGAGTGGCGCTGGAGAACTGTCAGAGTGGCGGACACCCGCTGTGGCTTAAG 354
OY      101 ProGlyTTPPhValGluCysGlnValSerGlnCysValSerSerSerProPheTyrCys 120
      355 CCAGGCTGGTTGTGAGAGTGCAGGTCAGCCAAATGTGTACAGATTCACCCCTTACTGC 414
OY      121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
      415 CAAACATGCTAGACTGGGGGCGCTGCACCCGCAACAGCGCTACTGTGTCCGCAAA 474
OY      141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSer 160
      475 GATACTGACTGTGGAGACTGCTGCTGCTCTATGAACATGGGAGATGGCGCTGTCC 534
OY      161 CysProThrSerThrLeuGlySerCysProGlnuArgCysAlaValAlaCysGlyTTPArg 180
      535 TGCCTCCAGAGACCCCTGGGAGCTGCAGAGCGCTGTGCGCTGTGTGTGGCTGAGG 594
DB      595 CAGATGTTCTGGGTCCAG 612
OY      181 GlnMetPheTTPValGln 186
      595 CAGATGTTCTGGGTCCAG 612
RESULT 5
HSU94502
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LOCUS      HSU94502      1257 bp      mRNA      linear      PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 1b mRNA,
alternatively spliced, complete cds.
ACCESSION  U94502
VERSION    U94502.1
KEYWORDS  GI:2071950
SOURCE    Homo sapiens.
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 1257)
AUTHORS  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLES   Scream, G.R., Xu, X.N., Olsen, A.L., Cowper, A.E., Tan, R.,
McMichael, A.J. and Bell, J.I.
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL   97272273
MEDLINE   9114039
PUBMED    2 (bases 1 to 1257)
REFERENCE Scream, G.R.
TITLES   Direct Submission
AUTHORS  Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES  Location/Qualifiers
source    1..1257
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BASE COUNT 202 a      421 c      408 g      226 t
ORIGIN
Alignment Scores:
Pred. No.:      2,08e-68      Length:      1257
Score:          1101.00      Matches:      186
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
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US-09-993-234-6_COPY_19_204 (1-186) x HSU94502 (1-1257)
OY      1 LeuLeuGLyAlAaRgAlAGInGLyGlyThrArGSeRProArGcYsAspCySaLaGLyAsp 20
      55 CTGCTGGGGGGCCCGGGCCAGGGGGGCGGCGACTCGAGCCCGAGGTGACTGTGCCGGTGC 114
OY      21 PheHisLysLysIleGlyLeuPheCysArGgLYCysProAlaGlyHisTyrLeuLys 40
      115 TTCCACAAGAGATGCTGTGTTTGTTCAGAGCGCTGCCAGGGGGCGACACTCTGAAG 174
DB      115 TTCCACAAGAGATGCTGTGTTTGTTCAGAGCGCTGCCAGGGGGCGACACTCTGAAG 174
OY      41 AlaProCysThnGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
      115 TTCCACAAGAGATGCTGTGTTTGTTCAGAGCGCTGCCAGGGGGCGACACTCTGAAG 174
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TITLE Death domain containing receptors
JOURNAL Patent: US 6153402-A 1 28-NOV-2000;
FEATURES Location/Qualifiers
source 1.1783
BASE COUNT 330 a 562 c 564 g 327 t
ORIGIN

Alignment Scores:
Pred. No.: 2.95e-68 Length: 1783
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-993-234-6_COPY_19_204 (1-186) x AR119656 (1-1783)

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OY 21 PheHisAlaValIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
    |||||||
DB 345 TTCACAGAAAGATGGTGTGTTTGTTCAGAGGCTGCCAGCGGGGCACTACCTGAAG 404

OY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
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OY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
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DB 465 TTGGCCCTGGAGAAACACCATTAATTCGAATGTCCCGCTGCCAGGCTGTGATGACGAG 524

OY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
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DB 525 GCCCTCCAGAGTGGCGTGGAACTGTTCAGCACTGGCCGACCCCTGTGTGTGAAG 584

OY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
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DB 585 CCAAGCTGGTGTGTGGAGTGCAGAGTCAAGCCAAATGTGTCAACATTCACCTTTACTGCG 644

OY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
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DB 645 CAACCAATGCTAGACACTGGGGGCGCTGCACCGCACACAGCGGTACTGTGTCCGCGAGA 704

OY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspArgLysValSer 160
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DB 705 GATACCTACTGTGGACCTGCTGCTGTCTATGAACAATGGCGATGGCTGTGCTGCC 764

OY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrPArg 180
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DB 765 TGGCCCAAGACACCTCGGGGAGCTGTCCAGAGCGCTGTGCTGTGTGTGGCTGGAAG 824

OY 181 GlnMetPheTrpValGln 186
    |||||||
DB 825 CAGATGTTCTGGGTCCAG 842

RESULT 10
HS083597 1528 bp mRNA linear PRI 27-JAN-1997
LOCUS HS083597
DEFINITION Human death domain receptor 3 (DDR3) mRNA, partial cds.
ACCESSION U83597
VERSION U83597.1 GI:1800292
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Chaudhary, P. M. and Hood, L. E.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-1997) Molecular Biotechnology, University of
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Washington, 1705 NE Pacific Street, HSB-K360, Seattle, WA 98195,
USA

FEATURES
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1.1238
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/function="mediates apoptosis when cross-linked"
/note="A TNFR1-related death-domain containing receptor;
DR3, WSL-LR, Apo-3, TRAMP; transmembrane form; similar to
human EST clone 298913, GenBank Accession Number N71143"
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gene
CDS

BASE COUNT 280 a 496 c 470 g 282 t
ORIGIN

Alignment Scores:
Pred. No.: 1.26e-67 Length: 1528
Score: 1091.00 Matches: 185
Percent Similarity: 99.46% Conservative: 0
Best Local Similarity: 99.46% Mismatches: 1
Query Match: 99.09% Indels: 0
DB: Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x HS083597 (1-1528)

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OY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
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DB 39 CTGCTGGGGGCGCCGCGCCAGGCGGCACCTGTGAGCCCAAGTGTGACTGTGCGGTGAC 98

OY 21 PheHisAlaValIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
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DB 99 TTCACAGAAAGATGGTGTGTTTGTTCAGAGGCTGCCAGCGGGCACTACCTGAAG 158

OY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
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DB 159 GCCCTTGCACAGGAGGCGCTGGGCACTCACTGCTGTGTGTGCCCAAGACACCTTC 218

OY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
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DB 219 TTGGCTTGGGAGAACCAACATTAATTCGAATGTGCCCTGCCAGGCTGTGATGACGAG 278

OY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
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DB 279 GCCCTCCAGAGTGGCGCTGGAACTGTTCACAGAGCGGCACCCGCTGTGCTGTGAAG 338

OY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
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DB 339 CCAAGCTGTGTGTGGAGTGCAGAGTCAAGCCAAATGTGTACAGAGTTCACCTTCTACTGCG 398

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DB 399 CAACCAATGCTAGACACTGGGGGCGCTGCACCGCACACAGCGGTACTGTGTCCGCGAGA 458

OY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspArgLysValSer 160
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1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProAlaArgCysAspCysAlaGlyAsp 20

REFERENCE	2 (bases 1 to 1355)
AUTHORS	Screation,G.R.
TITLE	Direct Submission
JOURNAL	Submitted (19-MAR-1997)
FEATURES	Molecular Immunology Group, Institute of Molecular Medicine, John Radcliffe Hospital, 9DU, UK
SOURCE	Location/Qualifiers 1..1355

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/function="mediates apoptosis"

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599..700
/note="Insertion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable retained intron leading
to premature transcriptional termination"
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Alignment Scores:
Pred. No.: 1,06e-66 Length: 1355
Score: 1077.00 Matches: 182
Percent Similarity: 98.91% Conservative: 0
Best Local Similarity: 98.91% Mismatches: 2
Query Match: 97.82% Indels: 0
Gaps: 0
DB: 9
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QY 1 LeuLeuGlyAlaIarGlaInGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
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QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 115 TTCACAGAAAGATGTGTGTTGTTGTCACAGAGGTGCCAGCGGGGACATACGGAAG 174
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 175 GCCCTTGGCAGGAGCCCGGCACTCCACCTGCTGTGTGCCCAAGACACCTTC 234
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 235 TTGGCCTGGGAGAACCCATTAATTTCTGAATGTGCCGCTGCAGGCTGTGATGAGCAG 294
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 295 GCCTCCAGAGTGGCGCTGGAGAACTGTTCAAGCAGTGGCCGACACCGGCTGTGGCTGAAG 354
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
DB 355 CCAGGCTGTTGTGTGAGTCCAGGTCCAGCAATGTGTCCAGATTCACCCCTTCTACTGC 414
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 415 CAACCAATGCTTAACAGTGGGGGCGCTGCACCGCACACAGGCTACTCTTTCGCGAGA 474
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSer 160
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QY 161 CysProThrSerThrLeuGlySerCysProGlnArgCysAlaValCysGlyTyrParg 180
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QY 181 GlnMetPheTyr 184
DB 595 CAGAGTAGGTGG 606
RESULT 13
AX331947 1743 bp DNA linear PAT 09-JAN-2002
LOCUS AX331947
DEFINITION Sequence 2456 from Patent W00194629.
ACCESSION AX331947

VERSION AX331947.1 GI:18122581
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Edner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 2456 13-DEC-2001;
Avalon Pharmaceuticals (US)
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/db_xref="taxon:9606"
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Score: 1077.00 Matches: 182
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Best Local Similarity: 98.91% Mismatches: 2
Query Match: 97.82% Indels: 0
Gaps: 0
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QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 183 TTCACAGAAAGATGTGTGTTGTTGTCACAGAGGTGCCAGCGGGGACATACGGAAG 242
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 243 GCCCTTGGCAGGAGCCCGGCACTCCACCTGCTGTGTGCCCAAGACACCTTC 302
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
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QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 363 GCCTCCAGAGTGGCGCTGGAGAACTGTTCAAGCAGTGGCCGACACCGGCTGTGGCTGAAG 422
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
DB 423 CCAGGCTGTTGTGTGAGTCCAGGTCCAGCAATGTGTCCAGATTCACCCCTTCTACTGC 482
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 483 CAACCAATGCTTAACAGTGGGGGCGCTGCACCGCACACAGGCTACTCTTTCGCGAGA 542
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSer 160
DB 543 GATACAGACTGTGGAGACTGCTGCTGCTGTATGAACATGGCGATGGCTGGCTGCC 602
QY 161 CysProThrSerThrLeuGlySerCysProGlnArgCysAlaValCysGlyTyrParg 180
DB 603 TGGCCACAGACACCTGGGGAGCTGTCCAGACGCTGTGCCCTGTGTGTGGCTGGAGG 662
QY 181 GlnMetPheTyr 184
DB 663 CAGAGTAGGTGG 674
RESULT 14
HSMSL1 1743 bp mRNA linear PRI 16-DEC-1996
LOCUS HSMSL1

DEFINITION	H.sapiens mRNA for WSL-1R, WSL-S1 and WSL-S2 proteins.
VERSION	Y09392
KEYWORDS	Y09392.1 GI:1669690
SOURCE	ws1-1 gene; WSL-1R protein; WSL-S1 protein; WSL-S2 protein.
ORGANISM	Homo sapiens.
REFERENCE	Hum sapiens.
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 1743)
JOURNAL	Kitson,J., Raven,T., Jiang,Y.P., Goeddel,D.V., Gilles,K.M.,
MEDLINE	Pun,K.T., Grinham,C.J., Brown,R. and Farrow,S.N.
PUBMED	A death-domain-containing receptor that mediates apoptosis
REFERENCE	Nature 384 (6607), 372-375 (1996)
AUTHORS	8934525
TITLE	2 (bases 1 to 1743)
JOURNAL	Kitson,J.
FEATURES	Direct Submission
SOURCE	Submitted (12-NOV-1996) J. Kitson, GAXO-Wellcome, Medicines
	Research Centre, Gunneis Wood Road, Stevenage, SGI 2NY, UK
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Dd	123 CTGGCTGGGGGGCCGGGGCCCGAGGGCGACTGTACCCAGGTGTGACTGTGCCGTGAC	182		
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Dd	183 TTCCACAGAGAAGATTGGTGCTGTGTGTGTGCAGAGGCTGCCACGGGGGCACTACTGAAG	242		
OY	41 AlAprOCystHrGluproCYsglyASnserThrCysleuValCyproglinaSPthrPhe	60		
Dd	243 GCCCCTTCGACAGGAGCCCTGGCGCACTCCACCCTGCTGTGTGCCAACACCTTC	302		
OY	61 leuAlATrprGLuAnNHISHASnSerGIucSYAlaArGYsglnAlacYaspgluIn	80		
Dd	303 TTGGCGCTGGAGAACCAACAATAATTCTGAAATGTGCCGCTGCCAGGCTGTATGACAG	362		
OY	81 AlASerGlnValAlaleuGluAnCysSerAlaValAlaASPthrArGYsglyCyslys	100		
Dd	363 GCGCTCCAGATGGCGCTGGAGAACTTTGACGAGTGCGGCACACCCGCTGTGCTGTAG	422		
OY	101 ProglYTrPheValGluCYsglnValSerGlnCysValSerSerSerpropheryCys	120		
Dd	423 CCAGCGTGGTTGTGTGAGAGCCAGGACCAATGTCACAGATTCACCCCTTACATGC	482		
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Dd	483 CAACCATGCTGACTGGGGGGCCCTGCACCGCACACAGGCTACTGTTCGGCAGA	542		
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Dd	543 GATTCGTACTGTGGACCTGCTGCTGCTTCTTATGAACATGGCGATGGCTGGCTGCC	602		
OY	161 CysProThrSerThrleuGlySerCysProgluArgCysAlaAlaValCysgLYTrParq	180		
Dd	603 TGCCCCACGAGACACCTGGGGAGCTGTCCAGAGGGGTGCCCTGTCTGTGGCTGGAG	662		
OY	181 GlmetPheTrp	184		
Dd	663 CAGAGTAGGTG	674		
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LOCUS	HSU94510			
DEFINITION	Human lymphocyte associated receptor of death 9 mRNA, alternatively			
ACCESSION	U94510			
VERSION	U94510.1			
KEYWORDS	GI:2071966			
SOURCE	Homo sapiens.			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
REFERENCE	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Sreter,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,			

TITLE McMichael, A.J. and Bell, J.I.
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1143)
AUTHORS Sreelaxan, G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

FEATURES
source

Location/Qualifiers
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Accession Number U94501, probable skipping of putative
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BASE COUNT 188 a 378 c 378 g 199 t
ORIGIN

Alignment Scores:

Pred. No.: 2,76e-66 Length: 1143
Score: 1070.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
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Query Match: 97.18% Indels: 0
DB: Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x HSD94510 (1-1143)

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DB 55 CTGCTGGGGGGCCGGCCGACGCGGCACTGTAGCCCACTGTGACTGTGCGCGTAC 114
QY 21 PheHisLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 40
|||||
DB 115 TTCCACAAGAGATGTGCTCTTTGTTGTGACAGAGCTGCCACGCGGGGCACTACCTGAAG 174
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
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DB 175 GCGCCCTTGACGAGAGCCCTGGGCACTCCACCTGCTGTGTGCTCCCAAGACACCTTC 234
QY 61 LeuAlaTrpGluAsnHisLysAsnSerGluCysAlaArgCysGlnAlaCysAspGln 80
|||||
DB 235 TTGGCCTGGGAGAACCACTAATTCGATGTGCCCCCTGCCAGCCTGTGATGAGCAG 294
QY 81 AlaSerGlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
|||||
DB 295 GCTCTCCAGGTGGCGCTGGAGAACTGTTCACAGCTGGCCGACACCCGCTGTGCTAAG 354
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTrpCys 120
|||||
DB 355 CCAGGCTGGTTGTGGAGTGCACAGTCCAAATGTGTACAGAGTTCACCTTACTTCG 414

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DB 415 CAACCATGGCTAGACTCGGGGCGCTGCACCGCACACAGGCTAATCTGTGCCGAGA 474
QY 141 AspThrArgCysGlyThrCysLeuProGlyPheTrpGluHisGlyAspGlyCysValSer 160
|||||
DB 475 GATCTGACTGTGGGACCTGCTGCTCTTATGAAATGGCGATGGCTGGCTGCC 534
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
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DB 535 TGCCCAAGACACCCCTGGGAGCTGTCCAGAGCGCTGTGCTGTGTGCTGAGAG 594
QY 181 Gln 181
DB 595 CAG 597

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140

GenCore version 5.1.4-p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:33:09 ; Search time 173.187 Seconds

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Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1101	100.0	1254	20 AAX00925	Death domain conta
3	1101	100.0	1254	21 AAC68777	Human death domain
4	1101	100.0	1634	21 AAT91180	Human apoptosis pr
5	1101	100.0	1634	22 AAH27782	Human genomic DNA
6	1101	100.0	1634	24 AAL47186	Human rheumatoid a
7	1101	100.0	1662	22 AAC91477	Human rheumatoid a
8	1101	100.0	1662	24 ABR40265	CDNA encoding huma
9	1101	100.0	1783	18 AAT89426	Death domain conta
10	1101	100.0	1783	20 AAX00924	Death domain conta
11	1101	100.0	1783	21 AAC68776	Human death domain
12	1101	100.0	1847	19 AAY28700	Human apoptosis in
13	1077	97.8	1743	24 ABL64119	Breast cancer rela
14	1041	94.6	1250	22 AAF83770	Nucleotide sequenc
15	979	88.9	816	24 ABL67258	Thyroid cancer rel
16	979	88.9	1438	18 AAT91179	Human apoptosis pr
17	964	87.6	787	24 AAL47187	Human rheumatoid a
18	767	69.7	4825	24 AAL47185	Human DR3 gene ass
19	767	69.7	10797	23 ABR42690	Genomic sequence #
20	615	55.9	1251	19 AAV28701	Mouse apoptosis in
21	216	19.6	2130	24 ABR63694	Rat sequence diffe
22	212.5	19.3	1049	18 AAT94007	CDNA for TBP(20-16
23	212	19.3	5870	21 AAL15044	Nucleotide sequenc
24	205.5	18.7	1301	18 AAT94022	CDNA for TBP(20-19
25	203.5	18.5	1202	18 AAT94008	CDNA for TBP(20-16
26	203	18.4	608	13 AAQ24441	Encodes truncated
27	203	18.4	1334	11 AAQ06282	Plasmid Tumour Nec
28	203	18.4	1368	14 AAQ49832	Lambda-derived TNF
29	203	18.4	1368	21 AAA95105	Human TNFR1 coding
30	203	18.4	2062	13 AAQ20973	TNF-alpha binding
31	203	18.4	2062	13 AAQ24440	Encodes TNF-alpha
32	203	18.4	2088	12 AAQ10883	30KD TNF inhibitor
33	203	18.4	2088	22 AAC83946	Human 30 kDa TNF 1
34	203	18.4	2111	12 AAQ10955	Encodes human 55KD
35	203	18.4	2111	20 AAZ09170	Human tumour necro
36	203	18.4	2111	22 AAT48859	Human TNFBP-associ
37	203	18.4	2111	24 ABR84039	Human CDNA differe
38	203	18.4	2111	24 ABR95862	Gene #2360 used to
39	203	18.4	2141	11 AAQ06285	Human Tumour Necro
40	203	18.4	2161	21 AAT48475	Human tumour necro
41	203	18.4	2161	24 ABR13194	Human tumour necro
42	203	18.4	2175	16 AAQ90513	p55 TNF-R gene. H
43	203	18.4	6889	17 AAT15931	DHFR/Inttron (WTas
44	203	18.4	6926	18 AAV04431	Vector pcDNA3-1gcl
45	202	18.3	2170	14 AAQ50870	p55 Tumour necrosi

ALIGNMENTS

RESULT 1
ID AAT89427 standard; cDNA; 1254 BP.
AC AAT89427;
XX
XX
XX 02-MAR-1998 (first entry)
DE Death domain containing receptor DR3 CDNA.
KW Death domain containing receptor; DR3; human; apoptosis;
XX Inflammation; NF-kappaB; ds.
XX
XX Homo sapiens.
OS
PH key Location/Qualifiers
FT sig_peptide 1..72
FT /*tag- a

FT mat_peptide 73..1251
 FT /tag= b
 XX MO9733904-A1.
 XX 18-SEP-1997.
 XX 17-OCT-1996; 96WO-US16849.
 XX 12-MAR-1996; 96US-0013285.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (UNMI) UNIV MICHIGAN.
 XX Dillion PJ, Dixit VM, Gentz RL, Ni J, Yu G;
 XX WPL; 1997-470812/43.
 DR P-PSDB; AAW31517.
 XX
 PT Death domain containing receptor polypeptide(s) DR3 and DR3-V1 -
 PT for activation of apoptosis and NF-kappaB, antagonists can be used
 PT to treat inflammatory diseases
 PS
 PS Claim 6; Page 75-77; 108pp; English.

CC This cDNA clone codes for human death domain containing receptor
 CC DR3 (see AAW31517), a novel member of the tumour necrosis factor
 CC receptor family. It was isolated from a HUVCC cDNA library.
 CC Related death domain containing receptor DR3-V1 cDNA (see AAT89426)
 CC was isolated from a human testis tumour cDNA library. The genes
 CC have also been identified in cDNA libraries of foetal liver,
 CC foetal brain, tonsil and leukocyte. Nucleic acids encoding full-
 CC length or mature DR3, or the extracellular, transmembrane,
 CC intracellular or especially the death domain of DR3, can be used to
 CC produce recombinant polypeptides in transformed host cells. These
 CC polypeptides can be used to treat diseases and disorders associated
 CC with the inhibition of apoptosis. Antagonists can be used to treat
 CC diseases and disorders associated with increased apoptosis and for
 CC treating inflammatory diseases and disorders.

SO Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:

Pred. No.: 7,956-75 Length: 1254
 Score: 1101.00 Matches: 186
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x AAT89427 (1-1254)

OY 1 LeuLeuGlyAlaArgAlaGlnGlyIleThrArgSerProArgCysAspCysAlaGlyAsp 20
 DB 55 CTGCTGGGGGGCCGGGGCCGAGGGGCGGACTGTAGCCCGAGGTGTGACTGCTCCGCTGAC 114
 OY 21 PheHisIysIysIleGlyLeuPheCysArgGlyCysProAlaGlyHisIleLeuIys 40
 DB 115 TTCACAGAGAGATGTGCTGTGTGTGTCAGAGGCTGCCAGCGGGGACACTGAG 174
 OY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
 DB 175 GCCCTTCACAGGAGCCCTGGGGCACTCCACTGCTGTGTGTGTCGCCAGACACCTTC 234
 OY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
 DB 235 TTGGGCTGGGGAACACCAATTAATTCATGATGTGCCCTCCAGGCGCTGTGTAGAGAG 294
 OY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysIys 100
 DB 295 GCGCTCCAGAGTGGCGCTGGAGAACTGTTCACCACTGGCGCCGACCCGCTGTGCTGTAG 354
 OY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerSerProPheTrpCys 120

DB 355 CCAGGCTGTTGTGAGAGCCAGGTACGCCAATGTGTCCAGCATTCACCTTCTACTGC 414
 OY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisIleThrArgLeuLeuCysSerArgArg 140
 DB 415 CAACCATGCTAGACTGGGGGGCCCTGCACCCGACACAGGCTACTGTGTCGCCGAGA 474
 OY 141 AspThrAspCysGlyThrCysLeuProGlyPheTrpGluHisGlyAspGlyCysValSer 160
 DB 475 GATACTGACTGTGGAGCTGCTGCTGCTTATGAACATGGGAGATGGCTGCTGCTTC 534
 OY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
 DB 535 TGCCCGACGAGACCCCTGGGGAGGCTGTCCAGAGCGCTGTGCCGTGTGCTGGAGG 594
 OY 181 GlnMetPheTrpValGln 186
 DB 595 CAGATGTCTGTGCTCCAG 612

RESULT 2

ID AAX00925 standard; cDNA; 1254 BP.

AC AAX00925;

XX 25-MAR-1999 (first entry)

DE Death domain containing receptor polypeptide (DR3) encoding cDNA.

KW Death domain; receptor; DR3-V1; DR3; recombinant; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..1254

FT /tag= a

FT /product= "Death domain containing receptor DR3"

FT sig_peptide 1..72

FT /tag= b

FT mat_peptide 73..1251

FT /tag= c

PN JP11000170-A.

PD 06-JAN-1999.

PF 12-MAR-1997; 97JP-0057503.

PR 06-FEB-1997; 97US-0037341.

PR 12-MAR-1996; 96US-0013285.

PR 17-OCT-1996; 96US-0028711.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (UNMI) UNIV MICHIGAN.

DR WPL; 1999-124390/11.

DR P-PSDB; AAW95538.

PT New death domain containing receptor and recombinant vector -

PT optionally comprising leader sequence

PS Claim 6; Fig 3; 50pp; Japanese.

XX The invention provides nucleotide sequences encoding death domain

XX containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone

XX is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is

XX contained in ATCC deposition No. 97457. Recombinant vectors comprising

XX the nucleic acid sequences and optionally the leader sequences are

XX used for the recombinant production of the proteins. The present

XX sequence represents a cDNA encoding the death domain containing

XX receptor polypeptide (DR3).

XX Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:

Pred. No.: 7.95e-75 Length: 1254
 Score: 1101.00 Matches: 186
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x AAC68777 (1-1254)

QY 1 LeuLeuGLYAlaArgAlaGlnGlyLysThrArgSerProArgCysAspCysAlaGlyAsp 20
 DB 55 CTGCTGGGGCCCGGGCCGAGGGGCGACCTGAGCCCGAGGTGTGACTGTGCGGGTAC 114
 QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlnHisTyrLeuLys 40
 DB 115 TTCACAGAGAAGATGTGCTGTTTGTGTGACAGAGCTGCCACGGGGGCACTACTGAG 174
 QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
 DB 175 GCCCCTTGACAGAGCCCTGCGCAACTCCACTGCTGTGTGTCCTCCCAAGACACTTC 234
 QY 61 LeuAlaTrpLysAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
 DB 235 TTGGCCCTGGGAGAACCACTTAATGTGAAATGTGCCGCGCAGGCTGTGATGAGCAG 294
 QY 81 AlaSerGlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
 DB 295 GCCTCCAGAGTGGCGCGGAGAACTGTTCAGCACTGCCACACCCGCTGTGCTGAG 354
 QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheThrCys 120
 DB 355 CCAGGCTGGTGTGTGGAGTCCAGGTCAGCCAAATGTGTGACAGTTCACCTCTACTGC 414
 QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
 DB 415 CAACCATGCTAGACTGGGGGCGCTGACACCGCACACAGGCTACTGTGTCCCGAGA 474
 QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSer 160
 DB 475 GATACGACGTGGGAGACTGCTGCGCTGTATGAAATGCGCATGGCGATGCGTCTCC 534
 QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaValCysGlyTTPArg 180
 DB 535 TGCCTCCAGCGACACCTGGGGAGCTGTCCAGAGCGGTGCTGCTGTGTGCTGAGG 594
 QY 181 GlnMetPheTrpValGln 186
 DB 595 CAGATGTCTGGGTCCAG 612
 RESULT 3
 AAC68777
 ID AAC68777 standard; cDNA; 1254 BP.
 AC AAC68777;
 DT 20-FEB-2001 (first entry)
 XX Human death domain containing receptor DR3 coding sequence.
 KW Human; death domain containing receptor; DR3; cancer;
 KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
 KW neurodegenerative disease; angiogenesis; ss.
 OS Homo sapiens.
 PN WO200064465-A1.
 PD 02-NOV-2000.
 PF 21-APR-2000; 2000MO-US10741.
 XX

PR 22-APR-1999; 99US-0130488.
 PR 28-MAY-1999; 99US-0136741.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (UNMI) UNIV MICHIGAN.
 PA (YUGG) YU G.
 PA (NIJU) NI J.
 PA (GENT) GENTZ R L.
 PA (DILL) DILLON P J.
 PA (DIXI) DIXIT V M.
 XX
 PI Yu G, NI J, Gentz RL, Dillon PJ, Dixit VM;
 DR WPI: 2000-687263/67.
 DR P-PSDB; AAB36265.
 XX
 PT Treating graft-versus-host disease, cancer, immunodeficiency or an
 PT autoimmune disease comprising administering an antibody to Death Domain
 PT containing Receptor proteins and a second therapeutic agent -
 PS Example 2B; Fig 2; 273pp; English.
 CC The present invention provides the protein and coding sequences for two
 CC death domain containing receptors, designated DR3 and DR3-V1. These
 CC receptors are involved in apoptosis, and the sequences given can be used
 CC in the treatment of cancers, infections, cardiovascular disorders such as
 CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
 CC and congenital heart defects, neurodegenerative diseases including
 CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
 CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
 CC and to promote angiogenesis and wound healing.
 SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;
 Alignment Scores:
 Pred. No.: 7.95e-75 Length: 1254
 Score: 1101.00 Matches: 186
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0
 US-09-993-234-6_COPY_19_204 (1-186) x AAC68777 (1-1254)
 QY 1 LeuLeuGLYAlaArgAlaGlnGlyLysThrArgSerProArgCysAspCysAlaGlyAsp 20
 DB 55 CTGCTGGGGCCCGGGCCGAGGGGCGACCTGAGCCCGAGGTGTGACTGTGCGGGTAC 114
 QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlnHisTyrLeuLys 40
 DB 115 TTCACAGAGAAGATGTGCTGTTTGTGTGACAGAGCTGCCACGGGGGCACTACTGAG 174
 QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
 DB 175 GCCCCTTGACAGAGCCCTGCGCAACTCCACTGCTGTGTGTCCTCCCAAGACACTTC 234
 QY 61 LeuAlaTrpLysAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
 DB 235 TTGGCCCTGGGAGAACCACTTAATGTGAAATGTGCCGCGCAGGCTGTGATGAGCAG 294
 QY 81 AlaSerGlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
 DB 295 GCCTCCAGAGTGGCGCGGAGAACTGTTCAGCACTGCCACACCCGCTGTGCTGAG 354
 QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheThrCys 120
 DB 355 CCAGGCTGGTGTGTGGAGTCCAGGTCAGCCAAATGTGTGACAGTTCACCTCTACTGC 414
 QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
 DB 415 CAACCATGCTAGACTGGGGGCGCTGACACCGCACACAGGCTACTGTGTCCCGAGA 474
 QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSer 160

Db 475 GATACGCTGCTGGAGCCCTGCTGCTTCTATGAACATGGGATGGCGCTGTC 534
QY 161 CysProthSerThrLeuGlySerCysProGluArgCysAlaIleValCysGlyTyrParg 180
Db 535 TGCCCGACGACGACCCCTGGAGGCTGTCCAGAGCGCTGTGCCCTGTGTGGCTGGAG 594
QY 181 GlnMetPheTyrValGln 186
Db 595 CAGATGTTCTGTGGTCCAG 612

RESULT 4

AA91180
ID AA91180 standard; cDNA; 1634 BP.
XX
AC AA91180;

DE 14-APR-1998 (first entry)

DE Human apoptosis protein Apo-3 cDNA clone FH20.57.

KM Apo-3; apoptosis; human; therapy; drug screening; ss.

OS Homo sapiens.

EH Key Location/Qualifiers

FT CDS 89..1342

FT sig_peptide 89..160

FT mat_peptide 161..1339

FT /note= "determined by hydrophathy analysis"

FT /tag= c

XX WO9737020-A1.

XX 09-OCT-1997.

XX 31-MAR-1997; 97WO-US05230.

XX 23-SEP-1996; 96US-0710802.

XX 01-APR-1996; 96US-0625328.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ;

XX WPI; 1997-503105/46.

XX

XX Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis

XX in mammalian cells

XX Example 1; Page 45-46; 70pp; English.

XX

XX cDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see

XX W26709), designated Apo-3, that stimulates or induces apoptotic

XX activity in mammalian cells. It was isolated from a human foetal

XX heart cDNA library by screening with probes (see 791183-84) based

XX on an EST sequence (Genbank locus W71984) that showed homology to

XX the intracellular domain of human TNFR1 and CD95. Amino acid

XX residues 1-181 of Apo-3 are identical to another novel apoptosis

XX polypeptide, Apo-2LI (see W26708). Nucleic acids encoding Apo-3

XX can be used diagnostically for tissue-specific typing and to

XX extracellular domain (amino acids 1-198) or death domain (amino

XX acids 338-417). Apo-3 can be used to induce apoptosis or

XX NF-kappa-B or JNK-mediated gene expression for therapeutic

XX purposes. Non-human transgenic animals containing cells that

XX express Apo-3 nucleic acid, and knockout animals containing

XX cells that have an altered Apo-3 gene, can be used in drug

XX screening and development.

XX Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:

Pred. No.: 1,08e-74 Length: 1634
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-993-234-6_copy_19_204 (1-186) x AA91180 (1-1634)

QY 1 LeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20

Db 143 CTGCTGGGGGCGCCGCGCCAGGCGCGCACTGAGCCCGAGCTGTGACTGTGCGCGTAC 202

QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40

Db 203 TTCCACAAGAAGATTGGTCTGTTTGTTCAGAGGCTGTCCAGCGGGGACTACCTGAAG 262

QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60

Db 263 GCCCTTGACAGGAGCGCTGGGCGCACTCCACCTGCTGTGTCTCCCAAGACCTTC 322

QY 61 LeuAlaTrrpGluAsnHisSerSerGluCysAlaArgCysGlnAlaCysAspGluGln 80

Db 323 TTGGCTGGAGAGAACCCATTAATTCGAATGTGCCCGCTGCAGGCTGTGATGAGCAG 382

QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyLys 100

Db 383 GCCCTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTTAAAG 442

QY 101 ProGlyTrrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120

Db 443 CCAGGCTGTGTTGTGGAGTCCAGGTCCAGGCAATGTGTGAGCTGACCTTCTACTGC 502

QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuGlySerArgArg 140

Db 503 CAACCATGCTTACAGCTGCGGGGCGCTGCACCGCACACAGGCTACTGTGCTCCGACAG 562

QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSer 160

Db 563 GATACGACTGTGGAGACCTGCTGCTGCTTATGACATGACATGCTGCTGCTGCTGCTG 622

QY 161 CysProthSerThrLeuGlySerCysProGluArgCysAlaIleValCysGlyTyrParg 180

Db 623 TGCCCGACGACGACCCCTGGGAGCTGTCCAGAGCGCTGTGCGCTGTGTGCTGGAGG 682

QY 181 GlnMetPheTyrValGln 186

Db 683 CAGATGTTCTGTGGTCCAG 700

Db

RESULT 5

AAH27782

ID AAH27782 standard; DNA; 1634 BP.

XX

XX AAH27782;

XX

XX 15-AUG-2001 (first entry)

XX

XX Human genomic DNA encoding a rheumatoid arthritis associated protein.

XX

XX Rheumatoid arthritis; transmembrane protein; human; ds.

XX

XX Homo sapiens.

XX

XX Key Location/Qualifiers

XX CDS 89..1342

XX /tag= a

XX /product= "Rheumatoid arthritis associated protein"

XX

XX WO200132921-A2.

XX

XX 10-MAY-2001.

XX

XX

XX

XX

XX

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XX 01-NOV-2000; 2000WO-JP07690.
XX
XX 01-NOV-1999; 99JP-0310805.
XX
XX (SHIO/) SHIOZAWA S.
XX
XX Shiozawa S, Konishi Y;
XX
XX WPI; 2001-308750/32.
XX
XX P-PSDB; AAB97370.
XX
XX
XX Diagnosing rheumatoid arthritis by probing digested human genomic DNA
XX or comparing expression of mRNA or polypeptide of a region of
XX transmembrane protein
XX
XX Claim 1; Page 14-18; 21pp; Japanese.
XX
XX This invention relates to a method of diagnosing chronic rheumatoid
XX arthritis by digesting human genomic DNA with EcoRI and hybridizing it
XX with a probe containing a fragment of the present sequence which
XX represents DNA encoding a transmembrane protein. The method is used for
XX the diagnosis of chronic rheumatoid arthritis, and for developing new
XX treatments.
XX
XX Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1,08e-74 Length: 1634
XX Score: 1101.00 Matches: 186
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX Gaps: 0
XX
XX
XX US-09-993-234-6_COPY_19_204 (1-186) x AAB27782 (1-1634)
XX
XX 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
XX 143 CTGCTGGGGGCGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 202
XX
XX 21 PheHisLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 40
XX 203 TTCACACAGAAAGATTGGTGTGTTTGTGTCAGAGGCTGCCAGCGGGGCGGCGGCGGCGG 262
XX
XX 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
XX 263 GCCCTTGCACAGGAGCCCTGCGGCACTCCACCTGCTGTGTTCCCAAGACACCTTC 322
XX
XX 61 LeuAlaTrpGluAsnHisAsnSerGlnCysAlaArgCysGlnAlaCysAspGluGln 80
XX 323 TTGGCTGGGAGACACACATATTGTAATGTGCCGCTCCAGGCGCTGTGATGAGAGAG 382
XX
XX 81 AlaSerGlnValAlaLeuGluAsnGlySerSerAlaValAlaAspThrArgCysGlyLys 100
XX 383 GCCCTCCAGGAGGCGGCTGGAGAACTGTTCACAGTGGCCGCGCACACCGCTGTGGCTGAAG 442
XX
XX 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerSerProPheTrpCys 120
XX 443 CCAGGCGGTGGTGGAGTGGCAGGTCCAGTCAATGTGTCCAGCACTTCACTTCTACTGC 502
XX
XX 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
XX 503 CAAACCAATGCTAGACTGCGGGGCGCTGCACCGCACACAGCGGTACTGTGTCCCGGAGA 562
XX
XX 141 AspThrAspCysGlyTrpCysLeuProGlyPheTrpGlnHisGlyAspArgLysValSer 160
XX 563 GATACCTACTGTGGACCTGCTGCTGGCTTCTATTAACATGGCGATGGCTGGTGTGCC 622
XX
XX 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
XX 623 TGCCCAAGAGACCCCTGGGGAGCTGTCCAGAGGCGTGTGGCTGTGTGTGGTGTGAGG 682
XX

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```

XX 181 GlnMetPheTrpValGln 186
XX 683 CAGATGTTCTGCTCCAG 700
XX
XX RESULT 6
XX AAL47186
XX ID AAL47186 standard; cDNA; 1634 BP.
XX
XX AAL47186;
XX
XX 22-AUG-2002 (first entry)
XX
XX Human rheumatoid arthritis associated DR3 gene related cDNA #1.
XX
XX Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
XX kw gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 89..1342
XX FT /*tag=a
XX FT /product="AAB17879"
XX
XX WO200234912-A1.
XX
XX 02-MAY-2002.
XX
XX 24-OCT-2001; 2001WO-JP09313.
XX
XX 24-OCT-2000; 2000JP-0324296.
XX
XX 27-MAR-2001; 2001JP-0090546.
XX
XX 30-MAR-2001; 2001JP-0099990.
XX
XX (NEW!) NEW IND RES ORG.
XX
XX (SHIO/) SHIOZAWA S.
XX
XX Shiozawa S, Konishi Y;
XX
XX WPI; 2002-417132/44.
XX
XX P-PSDB; AAB17879.
XX
XX Genomes, particularly DR3 genomic DNA, participating in rheumatoid
XX arthritis via mutation, useful in evaluating disease onset and its
XX possibility and providing therapy and remedies
XX
XX Example 1; Page 66-69; 84pp; Japanese.
XX
XX The present invention relates to the human DR3 gene, which is associated
XX with rheumatoid arthritis. Certain mutations in the gene can be linked to
XX the disease. The sequences can be used to evaluate disease onset and its
XX possibility and to provide therapy and remedies. The present sequence is
XX a coding sequence described in the exemplification of the invention.
XX
XX Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1,08e-74 Length: 1634
XX Score: 1101.00 Matches: 186
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX Gaps: 0
XX
XX
XX US-09-993-234-6_COPY_19_204 (1-186) x AAL47186 (1-1634)
XX
XX 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
XX 143 CTGCTGGGGGCGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 202
XX
XX 21 PheHisLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 40
XX 203 TTCACACAGAAAGATTGGTGTGTTTGTGTCAGAGGCTGCCAGCGGGGCGGCGGCGGCGG 262
XX

```

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QY 41 AlaProCysThrGluProCysGlnAsnSerThrCysLeuValCysProGlnAspThrPhe 60
D 253 GCGCTTGCAGGAGACCCCTGCGGACACCTGCTGTGTGTGTCACCAACACACCTTC 322
QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
D 323 TTGGCGCTGGAGAACACCATTAATCTGAATGTGCGCGCTGCAGACCTGTGATAGAG 382
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
D 383 GCGTCCGAGGAGGCGGTGGAACACTGTTCACAGAGCGCGACACCGCTGTGGCTGTAA 442
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheThrCys 120
D 443 CAGAGCGTGTGTGGAGTGCAGGTCCAGCAATGTGTACAGTCCACCTTCTACAGC 502
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
D 503 CACCAATGCTAGACTGGGGGCGCTGCACGACACAGGCTACTGTTCGCCGAG 562
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTrpGluHisGlyAspGlyCysValSer 160
D 563 GATACTGACTGTGGAGCTGCTGCTGCTTCTATGAAACATGGCGATGGCTGCTGCC 622
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
D 623 TGCCCGACGAGACACCTTGGGAGCTGTCCAGCGCTGTGCTGTGTGGTGAGG 682
QY 181 GlnMetPheTrpValGln 186
D 683 CAGATGTTCTGGGTCCAG 700
Db
RESULT 7
AAC91477
ID AAC91477 standard; cDNA; 1662 BP.
AC AAC91477;
XX
XX 21-MAR-2001 (first entry)
DT
XX
XX Human PRO779 cDNA.
DE
XX
XX Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW antihemetic; cardiast; antianaemic; immunosuppressive; antihypoid;
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
KW antiallergic; antiasthmatic; immune related disorder;
KW hepatobiliary disease; autoimmune disease; allergy; ss.
XX
OS Homo sapiens.
XX
PN WO200073452-A2.
XX
XX 07-DEC-2000.
PF
XX
XX 02-JUN-2000; 2000WO-US15264.
XX
XX
XX 02-JUN-1999; 99WO-US12252.
XX 20-JUL-1999; 99US-0144732.
XX 20-JUL-1999; 99US-0144738.
XX 28-JUL-1999; 99US-0146222.
XX 01-SEP-1999; 99WO-US20111.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 29-OCT-1999; 99US-0162506.
XX 30-NOV-1999; 99WO-US28313.
XX 01-DEC-1999; 99WO-US28634.
XX 09-DEC-1999; 99US-0170262.
XX 20-DEC-1999; 99WO-US10911.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04341.

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PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US04914.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PA (GERTH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;
PI Wood WI;
XX
DR WPI: 2001-025253/03.
DR P-PSDB: AAB50918.
XX
XX thirty three nucleic acids encoding PRO polypeptides which are useful
XX in the diagnosis and treatment of immune related disorders, e.g.
XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
XX thyroiditis and diabetes mellitus
PS
PS Claim 48; Fig 33; 218pp; English.
XX
XX The present sequence is one of thirty three nucleic acids encoding PRO
XX polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
XX antagonists are useful for treating and diagnosing immune related
XX disorders such as systemic lupus erythematosus, rheumatoid arthritis,
XX osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
XX systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
XX syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
XX anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
XX immune-mediated renal disease, demyelinating diseases of the central
XX and peripheral nervous systems (such as multiple sclerosis, idiopathic
XX demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
XX inflammatory demyelinating polyneuropathy), hepatobiliary diseases
XX (such as infectious, autoimmune chronic active hepatitis, primary
XX biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
XX inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
XX disease, autoimmune or immune-mediated skin diseases (such as bullous
XX skin diseases, erythema multiforme, contact dermatitis, psoriasis),
XX allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
XX food hypersensitivity and urticaria), immunological diseases of the
XX lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
XX and hypersensitivity pneumonitis), transplantation associated diseases
XX including graft rejection and graft-versus-host diseases.
SQ
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;
Alignment Scores:
Pred. No.: 1,1e-74 Length: 1662
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-993-234-6_COPY_19_204 (1-186) x AAC91477 (1-1662)
QY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
D 157 CTGCTGGGCGCGCGGCGGACGAGGCGGACGAGCCAGGTGTACTGTCCGGTGCAC 216
QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTrpLeuLys 40
D 217 TTCACAAAGAAATGTGTTGTGTTGTCAGAGGCTGCGCCAGCGGGGACATACCTGAAG 276
QY 41 AlaProCysThrGluProCysGlnAsnSerThrCysLeuValCysProGlnAspThrPhe 60
D 277 GCGCTTGCAGGAGACCCCTGCGGACACCTGCTGTGTGTGTCACCAACACACCTTC 336

```

QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 337 TTGGCTGGGAGAACCCCAATTCGAAATGTCGCCGCTGCCGCTGTGATGACAG 396
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 397 GCCCTCCAGGTGGCGCTGGAGAACTGTTCAGCACTGGCCGACACCCCTGTGGCTGTAA 456
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTrpCys 120
DB 457 CCAAGCTGTTGTGGAGTGCAGAGTCCAGCAATGTGTCAAGCACTTCACTTACTGTC 516
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 517 CCAACATGCTAGACCTCGGGGCTCCACCGCACACGGCTACTGTCTCCGAGAGA 576
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTrpGluHisGlyAspGlyCysValSer 160
DB 577 GATACCTACTGTGGAGACTGCTGCTGCTTCTATGAACTGGCGATGGCTGCTGCTCC 636
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
DB 637 TGCCCCAGAGACACCTGGGGAGCTGTCCAGAGCGTGTGCGCTGTGTGCTGGAGG 696
QY 181 GlnMetHetrPValGln 186
DB 697 CAGATGTCTGGGTCCAG 714
RESULT 8
ID ABK40265
AC ABK40265 standard; cDNA; 1662 BP.
XX
XX 15-JUL-2002 (first entry)
DE cDNA encoding human PRO779 polypeptide.
XX
XX Human: PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukemia; neuronal disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder;
KW gene therapy; cytostatic; neuroprotective; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200153486-A1.
XX
XX 26-JUL-2001.
XX
XX 11-FEB-2000; 2000WO-US03565.
XX
XX 08-MAR-1999; 99MO-US05028.
PR 11-MAR-1999; 99US-123972P.
PR 11-MAY-1999; 99US-133459P.
PR 02-JUN-1999; 99MO-US12252.
PR 22-JUN-1999; 99US-140650P.
PR 22-JUN-1999; 99US-140653P.
PR 20-JUL-1999; 99US-144758P.
PR 26-JUL-1999; 99US-145698P.
PR 28-JUL-1999; 99US-146232P.
PR 17-AUG-1999; 99US-149385P.
PR 31-AUG-1999; 99US-151689P.
PR 01-SEP-1999; 99MO-US20111.
PR 15-SEP-1999; 99MO-US21090.
PR 30-NOV-1999; 99MO-US28313.
PR 01-DEC-1999; 99MO-US28301.
PR 01-DEC-1999; 99MO-US28634.
PR 05-JAN-2000; 2000WO-US00219.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Goddard A, Godowski RJ, Gurney AL, Hillan KJ,
PI Marsters SA, Pan J, Pilleri RM, Roy MA, Smith V, Stone DM;

PI Watanabe CK, Wood WI;
XX WPI; 2002-205567/26.
DR P-PSDB: AAU86139.
XX
PT Thirty five nucleic acids encoding PRO polypeptides, useful for
PT treating benign or malignant tumours, leukaemias and lymphoid
PT malignancies, inflammatory, angiogenic and immunologic disorders -
PS Claim 50; Fig 23; 302pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides and the polynucleotide sequences encoding them. The
XX PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
XX useful for treating benign or malignant tumours (e.g. renal, kidney,
XX bladder, breast, etc), leukaemias and lymphoid malignancies, other
XX disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
XX macrophagal, stromal and blastocoele disorders, inflammatory, immune
XX and angiogenic disorders. The polynucleotide sequences are also
XX useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
XX polypeptides of the invention.
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;
Alignment Scores:
Pred. No.: 1,1e-74 Length: 1662
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-09-993-234-6_COPY_19_204 (1-186) x ABK40265 (1-1662)
QY 1 LeuGluGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 157 CTGGCTGGGGGCGCCGCGCCAGGCGCGCACTGTGAGCCCGAGTGTGACTGTGCGGTAC 216
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTrpLeuLys 40
DB 217 TTCACAAAGAAATGTGGTCTTTTGTTCGAGAGCTGCCCCAGCGGGGCACTACTGTAA 276
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 277 GCCCTTGACAGGAGCCCTGGCGCACTCCACTGTGTGTCCCAAGACACCTTC 336
QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 337 TTGGCTGGGAGAACCCCAATTCGAAATGTCGCCGCTGCCGCTGTGATGACAG 396
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 397 GCCCTCCAGGTGGCGCTGGAGAACTGTTCAGCACTGGCCGACACCCCTGTGGCTGTAA 456
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTrpCys 120
DB 457 CCAAGCTGTTGTGGAGTGCAGAGTCCAGCAATGTGTCAAGCACTTCACTTACTGTC 516
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 517 CCAACATGCTAGACCTCGGGGCTCCACCGCACACGGCTACTGTCTCCGAGAGA 576
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTrpGluHisGlyAspGlyCysValSer 160
DB 577 GATACCTACTGTGGAGACTGCTGCTGCTTCTATGAACTGGCGATGGCTGCTGCTCC 636
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
DB 637 TGCCCCAGAGACACCTGGGGAGCTGTCCAGAGCGTGTGCGCTGTGTGCTGGAGG 696
QY 181 GlnMetHetrPValGln 186
DB 697 CAGATGTCTGGGTCCAG 714

RESULT 9
AAT89426
ID AAT89426 standard; cDNA: 1783 BP.
XX
AC AAT89426;
XX
XX 02-MAR-1998 (first entry)
XX
DE Death domain containing receptor DR3-V1 cDNA.
XX
KM Death domain containing receptor; DR3-V1; human; apoptosis;
XX Inflammation; NF-kappaB; ds.
XX
OS Homo sapiens.
XX
FH Key
FH CDS Location/Qualifiers
FT 198..1484
FT /*tag= a
FT sig_peptide 198..302
FT /*tag= b
FT mat_peptide 304..1481
FT /*tag= c
XX
PN WO9733904-A1.
XX
PD 18-SEP-1997.
XX
PF 17-OCT-1996; 96MO-US16849.
XX
PR 12-MAR-1996; 96US-0013285.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
XX
PI Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
XX
DR WPI: 1997-470812/43.
DR P-PSDB; AAW31516.
XX
PT Death domain containing receptor polypeptide(s) DR3 and DR3-V1 -
PT for activation of apoptosis and NF-kappaB; antagonists can be used
PT to treat inflammatory diseases
XX
PS Claim 2; Page 71-73; 108pp; English.
XX
XX This cDNA clone, deposited as ATCC 97456, codes for human death
CC domain containing receptor DR3-V1 (see AAW31516), a novel member of
CC the tumour necrosis factor receptor family. It was isolated from a
CC cDNA library derived from cells of a human testis tumour. Related
CC death domain containing receptor DR3 cDNA (see AAT89427) was isolated
CC from a HUVEC cDNA library. The genes have also been identified in
CC cDNA libraries of foetal liver, foetal brain, tonsil and leukocyte.
CC Nucleic acids encoding full-length or mature DR3-V1 can be used to
CC produce recombinant polypeptides in transformed host cells. These
CC polypeptides can be used to treat diseases and disorders associated
CC with the inhibition of apoptosis. Antagonists, such as antibodies
CC raised against DR3-V1, can be used to treat diseases and disorders
CC associated with increased apoptosis and for treating inflammatory
CC diseases and disorders.
XX
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Alignment Scores:
Pred. No.: 1.19e-74 Length: 1783
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x AAT89426 (1-1783)

QY 1 LeuLeuGIYAlaArgAlaGlnGlyLThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 285 TTGCTGGGGGGCCCGGGCCAGGGCCAGCTGCTAGCCCGAGTGTGATGCGCGGTAC 344
QY 21 PheHisLysLysIleGlyLeuPheCysSerArgGlyCysProAlaGlnHisTyrLeuLys 40
Db 345 TTCCACAGAGAGATTGGTGTGTTTGTGGCAGAGCGTCCAGCGGGGCACTACTAGAG 404
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 405 GCCCTTGACAGGAGCCCTGGGCACTCCACCTGCTGTGTCTCCCAAGACACCTTC 464
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 465 TTGGCTGGGAGAACACCACTAATTCGAAATGTCCCGCTGGAGGCTGTGATGAGCAG 524
QY 81 AlaSerGlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 525 GCCCTCCAGGTGGCGCTGGAGAACCTGTTCAGCACTGGCCGACACCCCTGTGGCTTAA 584
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 585 CCAAGCTGTTGTGGAGTGCAGAGTTCAGCCATGTGTTCAGAGTTTCACTTACTGC 644
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 645 CAACCATGCTAGACTGGGGGCTGCACCGCACACAGGCTACTGTCTCCGAGAG 704
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisLysAspGlyCysValSer 160
Db 705 GATACGACTGTGGAGACTGCTGCTGCTGTATGAAATGCGCATGCTCGCTCGTCC 764
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180
Db 765 TGCCCCAGCAGACCTCGGGGAGCTGTCCAGAGACGCTGTGCCCTGTCTGTGCTGAG 824
QY 181 GlnMetPheTrpValGln 186
Db 825 CAGATGTCTGGGTCCAG 842

RESULT 10
AAX00924
ID AAX00924 standard; cDNA: 1783 BP.
XX
XX AAX00924;
XX
AC AAX00924;
XX
XX 25-MAR-1999 (first entry)
XX
DE Death domain containing receptor polypeptide (DR3-V1) encoding cDNA.
XX
XX Death domain; receptor; DR3-V1; DR3; recombinant; ds.
XX
OS Homo sapiens.
XX
FH Key
FH CDS Location/Qualifiers
FT 198..1484
FT /*tag= a
FT /*product= "Death domain containing receptor DR3-V1"
FT sig_peptide 198..300
FT /*tag= b
FT mat_peptide 301..1481
FT /*tag= c
XX
XX JP11000170-A.
XX
XX
XX 06-JAN-1999.
XX
XX 12-MAR-1997; 97JP-0057503.
XX
XX 06-FEB-1997; 97US-0037341.
XX 12-MAR-1996; 96US-0013285.
XX 17-OCT-1996; 96US-0028711.
XX

QY 41 AlAPrOCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 405 GCCCTTGGACGAGAGCCCTGGCGCAACTGCACCTGCTGTGTGTCCTCCCAACACCTTC 464
QY 61 LeuAlaTrpGlnAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGln 80
DB 465 TTGGCTTGGAGAACCCACATTAATTCGTAAATGTGCCCGCTGGCAGGCGCTGATGAGCAG 524
QY 81 AlaSerGlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyAsp 100
DB 525 GCCCTCCAGGTGGCGCTGGAGAACTGTTCCAGCAGTGGCCGACACCGCTGTGGCTGTAG 584
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerSerProPheThrCys 120
DB 585 CCAGGCTGTGTGGAGTGGCAGGTGACCAATGTGTGACAGATTCACCTTCTACTGC 644
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArg 140
DB 645 CAACCATCCTAGACTGGGGGGCCCTGCACCGCACACACGCTACTCTGTCCCGCAGA 704
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheThrGluHisGlyAspGlyCysValSer 160
DB 705 GATACCTGCTGGGACCTGCTGCTGCTTATGAACTGGCGATGGCTGGCTGCTCC 764
QY 161 CysProThrSerThrLeuGlySerCysProGlnArgCysAlaAlaValCysGlyTrpArg 180
DB 765 TGCCCGACGAGACCCCTGGGGAGCTGTCCAGAGCGCTGTGCGCTGTGCTGGAGG 824
QY 181 GlnMetPheTrpValGln 186
DB 825 CAGATGTTCTGGGTCCAG 842

RESULT 12

AAV28700 standard; cDNA; 1847 BP.

AAV28700;

20-AUG-1998 (first entry)

Human apoptosis inducing receptor coding sequence.

Apoptosis inducing receptor; ATR protein; human; cell death regulator;
Type I transmembrane protein; tumour cell death; autoimmune disease;
therapy. ss.

Homo sapiens.

Key location/Qualifiers
CDS 236..1489
FT /tag= a
FT /product= AIR

W09814565-A1.

09-APR-1998.

03-OCT-1997; 97WO-US17876.

04-OCT-1996; 96US-0044456.

(IMMV) IMMUNEX CORP.

Perkins PA;

WPI; 1998-240077/21.

P-PSDB; AAM57045.

DNA encoding apoptosis inducing receptor - which is Type I
transmembrane protein, useful for regulating cell death

Claim 2; Page 28-30; 45pp; English.

CC This sequence encodes the human apoptosis inducing receptor (AIR) of the
CC invention. AIR is a Type I transmembrane protein, soluble forms of which
CC can be used to regulate cell death in a therapeutic setting. Soluble AIR
CC can also be used in vitro to block apoptosis or AIR-expressing cells, or
CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain
CC of AIR can be used to develop assays for inhibitors of AIR-induced cell
CC death, which is useful to regulate cell death in a therapeutic setting as
CC well as in vitro. Agonists of AIR activity can be used to kill tumour
CC cells that express AIR, or T cells expressing AIR in autoimmune diseases.
XX
XX
SQ Sequence 1847 BP; 316 A; 605 C; 579 G; 347 T; 0 other;

Alignment Scores:

Pred. No.:	1.24e-74	Length:	1847
Score:	1101.00	Matches:	186
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	19	Gaps:	0

US-09-993-234-6_COPY_19_204 (1-186) x AAV28700 (1-1847)

QY 1 LeuAlaTrpGlnAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGln 20
DB 290 CTGCTGGGGGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 349
QY 21 PheHisLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 40
DB 350 TTCACACAGAGAGATGTGCTGTTTGTTCAGAGGCTGCGCCACGGGGGACATCTGAAG 409
QY 41 AlAPrOCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 410 GCCCTTGGACGAGAGCCCTGGCGCAACTGCACCTGCTGTGTGTCCTCCCAACACCTTC 469
QY 61 LeuAlaTrpGlnAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGln 80
DB 470 TTGGCTTGGAGAACCCACATTAATTCGTAAATGTGCCCGCTGGCAGGCTGATGAGCAG 529
QY 81 AlaSerGlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyAsp 100
DB 530 GCCCTCCAGGTGGCGCTGGAGAACTGTTCCAGCAGTGGCCGACACCGCTGTGGCTGAG 589
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerSerProPheThrCys 120
DB 590 CCAGGCTGTGTGGAGTGGCCAGGTGCAACATGTGTGACGAGATTCACCTTCTACTGC 649
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArg 140
DB 650 CAACCATCCTAGACTGGGGGGCCCTGCACCGCACACGCTACTCTGTCCCGCAGA 709
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheThrGluHisGlyAspGlyCysValSer 160
DB 710 GATACCTGCTGGGACCTGCTGCTGCTTATGAACTGGCGATGGCTGGCTGCTCC 769
QY 161 CysProThrSerThrLeuGlySerCysProGlnArgCysAlaAlaValCysGlyTrpArg 180
DB 770 TGCCCGACGAGACCCCTGGGGAGCTGTCCAGAGCGCTGTGCGCTGTGCTGGAGG 829
QY 181 GlnMetPheTrpValGln 186
DB 830 CAGATGTTCTGGGTCCAG 847

RESULT 13

ABL64119 standard; DNA; 1743 BP.

ABL64119;

15-MAY-2002 (first entry)

Breast cancer related gene sequence SEQ ID NO:2456.

Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

DE Nucleotide sequence of human TR3 gene.
 XX
 XX TR3; cell proliferation; leukemia; immunosuppressive; cytostatic;
 KM dermatological; antidiabetic; antidiabetic; neuroprotective; cardiant;
 KM antihypertoid; antiinflammatory; antiallergic; T-cell-inhibitor; ds.
 XX
 OS Homo sapiens.
 FH
 FH Key Location/Qualifiers
 FT CDS 1..1250
 FT /tag= a
 FT /transl_except= "(pos:481..482, aa:Asp)"
 FT /note= "this codon has an apparent 1 nucleotide
 FT deletion which alters the reading frame"
 FT /transl_except= "(pos:558..559, aa:Cys)"
 FT /note= "this codon has an apparent 1 nucleotide
 FT deletion which alters the reading frame"
 FT /transl_except= "(pos:638..639, aa:Ileu)"
 FT /note= "this codon has an apparent 1 nucleotide
 FT deletion which alters the reading frame"
 FT /transl_except= "(pos:718..719, aa:Met)"
 FT /note= "this codon has an apparent 1 nucleotide
 FT deletion which alters the reading frame"
 FT sig_peptide 1..72
 FT /tag= b
 FT mat_peptide 73..1247
 FT /tag= c
 XX
 PN WO200135995-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-US31692.
 XX
 PR 19-NOV-1999; 99US-0166583.
 XX
 PA (TITP/) TITTLE T V.
 PA (WEGM/) WEGMANN K W.
 XX
 PI Title TV, Wegmann KM;
 XX
 DR WPI; 2001-343711/36.
 DR P-PSDB; AAB84941.
 XX
 PT Composition for treatment of T-cell mediated disease e.g. arthritis,
 PT cancer comprises a biologically active TR3-specific binding agent
 PT especially a monoclonal antibody -
 XX
 PS Disclosure; Page 72; 77pp; English.
 XX
 CC The invention relates to a composition comprising a biologically active
 CC TR3-specific binding agent (I) that binds to TR3 and inhibits the
 CC proliferation of cells expressing TR3. (I) identified by the methods are
 CC useful for treating a subject suspected of having a disease associated
 CC with a proliferation of cells expressing TR3 especially leukemias or
 CC lymphomas or a T-cell mediated disease especially autoimmune diseases
 CC such as myasthenia gravis, systemic lupus erythematosus, rheumatoid
 CC arthritis, diabetes, multiple sclerosis, sarcoidosis, myocarditis,
 CC thyroiditis and tumours. (I) is also useful for treating a subject
 CC suspected of having graft-versus-host disease, rejection of a
 CC transplanted organ such as heart, liver, lung, kidney, pancreas, bowel,
 CC skin or an appendage, or inflammatory diseases, allergies and contact
 CC dermatitis. The present sequence represents the nucleotide sequence of
 CC human TR3 gene.
 CC
 SQ Sequence 1250 BP; 201 A; 419 C; 406 G; 224 T; 0 other;

DB: 22 Gaps: 0
 US-09-993-234-6_copy_19_204 (1-186) x AAF83770 (1-1250)
 QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProAlaGlyAspCysAlaGlyasp 20
 DB 55 CTGCTGGGGGGCCCGCCAGGCGCGACCTGTACCCAGGTGACTGTGCCGTGAC 114
 QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
 DB 115 TTCACAGAGAGATTGCTGTGTTGTTGTCAGAGGCTGCCAGCGGGCAGCTACTGAA 174
 QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuAlaCysProGlnAspThrPhe 60
 DB 175 GCCCTTGACAGGAGCCCTGCGCAATCCACCTGCTGTGTGTGCCAAGACACTTC 234
 QY 61 LeuAlaTTPGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGln 80
 DB 235 TTGGCTGGGAGAACACCATTAATCTGAAATGTCGCCCTGCCAGGCTGTGATAGCAG 294
 QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
 DB 295 GCTCCAGAGTGGCGCTGGAGAACTGTTACAGCAGTGGCCGACACCCGCTGTGCTAAG 354
 QY 101 ProGlyTTPPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
 DB 355 CCAGGCTGTGTTGTGGAGTGCAGGTCAGCCAAATGTGTCAGAGATGTCACCCCTTACTGC 414
 QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLysSerArgArg 140
 DB 415 CAAACATGCTTACTGACTGCGGGCCCTGCACCCGACACAGGCTTCTGTTCCGCCAGA 474
 QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
 DB 475 GATFAC-GACTGTGGGACCTGCTGCTGTCTGTGAACATGGGATGCTGCGTTC 533
 QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTTPArg 180
 DB 534 TGCCCCACGACGACCCCTGGGAGCGT-CCAGAGCGCTGTGCGCTGTGTGGTGGAG 592
 QY 181 GlnMetPheTTPValGln 186
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 ID ABL67258 standard; DNA; 816 BP.
 XX
 AC ABL67258;
 XX
 DT 15-MAY-2002 (first entry)
 DE
 XX
 XX Thyroid cancer related gene sequence SEQ ID NO:5595.
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200194629-A2.
 PD
 PD 13-DEC-2001.
 PF 30-MAY-2001; 2001WO-US10838.
 XX
 XX
 XX 05-JUN-2000; 2000US-209473P.
 XX 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-233133P.
 PR 18-SEP-2000; 2000US-233617P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.

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Pred. No.: 2.88e-70 Length: 1250
 Score: 1041.00 Matches: 184
 Percent Similarity: 98.92% Conservative: 0
 Best Local Similarity: 98.92% Mismatches: 2
 Query Match: 94.55% Indels: 2

147

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GenCore version 5.1.4_p5_4578
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Run on: April 6, 2003, 16:28:24 ; Search time 31.3989 Seconds
(without alignments)
1816.682 Million cell updates/sec

Title: US-09-993-234-6_COPY_19_204
Perfect score: 1101
Sequence: 1 LIGARAGGTRSPRCDCAGD.....GSCPERCAAVCGMRQMFVQ 186

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=human40.cdi
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued_Patents_NA:*

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- 2: /cgn2.6/prodata/1/lna/5B_COMB.seq:*
- 3: /cgn2.6/prodata/1/lna/5A_COMB.seq:*
- 4: /cgn2.6/prodata/1/lna/5B_COMB.seq:*
- 5: /cgn2.6/prodata/1/lna/PCTUS_COMB.seq:*
- 6: /cgn2.6/prodata/1/lna/Backfilesl.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1101	100.0	1254	3	US-08-815-469-3
2	1101	100.0	1634	4	US-08-928-069-11
3	1101	100.0	1634	4	US-08-828-683A-9
4	1101	100.0	1783	3	US-08-815-469-1
5	979	88.9	1438	4	US-08-928-069-5
6	979	88.9	1438	4	US-08-828-683A-5
7	692	62.9	433	4	US-08-928-069-2
8	692	62.9	433	4	US-08-828-683A-2
9	213	19.3	1956	2	US-08-762-308-10
10	212.5	19.3	1049	4	US-08-804-166-1
11	212.5	19.3	1049	4	US-08-910-991-1
12	205.5	18.7	1301	4	US-08-804-166-7

13	205.5	18.7	1301	4	US-08-910-991-7	Sequence 7, Appl1
14	205	18.6	600	1	US-08-050-319B-47	Sequence 47, Appl1
15	205	18.6	600	2	US-08-465-982-47	Sequence 47, Appl1
16	203.5	18.5	1202	4	US-08-804-166-3	Sequence 3, Appl1
17	203.5	18.5	1202	4	US-08-910-991-3	Sequence 3, Appl1
18	203	18.4	2062	1	US-08-050-319B-24	Sequence 24, Appl1
19	203	18.4	2062	2	US-08-465-982-24	Sequence 24, Appl1
20	203	18.4	2161	3	US-09-106-038A-1	Sequence 1, Appl1
21	203	18.4	2161	4	US-09-505-250-3	Sequence 3, Appl1
22	203	18.4	2175	1	US-08-321-668-1	Sequence 1, Appl1
23	203	18.4	2175	1	US-08-837-941-1	Sequence 1, Appl1
24	203	18.4	2175	1	US-08-126-016-1	Sequence 1, Appl1
25	203	18.4	2175	4	US-08-054-970-1	Sequence 1, Appl1
26	203	18.4	6889	1	US-08-286-740-2	Sequence 2, Appl1
27	203	18.4	6889	5	PCT-US95-09576-2	Sequence 2, Appl1
28	203	18.4	6896	2	US-08-627-151A-6	Sequence 6, Appl1
29	201	18.3	1147	4	US-08-604-166-5	Sequence 5, Appl1
30	201	18.3	1147	4	US-08-910-991-5	Sequence 5, Appl1
31	200.5	18.2	483	4	US-09-326-394-1	Sequence 1, Appl1
32	200.5	18.2	1478	4	US-09-149-922-6	Sequence 6, Appl1
33	191	17.3	543	4	US-09-513-007-3	Sequence 3, Appl1
34	191	17.3	2440	4	US-09-513-007-1	Sequence 1, Appl1
35	190	17.3	1724	5	PCT-US96-12374-1	Sequence 1, Appl1
36	189	17.2	1724	4	US-08-509-024-1	Sequence 1, Appl1
37	189	17.2	1724	4	US-09-333-279-1	Sequence 1, Appl1
38	182	16.5	579	4	US-09-146-950-3	Sequence 3, Appl1
39	182	16.5	591	4	US-09-146-950-19	Sequence 19, Appl1
40	182	16.5	1596	4	US-09-146-950-17	Sequence 17, Appl1
41	182	16.5	1929	4	US-09-146-950-1	Sequence 1, Appl1
42	182	16.5	4622	4	US-08-509-024-6	Sequence 6, Appl1
43	182	16.5	4622	4	US-09-333-279-6	Sequence 6, Appl1
44	170.5	15.5	477	1	US-08-050-319B-53	Sequence 53, Appl1
45	170.5	15.5	477	2	US-08-465-982-53	Sequence 53, Appl1

ALIGNMENTS

RESULT 1
US-08-815-469-3
; Sequence 3, Application US/08815469
; Patent No. 6153402
GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reinher L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; City: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE: HERewith
; CLASSIFICATION: 435
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 6153402 Yet Assigned
; FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285


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OY      121  GINPFCYSLEAASPCYSGLVAILENHISARHGISHTHARGLEULEAUCYSSEATARG 1408
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DB       503  CACCATTCCTTAGACTGCGGGGCCCTGCACCCGACACAGGGTACTGTGTCCCCGAGA 5623
OY      141  ASPTTHASPcysgltYrHCysleuProglYPhetYrgIunHislaSPglYCysValSer 1606
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DB       563  GATACTGACTGCTGGAGACTGCGCTGCGTTTATGAACAATGGCAGTGGCTGTCC 6222
OY      161  CysProThrSerThrLeuglySerCysProGluaRgcysalaalavalCysgltYTParg 1800
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DB       623  TGCCCCAGACACCACCTGGGGAGCGTGTCACAGAGCGCTGTGCGCTGTGTGGCTGGAG 6822
OY      181  GlnmetPheTrpValGln 186
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DB       683  CAGATGTTCTGGGTCCAG 700

RESULT 3
US-08-828-683A-9
: Sequence 9, Application US/08828683A
: Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipatn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-828-683A-9

Alignment Scores:
Pred. No.:          2,08e-90           Length:    1634
Score:              1101.00           Matches:     186
Percent Similarity: 100.00%           Conservative: 0
Best local Similarity: 100.00%         Mismatches:  0
Query Match:        100.00%           Indels:      0
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Oy      21 PheHisLysLysIleGlyLeuPheCysAsnArgLysCysProAlaGlnHisIstYLeuLys 40
Db      203 TTCACAGAGAAATATGGCTGTCTTTTGTGTGAGAGAGCTGCCAAGGGGGCACTACCTGAAG 262
Oy      41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db      263 GCCCTTCCAGGGAGCCCTGGCGGCACTCCACCTGCCCTGTGTGTCCCAAGACACTTC 322
Oy      61 LeuAlaTrpGluAsnHisAsnSerGlnCysAlaArgCysGlnAlaCysAspGluGln 80
Db      323 TTGGCTCTGGGAGAACCAACCAATTAATTCGAATGTGCCGCTGCCAAGGCTTGTATGAGCAG 382
Oy      81 AlaSerGlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db      383 GCGCTCCAGGTGGGGGCTGTGAATACTGTTCACAGACTGGCCGACACCCGCTGTGGCTGAAG 442
Oy      101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTrpCys 120
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Oy      121 GlnProCysLeuAspPysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerAlaArg 140
Db      503 CAACCATCCCTAAGACTGGGGGGCCCTCACCAGCCACACAGCGCTACCTTTCCCCAGG 562
Oy      141 AspThrAspCysGlyTrpCysLeuProGlyPheTrpGlnHisGlyAspGlyCysValSer 160
Db      563 GATACTGACTGTGGGACCTGCTGCTGCTCTCTATATAACATGGCATGGCTCGCTGTCC 622
Oy      161 CysProThrSerThrLeuGlySerCysPysProGluArgCysAlaAlaValCysGlyTrpArg 180
Db      623 TGCCCCAGACACACCTGGGGGAGCTGTCCAGAGCGCTGTGCCGCTGCTGTGCTGGAGG 682
Oy      181 GlnMetPheTrpValGln 186
Db      683 CAGATGTTCTGGGTCCAG 700

RESULT 4
US-08-815-469-1
: Sequence 1, Application US/08815469
: Patent No. 6153402
: GENERAL INFORMATION:
: APPLICANT: Yu, Guo-Liang
: APPLICANT: Ni, Jian
: APPLICANT: Dixit, Vishva
: APPLICANT: Gentz, Reiner L.
: APPLICANT: Dillon, Patrick J.
: TITLE OF INVENTION: Death Domain Containing Receptors
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
: STREET: 1100 New York Ave., NW, Suite 600
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/815,469
: FILING DATE: HEREWITH
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: No. 6153402 Yet Assigned
: FILING DATE: 06-FEB-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/028,711
: FILING DATE: 17-OCT-1996
: PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 198..1481
US-08-815-469-1

Alignment Scores:
Pred. No.: 2,346-90 Length: 1783
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

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DB 285 CTTGCTGGGGGCCCCGGCCGAGGCGGCGCTGAGCCCGAGGCTGACGTCGGCTGAC 344
QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 345 TTCACAGAAAGATTGGTGTGTTTTCACAGAGGCTGCCCGGGGCGACTACCTGAAG 404
QY 41 AlaProCysThrGluProCysGlnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 405 GCCCTTCAGAGGAGCCGCGGCAACTCCACTGCTGTGTGCCCAAGCAACTTC 464
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 465 TTGGCTGGGAGAACCCATTAATCTGAATGTGCCCGCTGCAGGCTGTGATGAGCAG 524
QY 81 AlaSerGlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 525 GCCTCCAGAGTGGCGCTGAGAACTGTTCAAGTGGCCGACACCCGCTGTGGCTGAG 584
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerSerProPheTyrCys 120
DB 585 CCAGGCTGGTTGTGGAGTGCAGAGTCACCAATGTGTAGAGCATTCACCTTACTTC 644
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisTyrArgLeuLeuCysSerArgArg 140
DB 645 CAACATGCTGCTAGCTGCGGGGCGCTGCACCGCCACACAGCGCTACTGTTCCGACAG 704
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspThrLysValSer 160
DB 705 GATATGACTGTGGAGCTGCTGCTGCTGTATGAACATGGGAGTGGCGGTGTC 764
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrPar 180
DB 765 TGCCCCAGAGAGACCTGGGAGGCTGCAGAGCGCTGTGCTGTGGCTGGAG 824
QY 181 GlnMetPheTrpValGln 186
DB 825 CAGAGTTCTGTGGTCCAG 842
RESULT 5
US-08-928-069-5

Sequence 5, Application US/08928069
Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-928-069-5

Alignment Scores:
Pred. No.: 1,756-79 Length: 1438
Score: 979.00 Matches: 169
Percent Similarity: 93.92% Conservative: 1
Best Local Similarity: 93.37% Mismatches: 3
Query Match: 88.92% Indels: 8
Gaps: 1

US-09-993-234-6_COPY_19_204 (1-186) x US-08-928-069-5 (1-1438)

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QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 491 TTCACAGAAAGATTGGTGTGTTTTCACAGAGGCTGCCCGGGGCGACTACCTGAAG 550
QY 41 AlaProCysThrGluProCysGlnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 551 GCCCTTCAGAGGAGCCCTGCGGCAACTCCACTGCTGTGTGTCACCAAGACACTTC 610
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 611 TTGGCTGGGAGAACCCATTAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 670
QY 81 AlaSerGlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 671 GCCTCCAGAGTGGCGCTGAGAACTGTTCAAGTGGCGGAGACACCCGCTGTGGCTGAG 730
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerSerProPheTyrCys 120
DB 731 CCAGGCTGTGTGGAGTGGCGAGGTCAGCAATGTGTACAGCATTCACCTTACTTC 790

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-928-069-2

Alignment Scores:
Pred. No.: 2,66e-54 Length: 433
Score: 692.00 Matches: 133
Percent Similarity: 93.10% Conservative: 2
Best Local Similarity: 91.72% Mismatches: 6
Query Match: 62.85% Indels: 5
DB: Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x US-08-928-069-2 (1-433)

QY 1 LeuLeuGlyAlaArGAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
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DB 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAla-GlyHisTyrLeu 40
61 TTCACAGAGAGATTGCTGTGTGTGTCAGAGGCTGCCAGCGGGGCAACTACTGTA 120
QY 40 sAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPh 60
121 GGGCCCTTGACAGGAGCCCTGGCC -AACTCCACCTGCTGTGTGTGTCGCCAAGACACTT 179
DB 60 eleuAlaTrpGluAsnHisHisAsnSerGluCysAlaArGysGlnAlaCysAspGlu 80
180 CTGGGCTGGGAGAACACCATTAATCTGAATGTGCCCTGCCAGGCTGTGATGAGA 239
QY 80 nAlaSerGlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyAsy 100
240 GGCCTCCAGGTGGGCTGGAGACTGTTCAGCAGTGGCCGACCCGCTGGCTGTGA 299
DB 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAla-GlyHisTyrLeu 40
100 sProGlyTrpPheValGluCysGln-ValSerGlnCysValSerSer-SerProPheTyr 119
300 GAGGGCTGGTGTGGAGTGTGCAGGGTCAGGCAATGTGTCAAGCAATTCACCCCTTGA 359
QY 120 CysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCys-SerAr 139
360 TGCACAACATGCTAGACTGCGGGGCTGCACAGCAGACACAGGCTAATNTGTTCCG 419
DB 139 gArGAsp 141
420 CAGAGAT 426

RESULT 8
US-08-828-683A-2
Sequence 2, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
FAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-828-683A-2

Alignment Scores:
Pred. No.: 2,66e-54 Length: 433
Score: 692.00 Matches: 133
Percent Similarity: 93.10% Conservative: 2
Best Local Similarity: 91.72% Mismatches: 6
Query Match: 62.85% Indels: 5
DB: Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x US-08-828-683A-2 (1-433)

QY 1 LeuLeuGlyAlaArGAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
1 CTGCTGGGGGCCCCGGCCAGNGCCGACCTGAGCCCGGAGGTGAGTGTGCGGGTGAC 60
DB 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAla-GlyHisTyrLeu 40
61 TTCACAGAGAGATTGCTGTGTGTGTCAGAGGCTGCCAGCGGGGCAACTACTGTA 120
QY 40 sAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPh 60
121 GGGCCCTTGACAGGAGCCCTGGCC -AACTCCACCTGCTGTGTGTGTCGCCAAGACACTT 179
DB 60 eleuAlaTrpGluAsnHisHisAsnSerGluCysAlaArGysGlnAlaCysAspGlu 80
180 CTGGGCTGGGAGAACACCATTAATCTGAATGTGCCCTGCCAGGCTGTGATGAGA 239
QY 80 nAlaSerGlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCys 100
240 GGCCTCCAGGTGGGCTGGAGACTGTTCAGCAGTGGCCGACCCGCTGGCTGTGA 299
DB 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAla-GlyHisTyrLeu 40
100 sProGlyTrpPheValGluCysGln-ValSerGlnCysValSerSer-SerProPheTyr 119
300 GAGGGCTGGTGTGGAGTGTGCAGGGTCAGGCAATGTGTCAAGCAATTCACCCCTTGA 359
QY 120 CysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCys-SerAr 139
360 TGCACAACATGCTAGACTGCGGGGCTGCACAGCAGACACAGGCTAATNTGTTCCG 419
DB 139 gArGAsp 141
420 CAGAGAT 426

RESULT 9
US-08-762-308-10
Sequence 10, Application US/08762308
Patent No. 5925548
GENERAL INFORMATION:
APPLICANT: Beutler, Bruce A.
TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY
TITLE OF INVENTION: SIGNAL


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Db 329 CAAGAGGCGAGTGGCGATGATGTGTCTCCCAAGAAAAATATATCCACCCTCAAAATAT 388
QY 27 LeupheCysArGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 46
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Db 389 TCCATTGTGCTGACCAAGTCCCAAGAGACCTACTTGTACAAATGACGTCCAGGCCG 448
QY 47 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 66
   ||||| ||| |||||
Db 449 GCGCAGGATACGACGACGCGGAGAGACGCGCTCTCCCTTCACCCCTTCAGAAAAACAC 508
QY 67 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluAlaSerGlnAlaAlaLeu 86
   ||||| ||| |||||
Db 509 CTCAGA---CACTGCTCTGACGTGCTCCAAATGCCGAAGAAATGGGTGAGGTGAGATC 565
QY 87 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysAlaSerProGlyTrpPheValGlu 106
   ||||| ||||| |||||
Db 566 TCTTCTTGACAGTGGACCGGACCGGTGTGTGCTGACGAGAAACAGATACCGGCAT 625
QY 107 Cys-----GlnValSerGlnCysValSerSerProPheTrpCysGlnProCys 123
   ||||| ||| |||||
Db 626 TATTGAGTGAACCTTTTCCAGTGC-----TTCAATTGACAGCTCTGTC 670
QY 124 LeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 143
   ||||| ||| |||||
Db 671 CTCAT---GGACCGCTGCAC-----CTCTCTGCGCAGAGAAACAGAACACC 715
QY 144 CysGlyThrCysLeuProGlyPheTrpGlnHisGlyAspGlyCysValSerCysProThr 163
   ||||| ||||| |||||
Db 716 GTGTGACCTGCGCATGACAGTCTTCTTAAGAGAAACAGAGTGTGTCTCCGTGCCGT 775
QY 164 SerThrLeuGlySerCysProGlu 171
   ||||| ||| |||||
Db 776 GCTGCCCCAGGT---TGCCCAAGAA 796

RESULT 11
US-08-910-991-1
; Sequence 1, Application US/08910991
; Patent No. 6194177
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chapel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,991
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/804,166
; FILING DATE: 20 February 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,936
; FILING DATE: 20 February 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: TUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: CAMPBELL-2B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528

```

```

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1049 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 278..1047
; US-08-910-991-1

Alignment Scores:
Pred. No.: 1,44e-10 Length: 1049
Score: 212.50 Matches: 52
Best Similarity: 42.26% Conservative: 19
Best Local Similarity: 30.95% Mismatches: 82
Query Match: 19.30% Indels: 13
DB: 4 Gaps: 6

US-09-993-234-6_COPY_19_204 (1-186) x US-08-910-991-1 (1-1049)
QY 7 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisTyrSlyIleGly 26
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Db 329 CAAGAGGCGAGTGGCGATGATGTGTCTCCCAAGAAAAATATATCCACCCTCAAAATAT 388
QY 27 LeupheCysArGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 46
   ||||| ||| |||||
Db 389 TCCATTGTGCTGACCAAGTCCCAAGAGACCTACTTGTACAAATGACGTCCAGGCCG 448
QY 47 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 66
   ||||| ||| |||||
Db 449 GCGCAGGATACGACGACGCGGAGAGACGCGCTCTCCCTTCACCCCTTCAGAAAAACAC 508
QY 67 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluAlaSerGlnAlaAlaLeu 86
   ||||| ||| |||||
Db 509 CTCAGA---CACTGCTCTGACGTGCTCCAAATGCCGAAGAAATGGGTGAGGTGAGATC 565
QY 87 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysAlaSerProGlyTrpPheValGlu 106
   ||||| ||||| |||||
Db 566 TCTTCTTGACAGTGGACCGGACCGGTGTGTGCTGACGAGAAACAGATACCGGCAT 625
QY 107 Cys-----GlnValSerGlnCysValSerSerProPheTrpCysGlnProCys 123
   ||||| ||| |||||
Db 626 TATTGAGTGAACCTTTTCCAGTGC-----TTCAATTGACAGCTCTGTC 670
QY 124 LeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 143
   ||||| ||| |||||
Db 671 CTCAT---GGACCGCTGCAC-----CTCTCTGCGCAGAGAAACAGAACACC 715
QY 144 CysGlyThrCysLeuProGlyPheTrpGlnHisGlyAspGlyCysValSerCysProThr 163
   ||||| ||||| |||||
Db 716 GTGTGACCTGCGCATGACAGTCTTCTTAAGAGAAACAGAGTGTGTCTCCGTGCCGT 775
QY 164 SerThrLeuGlySerCysProGlu 171
   ||||| ||| |||||
Db 776 GCTGCCCCAGGT---TGCCCAAGAA 796

RESULT 12
US-08-804-166-7
; Sequence 7, Application US/08804166
; Patent No. 6193972
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chapel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.

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COUNTRY: USA
ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,166
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: CAMPBELL-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1301 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 279..1287
US-08-804-166-7

Alignment Scores:
Pred. No.: 8.18e-10 Length: 1301
Score: 205.50 Matches: 51
Percent Similarity: 40.91% Conservative: 21
Best Local Similarity: 28.98% Mismatches: 83
Query Match: 18.66% Indels: 21
DB: 4 Gaps: 7

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QY 7 GlnGlyGlyThrArgSerProAlaGlyAspArgCysAlaGlyAspPheHisLysIleGly 26
DB 330 CAAGAGGAGGAGCGCATGATGTGTCTCCCAAGAAATATATTCACCCCTCAAAATAT 389
QY 27 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 46
DB 390 TCGATTGCTGTACCAAGTCCCAAGAGAACCTACTGTACAAATGACTGTCCAGGCCG 449
QY 47 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 66
DB 450 GGGCAGGATACGAGCTGCGAGGAGGTGTGAGAGCGGCTCCCTTCACCGCTTCAGAAAC 509
QY 67 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 86
DB 510 CTCAGG---CACTGCTCAGCTCTCCCAATGCGCAAGAAATGGGTGAGTGGAGATC 566
QY 87 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 106
DB 567 TCTTTTTCACAGTGGACGGACCGGCTGTGTGGCTGCAGGAAACAGTACCGGCAT 626
QY 107 Cys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnProCys 123
DB 627 TATTGAGTGAACACCTTTTCCAGTGC-----TTCAATTGCGACCCCTGTGC 671
QY 124 LeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 143
DB 672 CTCGAAT---GGAGCGGTGCAC-----CTCTCGTCGACGAGAAACAGAACAC 716
QY 144 CysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThr 163
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DB 717 GTGTGACCTGCGCATGAGGTTCTTTCTAAGAAACAGAGTGTCTCTCTG----- 770
QY 164 SerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys 177
DB 771 -----AGTAACTGTAAAGAAACCTGGAGTGCACGAAGTTGTGC 809

RESULT 13
US-08-910-991-7
; Sequence 7, Application US/08910991
; Patent No. 6194177
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappell, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,991
FILING DATE:
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/804,166
FILING DATE: 20 February 1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CAMPBELL-2B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1301 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 279..1287
US-08-910-991-7

Alignment Scores:
Pred. No.: 8.18e-10 Length: 1301
Score: 205.50 Matches: 51
Percent Similarity: 40.91% Conservative: 21
Best Local Similarity: 28.98% Mismatches: 83
Query Match: 18.66% Indels: 21
DB: 4 Gaps: 7

US-09-993-234-6_COPY_19_204 (1-186) x US-08-910-991-7 (1-1301)
QY 7 GlnGlyGlyThrArgSerProAlaGlyAspArgCysAlaGlyAspPheHisLysIleGly 26
DB 330 CAAGAGGAGGAGCGCATGATGTGTCTCCCAAGAAATATATTCACCCCTCAAAATAT 389
QY 27 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 46
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Db 390 TCGATTGCTTACCAAGTCCCAAGAACCTTACTTGTACATGACGTGCGAGCCCG 449
Qy 47 CysGlySerThrCysLeuValCysProGlnAspThrPheLeuAlaIrpGlnAsnHis 66
Db 450 GGGCAGAGATACGACGTGAGAGAGTGTAGACGGGTCTCTTCAACCGCTTCAAAAAACAC 509
Qy 67 HisAsnSerGluCysAlaIrpGlySerGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 86
Db 510 CTCAGA---CACTGCTCAGCTGCTCCAAATGCGGAAGAAATGGCTGTCAGTGCAGATC 566
Qy 87 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLeuProGlyIrrPheValGlu 106
Db 567 TCTTCTTGACAGTGGACCGGACACCGTGTGTGCTGACGAGAAACACGACGCGCAT 626
Qy 107 Cys-----GlnValSerGlnCysValSerSerProPheThrCysGlnProCys 123
Db 627 TATTGAGTGAAGAACCTTTTCCAGTGC-----TTCAATGTGACCGCTCTGC 671
Qy 124 LeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 143
Db 672 CTCAT---GGGACCGTGCAC-----CTCTCCTGCCAGAGAAACAGAACACAC 716
Qy 144 CysGlyThrCysLeuProGlyPheThrGluHisGlyAspGlyCysValSerCysProThr 163
Db 717 GTGTGACCTGCTGACAGTGTCTTCTTAAGAGAAACAGTGTCTCTCTG----- 770
Qy 164 SerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys 177
Db 771 -----AGTAACGTGAAGAAAGCCGTGAGTGCACGAACTGTGC 809

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RESULT 14
US-08-050-319B-47
; Sequence 47, Application US/08050319B
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M. Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Reed & Robblins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050.319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robblins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 600 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS

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; LOCATION: 1..597
US-08-050-319B-47
Alignment Scores:
Pred. No.: 3.26e-10 Length: 600
Score: 205.00 Matches: 53
Percent Similarity: 40.88% Conservative: 21
Best Local Similarity: 29.28% Mismatches: 83
Query Match: 18.62% Indels: 24
DB: 1 Gaps: 8

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US-09-993-234-6_COPY_19_204 (1-186) x US-08-050-319B-47 (1-600)
Qy 2 LeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPhe 21
Db 100 CTAGGGGACAGGAGAGAG-----ACAGTATGTTGTGTGTCACACAGAGAAATATATTC 150
Qy 22 HisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisThrLeuLysAla 41
Db 151 CACCCCTCAAAATATATTCGATTGTGTACCAAGTGCACCAAGAAACCTTACTTGTACAT 210
Qy 42 ProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeu 61
Db 211 GACTGTCCAGGCCCGGCGAGATGACGACTGCAGAGATGTGAGAGCGGCTCTTACAC 270
Qy 62 AlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAla 81
Db 271 GCTTACAGAAACACCTCTAGA---CACTGCCCTCAGCTGCTCCAAATGCCGAAAGAAATG 327
Qy 82 SerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysPro 101
Db 328 GGTTCAGGTGGAGATCTCTTTCACAGTGCACCGGACACCGGTGTGGTGCAGAGAG 387
Qy 102 GlyTrpPheValGluCys-----GlnValSerGlnCysValSerSerProPhe 118
Db 388 AACCGATACCGGCAATTATGAGTGAAGAAACCTTTCCAGTGC-----TTG 432
Qy 119 TyrCysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSer 138
Db 433 AATTGACAGCTGCTGCTCAAT---GGACCGTGCAC-----CTCTCCCTCCAG 477
Qy 139 ArgArgAspThrAspCysGlyThrCysLeuProGlyPheThrGluHisGlyAspGlyCys 158
Db 478 GAGAAACAGAACCCGTGACCTGCATGCGAGTGTCTTCTTAAGAGAAACGAGTGT 537
Qy 159 ValSerCysProThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaVal 176
Db 538 GTCTCTCTG-----AGTAACGTGAAGAAAGCCGTGAGTGCACGAAATGTG 582
Qy 177 Cys 177
Db 583 TGC 585

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RESULT 15
US-08-465-982-47
; Sequence 47, Application US/08465982
; Patent No. 5863786
; GENERAL INFORMATION:
; APPLICANT: M. Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Reed & Robblins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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150

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GenCore version 5.1.4_p5.4578
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 6, 2003, 21:08:18 ; Search time 70.8236 Seconds

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2303.655 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 593429 segs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published.Applications_NA_QFRT-fastap -SUFFIX=trmb -MINMATCH=0.1
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-TRANS=human40.ccl -LIST=45 -DOCALLIGN=200 -THR_SCORE=ptc -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-FGAPEXT=7 -TGAPOP=10 -TGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published.Applications_NA:*

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3:	/cgnt2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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7:	/cgnt2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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14:	/cgnt2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1101	100.0	1634	9	US-10-081-280-9 Sequence 9, Appl1
3	1101	100.0	1634	9	US-10-112-793-9 Sequence 9, Appl1
4	1101	100.0	1634	9	US-10-112-193-11 Sequence 11, Appl1

5	1101	100.0	1634	10	US-09-993-234-9 Sequence 9, Appl1
6	1101	100.0	1783	10	US-09-333-966-1 Sequence 1, Appl1
7	1077	97.8	1743	9	US-09-954-531-1389 Sequence 189, Ap
8	979	88.9	816	10	US-09-964-824A-292 Sequence 292, App
9	979	88.9	1438	9	US-10-081-280-5 Sequence 5, Appl1
10	979	88.9	1438	9	US-10-112-793-5 Sequence 5, Appl1
11	979	88.9	1438	9	US-10-112-193-5 Sequence 5, Appl1
12	979	88.9	1438	10	US-09-884-733-5 Sequence 5, Appl1
13	979	88.9	1438	10	US-09-993-234-5 Sequence 5, Appl1
14	767	69.7	10797	10	US-10-092-154-1577 Sequence 1577, Ap
15	767	69.7	10797	10	US-09-764-847-1577 Sequence 1577, Ap
16	692	62.9	433	9	US-10-081-280-2 Sequence 2, Appl1
17	692	62.9	433	9	US-10-112-793-2 Sequence 2, Appl1
18	692	62.9	433	9	US-10-112-193-2 Sequence 2, Appl1
19	692	62.9	433	10	US-09-884-733-2 Sequence 2, Appl1
20	692	62.9	433	10	US-09-993-234-2 Sequence 2, Appl1
21	216	19.6	2130	10	US-09-917-800A-1601 Sequence 1601, Ap
22	212.5	19.3	1049	10	US-09-756-186-1 Sequence 1, Appl1
23	212	19.3	5870	10	US-09-838-718A-8 Sequence 8, Appl1
24	208	18.9	1674	9	US-09-359-595-12 Sequence 7, Appl1
25	205.5	18.7	1301	10	US-09-756-186-7 Sequence 7, Appl1
26	203.5	18.5	570	9	US-09-899-429A-17 Sequence 17, Appl1
27	203.5	18.5	600	9	US-09-899-429A-11 Sequence 11, Appl1
28	203.5	18.5	1202	10	US-09-756-186-3 Sequence 3, Appl1
29	203	18.4	519	9	US-09-899-429A-15 Sequence 15, Appl1
30	203	18.4	549	9	US-09-899-429A-9 Sequence 9, Appl1
31	203	18.4	603	9	US-09-899-429A-13 Sequence 13, Appl1
32	203	18.4	1334	9	US-09-899-429A-7 Sequence 7, Appl1
33	203	18.4	1334	9	US-09-898-234-11 Sequence 11, Appl1
34	203	18.4	1334	9	US-09-792-356-11 Sequence 11, Appl1
35	203	18.4	1334	10	US-09-899-422-11 Sequence 11, Appl1
36	203	18.4	1368	9	US-09-898-234-1 Sequence 1, Appl1
37	203	18.4	1368	9	US-09-899-429A-1 Sequence 1, Appl1
38	203	18.4	1368	9	US-09-792-356-1 Sequence 1, Appl1
39	203	18.4	1368	10	US-09-899-422-1 Sequence 1, Appl1
40	203	18.4	2111	10	US-09-880-107-2360 Sequence 2360, Ap
41	203	18.4	2141	9	US-09-898-234-16 Sequence 16, Appl1
42	203	18.4	2141	9	US-09-899-429A-26 Sequence 26, Appl1
43	203	18.4	2141	9	US-09-792-356-16 Sequence 16, Appl1
44	203	18.4	2141	10	US-09-899-422-16 Sequence 16, Appl1
45	203	18.4	2175	12	US-10-120-397-1 Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-333-966-3
Sequence 3, Application US/09333966
Patent No. US2002009773A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:

QY	61	LeuLlaIrrpGluAsnAlnHsAsnSerGluCysAlaIrrgCysGlnAlaCysAspGluGln	80
Db	323	TTGGCCCTGGGAGAACCAACCAATTCCTGAAATGTCCCGCCGTCCAGGGCTGTGAAGACAG	382
QY	81	AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGluCysLys	100
Db	383	GCCCTCCAGGGGGCGCTGGAGAAACTGTTCAGCAAGTGGCCGACACCCTGGGCTGTAAAG	442
QY	101	ProGlyIrrpIrrpValGluCysGlnValSerGlnCysValSerSerSerProPheTyrCys	120
Db	443	CCAGGCTGGTGTGGAGATGGCCAGAGTCCAGCCAAATGTCTCAGCAACTTACCTTCATGTC	502
QY	121	GlnProCysLeuAspPcysGluAlaLeuHsIrrGhtIrrThrArgLeuLeuCysSerArgArg	140
Db	503	CAACCAATGCCCTCAAGACTGGGGGGCCCTGTGCACGCCACACAGGGCTACTCTGTTCGCCGAGA	562
QY	141	AspThrAspCysGluTyrThrCysLeuProGluPheTyrGluHsGluAspGluCysValSer	160
Db	563	GATACCTGACTGTGGAGACTGGCTGCTGCGCTTATATACATGGCATGGGTGGGTGTCC	622
QY	161	CysProThrSerThrLeuGluGlySerCysProGluArgCysAlaAlaValAlaCysGluTTPArg	180
Db	623	TGCCCCACGACACACCCTGGGGAGCTGTTCACAGAGCGCTGTGCGCTGTCTGTGGCTGGAGG	682
QY	181	GlnMetPheIrrpValGln	186
Db	683	CAGATGTTCTGGCTCCAG	700

US-10-112-793-9	
Alignment Scores:	
Pred. No.:	2.06e-103
Score:	1101.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	9
US-09-993-234-6_COPY_19_204 (1-186) x US-10-112-793-9 (1-1634)	
	Length: 1634
	Matches: 186
	Conservative: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0

APPLICATION NUMBER: US/10/112,193
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,069
FILING DATE: 11-Sep-1997
APPLICATION NUMBER: 60/026943
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-112-193-11

Alignment Scores:
Pred. No.: 2,066-103 Length: 1634
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x US-10-112-193-11 (1-1634)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 143 CTGGCTGGGGGGCCGGGGCCAGGCGGCACTGCTAGCCGCCAGGTGTGACTGTCCGGTGC 202
QY 21 PheHisLysLysLleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 203 TTCCACAGAGAAATGTGCTGTTTGTTCAGAGGCTGCGCCAGCGGCGACATCACTGAAG 262
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 263 GCCCTTCGACGAGACCCCTCGCGGCACTCCACTGCTGTGTGTCCTCCAAAGACCTTC 322
QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 323 TTGGCTGGGAGAACACCAATATTCTGAATGTGCCCGCTGCCAGCGCTGTATGACGAG 382
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 383 GCCTCCAGAGTGGCGCTGGAGAACTGTCAGACGTGGCGGACACCCGCTGTGGCTGTAAG 442
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheThrCys 120
DB 443 CCAGGCTGTGTGTGATGTCAGGCTCAGCCCAATGTGTACAGATGTCACCCCTTACTGC 502
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 503 CAACATCCTCAAGACTGGGGGCGCTGCACGCGCCACACAGCGCTACTGTCCCGCAGA 562
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheThrGluHisGlyAspGlyCysValSer 160
DB 563 GATACTGTGCTGTGGACCTGCTGCTGCTTCTATGAACTGGGATGGGCTGCTGCTGCC 622
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
DB 623 TGCCCCACGAGACCTTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGAG 682
QY 181 GlnMetPheTrpValGln 186
DB 683 CAGATGTTCTGGTGCAG 700

RESULT 5
US-09-993-234-9

Sequence 9, Application US/09993234
Patent No. US20020146768A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/993,234

FILING DATE: 19-No. US20020146768A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,683

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1007P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5416

TELEFAX: 910/371-7168

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 1634 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-993-234-9

Alignment Scores:

Pred. No.: 2,066-103 Length: 1634
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x US-09-993-234-9 (1-1634)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 143 CTGGCTGGGGGGCCGGGGCCAGGCGGCACTGCTAGCCGCCAGGTGTGACTGTCCGGTGC 202
QY 21 PheHisLysLysLleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 203 TTCCACAGAGAAATGTGCTGTTTGTTCAGAGGCTGCGCCAGCGGCGGCGCTACTGAAG 262
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 263 GCCCTTCGACGAGACCCCTCGCGGCACTCCACTGCTGTGTGTGTCCTCCAAAGACCTTC 322
QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 323 TTGGCTGGGAGAACACCAATATTCTGAATGTGCCCGCTGCCAGCGCTGTATGACGAG 382
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100

Db 383 GCTCCAGGTGGCGCTGGAGAACTGTTCAAGACTGGCCAGACCCGCTGTGCTTAAG 442
Qy 101 ProglyTTPheValGluCysGlnValSerGlnCysValSerSerProphetyrCys 120
Db 443 CAGGGCTGGTTGTGGAGTCCAGGTGACCAATGTGTGACAGAGTTACCTTCTACTGC 502
Qy 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArg 140
Db 503 CAACCATGCTTACAGCTGGGGGGCCCTGCACCGCACACAGGCTACTCTTCCCGCAGA 562
Qy 141 AspThrAspCysGlyThrCysLeuProGlyPheThrGlnHisGlyAspGlyCysValSer 160
Db 563 GATACGACTGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 622
Qy 161 CysProThrSerThrLeuGlySerCysProGlyAspGlyAlaValCysGlyTTPArg 180
Db 623 TGCCCGACGAGCAACCTGGGGAGCTGTCCAGAGCGCTGTGCTGCTGCTGCTGAGG 682
Qy 181 GlnMetPheTTPValGln 186
Db 683 CAGATGTTCTGGGTCCAG 700

RESULT 6

US-09-333-966-1
Sequence 1, Application US/09333966
Patent No. US200200973A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: NI, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
APPLICATION NUMBER: No. US200200973A1 yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steife, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 198..1481
US-09-333-966-1

Alignment Scores:
Pred. No.: 2,28e-103 Length: 1783
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x US-09-333-966-1 (1-1783)

Qy 1 LeuLeuGlnAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 285 CTGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 344
Qy 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisLysLeuLys 40
Db 345 TTCACAGAGAGATGGTGTGTTGTTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAG 404
Qy 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 405 GCCCTTGACAGAGAGCGCTGGGGGCACTCCACCTGCTGTGTCTCCCAAGACACCTTC 464
Qy 61 LeuAlaTTPGlnAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 465 TTGGCTGGGGGAGAACCACTAATTCGAATGTGCCCGCTCCAGCGCTGTGATGACAG 524
Qy 81 AlaSerGlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCys 100
Db 525 GCTCCAGAGGTGGCGCTGGAGAACTGTTCAGCACTGGCGGACCCGCTGGGTGAAG 584
Qy 101 ProglyTTPheValGluCysGlnValSerGlnCysValSerSerProphetyrCys 120
Db 585 CCAGGCTGGTTGTGGAGTGCAGGTGCAGGCAATGTGTGACACATTACCTTCTACTGC 644
Qy 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArg 140
Db 645 CAACCATGCTTACAGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 704
Qy 141 AspThrAspCysGlyThrCysLeuProGlyPheThrGlnHisGlyAspGlyCysValSer 160
Db 705 GATACGACTGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 764
Qy 161 CysProThrSerThrLeuGlySerCysProGlyAspGlyAlaValCysGlyTTPArg 180
Db 765 TGCCCGACGAGCAACCTGGGGAGCTGTCCAGAGCGCTGTGCTGCTGCTGCTGAGG 824
Qy 181 GlnMetPheTTPValGln 186
Db 825 CAGATGTTCTGGGTCCAG 842

RESULT 7

US-09-954-531-1389
Sequence 1389, Application US/09954531
Patent No. US20020165180A1
GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034

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; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: Patent version 3.0
; SEQ ID NO: 1389
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-1389

Alignment Scores:
Pred. No.: 6,25e-101 Length: 1743
Score: 1077.00 Matches: 182
Percent Similarity: 98.91% Conservative: 0
Best Local Similarity: 98.91% Mismatches: 2
Query Match: 97.82% Indels: 0
DB: Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x US-09-954-531-1389 (1-1743)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
   |||||||
DB 123 CTGCTGGGGGCCCCGGCCAGGCGGCGACTGTAAGCCAGGTGTACTGTGCGGTGAC 182

QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
   |||||||
DB 183 TTCACAAAGATGTGCTGTTTGTTCACAGAGCTGCCACGGGGGACACTGGAAG 242

QY 41 AlaProCysThGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
   |||||||
DB 243 GCCCTTGACAGGAGCCCTGCGCAACTCCACTGCTGTGTGTGCCAAGACACTTC 302

QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
   |||||||
DB 303 TTGGCTGGGGAACACCATTAATCTGATGTGCCCTGCGAGCCGTGATGAGCAG 362

QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
   |||||||
DB 363 GCCTCCAGCTGGCGCTGAGAACTGTTACAGAGTGGCGGACACCCGCTGTGTTAAG 422

QY 101 ProGlyTyrPheValGluCysGlnValSerGlnCysValSerSerSerProPheTyrCys 120
   |||||||
DB 423 CCAGCTGTGTTGTGAGAGCCAGGTCACCATGTGTGACAGAGTTCACCTTACTGTC 482

QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
   |||||||
DB 483 CAACATGCTAGACTGGGGGGCCCTGCACCCGACACAGGCTACTCTGTTCCGCAAG 542

QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSer 160
   |||||||
DB 543 GATTAAGTGTGGAGCTGCTGCTGCTGCTTGAACATGGAGGAGTGGCTGCTGTC 602

QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaValCysLysTyrParg 180
   |||||||
DB 603 TGCCCCAGAGACCTGGGGAGAGTGTCCAGAGCCCTGTGCTGTGTGTGGAGAG 662

QY 181 GlnMetPheTyr 184
   |||
DB 663 CAGAGTAGGTGG 674

RESULT 8
US-09-964-824A-292
; Sequence 292, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrihan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
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; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: Patent version 3.0
; SEQ ID NO: 292
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-292

Alignment Scores:
Pred. No.: 2,53e-91 Length: 816
Score: 979.00 Matches: 169
Percent Similarity: 93.92% Conservative: 1
Best Local Similarity: 93.37% Mismatches: 3
Query Match: 88.92% Indels: 8
DB: Gaps: 1

US-09-993-234-6_COPY_19_204 (1-186) x US-09-964-824A-292 (1-816)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
   |||||||
DB 39 CTGCTGGGGGCCCCGGCCAGGCGGCGACTGTAAGCCAGGTGTACTGTGCGGTGAC 98

QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
   |||||||
DB 99 TTCACAAAGATGTGCTGTTTGTTCACAGAGCTGCCACGGGGGACACTGGAAG 158

QY 41 AlaProCysThGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
   |||||||
DB 159 GCCCTTGACAGGAGCCCTGCGCAACTCCACTGCTGTGTGTGCCAAGACACTTC 218

QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
   |||||||
DB 219 TTGGCTGGGGAACACCATTAATCTGATGTGCCCTGCGAGGCTGTGATGAGCAG 278

QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
   |||||||
DB 279 GCCTCCAGCTGGCGCTGAGAACTGTTACAGAGTGGCGGACACCCGCTGTGTTAAG 338

QY 101 ProGlyTyrPheValGluCysGlnValSerGlnCysValSerSerSerProPheTyrCys 120
   |||||||
DB 339 CCAGCTGTGTTGTGAGAGTCCAGGTCACCATGTGTGACAGAGTTCACCTTACTGTC 398

QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
   |||||||
DB 399 CAACATGCTAGACTGGGGGGCCCTGCACCGGACACAGGCTACTCTGTTCCGCAAG 458

QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSer 160
   |||||||
DB 459 GATTAAGTGTGGAGCTGCTGCTGCTGCTTGAACATGGAGGAGTGGCTGCTGTC 518

QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaValCysLysTyrParg 180
   |||||||
DB 519 TGCCCCAGAGTATTCCTA-----GCTGTGCTGGAGTGGAGG 554

QY 181 Gln 181
   |||
DB 555 GAA 557

RESULT 9
US-10-081-280-5
; Sequence 5, Application US/10081280
; Patent No. US2002016517A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-081-280-5

Alignment Scores:
Pred. NO: 4.97e-91 Length: 1438
Score: 979.00 Matches: 169
Percent Similarity: 93.92% Conservative: 1
Best local Similarity: 93.37% Mismatches: 3
Query Match: 88.92% Indels: 8
DB: 9 Gaps: 1

US-09-993-234-6_COPY_19_204 (1-186) x US-10-081-280-5 (1-1438)
0Y 1 LeuenuGjAlaAtgAlaGlnGlyGlyThrArgSerProArGysAspCysAlaGlyAsp 20
Db 431 CTGCTGGGGGGCCGGCCGACAGGGGGGACACTGTGAGCCCGAGGTGTGACTGTGGCGGGTAC 490
0Y 21 PheHisIstLysIleGlyLeuPhePheCysAsrGlyCysProAlaGlyHisTyrLeuLys 40
Db 491 TTCCACAAGAGATTGGTGTCTTTTGTGTGCAGAGCGTCCCGACGGGGGCACTACGTGAAG 550
0Y 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 551 GCCCTTGCACGGAGCCCTGGCGCAACTCCACTGCTGTGTGTCCCAAGACACTTC 610
0Y 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluIn 80
Db 611 TTGGCTGGGGGAACCAACCAATTAATTCGAATGTCCCGCTGCCAGGGCTGTGATGAGCAG 670
0Y 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 671 GCTCTCCAGGTGGGGCGTGGAGAACTGTTCAGCACTGGCCGACACGCCCTGTGGCTGTAAAG 730
0Y 101 ProGlyTyrPheValAlaGlyCysGlnValSerGlnCysValSerSerSerProPheTyrCys 120
Db 731 CCAGGCTGGTTTGTGTGAGTGCACAGTCCAGCCAAATGTCTCAGCAAGTTCACCCCTTCTACTGC 790
0Y 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 791 CACCATCTCCAGTACACTGGGGGGCCCTGCACGCCCAACACAGGGCTACTCTGTCCCGAGA 850

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Qy      141  ASPTLRARPCCYSGIYTHCYSLAEPROGLYPHERYCRILNHSIGLYASPSGIYCSVALSER 160
Db      851  CATACTGACTGTGGAGCCTGCCTCGCTGGCTTCATGACATGGCCAGTGGCTGCGTGCC 910
Qy      161  CYSPEOTHRISERTIRLEUGLISERCYSPROGLUARGCYSAIAAALVALCYSGIYTTPARG 180
Db      911  TGCCCCACCATTAATTCCTA-----GCTGTGCGTGGATGGAGG 946
Qy      181  Gln 181
Db      947  GAA 949

RESULT 10
US-10-112-793-5
Sequence 5, Application US/10112793
Publication No. US20020192729A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Maischang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-793-5

Alignment Scores:
Pred. No.:          4,97e-91          Length:       1438
Score:              979.00            Matches:       169
Percent Similarity: 93.92%           Conservative:   1
Best Local Similarity: 93.37%         Mismatches:    3
Query Match:        88.92%            Indels:        8
DB:                  9                Gaps:          1

US-09-993-234_6_COPY_19_204 (1-186) x US-10-112-793-5 (1-1438)
Qy      1  LEULENGLYALAAYGALINGLYELYTHARSETPRQARGCYSAAPCYSAIAGLYASP 20
Db      431  CTGCTGGGGGCCCGGGCCAGGGGCGCACTGTATGCCCCAGGTGTGACTGTGCGCGTGAC 490

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QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 491 TTCCACAGAGAGATGGTGTCTTTGTTGACAGAGCTGCCACGGGGGACACTACTGTAAG 550
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 551 GCCCTTGACAGAGAGCTGCGGACACTGCCACTGCTGTGTGTCTCCCAAGACACTTTC 610
QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 611 TTGGCCTGGGAGAACCACTAATTTGAAATGTGCCCGCTGGCCAGCTGTGATGACAGAC 670
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 671 GCTCCAGAGGCGCGGAGAACTGTTCAAGCACTGGCCACACCCCTGTGGCTGTAAAG 730
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
DB 731 CCAAGGCTGTTGTGGAGTCCAGGTCCAGGTCAAGCAATGTGTCCAGGTTCCACTTCTACTGC 790
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 791 CAACCAATGCTTAGACTGCGGGGCTGCACCGCACACAGGGCTACTGTTCCTCCGAGAG 850
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
DB 851 GATACGACTGTGGAGCTGCTGCTGCTGTATGAAATGCGATGGCTGCTGCTGCTGC 910
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaValCysGlyTyrParg 180
DB 911 TGCCCAAGCAATTTCCCTA-----GCTGTCTGGGATGGAGG 946
QY 181 Gln 181
DB 947 GAA 949

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RESULT 11
 US-10-112-193-5
 ; Sequence 5, Application US/10112193
 ; Publication No. US20030004313A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/112,193
 ; FILING DATE: 28-Mar-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/928,069
 ; FILING DATE: 11-Sep-1997
 ; APPLICATION NUMBER: 60/026943
 ; FILING DATE: 23-Sep-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Marschang, Diane L.
 ; REGISTRATION NUMBER: 35,600
 ; REFERENCE/DOCKET NUMBER: P1052R1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-5416
 ; TELEFAX: 650/952-9881

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; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-193-5

Alignment Scores:
Pred. No.: 4,97e-91 Length: 1438
Score: 979.00 Matches: 169
Percent Similarity: 93.92% Conservative: 1
Best Local Similarity: 93.37% Mismatches: 3
Query Match: 88.92% Indels: 8
DB: 9 Gaps: 1

US-09-993-234-6_COPY_19_204 (1-186) x US-10-112-193-5 (1-1438)
QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 431 CTGCTGGGGGCGCGGCGCCAGGCGGCACTGTAAGCCCAAGGTGTACTGTGCGGGTAC 490
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 491 TTCCACAGAGAGATGGTGTCTTTGTTGACAGAGCTGCCACGGGGGACACTACTGTAAG 550
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 551 GCCCTTGACAGAGAGCTGCGGACACTGCCACTGCTGTGTGTCTCCCAAGACACTTTC 610
QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 611 TTGGCCTGGGAGAACCACTAATTTGAAATGTGCCCGCTGGCCAGCTGTGATGACAGAC 670
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 671 GCTCCAGAGGCGCGGAGAACTGTTCAAGCACTGGCCACACCCCTGTGTGTCTCCCAAGACACTTTC 730
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
DB 731 CCAAGGCTGTTGTGGAGTCCAGGTCCAGGTCAAGCAATGTGTCCAGGTTCCACTTCTACTGC 790
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 791 CAACCAATGCTTAGACTGCGGGGCTGCACCGCACACAGGGCTACTGTTCCTCCGAGAG 850
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
DB 851 GATACGACTGTGGAGCTGCTGCTGCTGTATGAAATGCGATGGCTGCTGCTGCTGCTGC 910
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaValCysGlyTyrParg 180
DB 911 TGCCCAAGCAATTTCCCTA-----GCTGTCTGGGATGGAGG 946
QY 181 Gln 181
DB 947 GAA 949

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RESULT 12
 US-09-884-733-5
 ; Sequence 5, Application US/09884733
 ; Patent No. US20020123116A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; TITLE OF INVENTION: Apo-2 Ligand Inhibitor
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/884,733
FILING DATE: 19-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/304,003
FILING DATE: 14-JUNE-2000
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-884-733-5
Alignment Scores:
Pred. No.: 4.97e-91 Length: 1438
Score: 979.00 Matches: 169
Percent Similarity: 93.92% Conservative: 1
Best Local Similarity: 93.37% Mismatches: 3
Query Match: 88.92% Indels: 8
DB: 10 Gaps: 1
US-09-993-234-6_COPY_19_204 (1-186) x US-09-884-733-5 (1-1438)
QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 431 CTGCTGGGGCCCGGGCCAGGCGGCGCAGCTGAGCCCGAGTGTGACTGCGCGGTAC 490
QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 491 TTCACAGAAGAAGATGCTGTTTGTTCAGAGAGCTGCCAGCGGGGACACTACTGAAG 550
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 551 GCCCTTCGACAGGAGCGCTGGGCACTCCACCTGCTGTGTCCCAAGACACCTTC 610
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 611 TTGGCCCGGAGAGACCACTAATTCGAATGTGCCGCTGCCAGGCTGTGATGAGCAG 670
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 671 GCCCTCCAGGTGGCGCTGGAGAACTGTTCAGCACTGGCCAGACCCCGCTGGCTGAAG 730
QY 101 ProGlyTyrPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
DB 731 CCAAGGCTGTTTGTGAGAGTCCAGAGTCCAGCAATGTGTACAGCACTTCTACTGC 790
QY 121 GluProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 791 CAACACATGCTAGACCTCGGGGCGCTCCACCGCACAGGGCTACCTGTTCCCGAGA 850
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
DB 851 GATATCACTAGCTGGAGACTGCTGCTGCTTCTATGAACATGGCGATGGTGGCTGCTCC 910
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180

||||| 11 ||||| 11111111
DB 911 TGCCCAAGTAATTCCTA-----GCTGTCGTGGATGAGG 946
QY 181 Gln 181
DB 947 GAA 949
RESULT 13
US-09-993-234-5
Sequence 5, Application US/09993234
Patent No. US20020146768A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/993,234
FILING DATE: 19-NO. US20020146768A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,683
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-993-234-5
Alignment Scores:
Pred. No.: 4.97e-91 Length: 1438
Score: 979.00 Matches: 169
Percent Similarity: 93.92% Conservative: 1
Best Local Similarity: 93.37% Mismatches: 3
Query Match: 88.92% Indels: 8
DB: 10 Gaps: 1
US-09-993-234-6_COPY_19_204 (1-186) x US-09-993-234-5 (1-1438)
QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 431 CTGCTGGGGCCCGGGCCAGGCGGCGCAGCTGAGCCCGAGTGTGACTGCGCGGTAC 490
QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 491 TTCACAGAAGAAGATGCTGTTTGTTCAGAGAGCTGCCAGCGGGGACACTACTGAAG 550
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 551 GCCCTTCGACAGGAGCGCTGGGCACTCCACCTGCTGTGTCCCAAGACACCTTC 610

QY	61	LeuAlaItrpGluAsnHisHisAsnSerGluCysAlaItrgCysGlnAlaCysAspGluGln	80
Db	611	TTGGCCCTGGGAGAACCCACCAATATTCTGAATGTGCCCGCTGCCAGGCGCTGAGAGACAG	670
QY	81	AlaSerGlnValAlaIaLeuGluAsnCysSerAlaValAlaAspIrrAspCysGlyCysLys	1000
Db	671	GGCTCCCAAGGTGGCGCTGGAGAACTGTTCACACATGGGCCAGACACCCCGCTGGCTGTAA	730
QY	101	ProGlyTrrPheValGluCysGlnValSerGlnCysValSerSerSerProPheTyrCys	1200
Db	731	CCAGGCTGGTTGTGGATGGCAGGTCCAGCCAAAGTGTCCAGCACTGACCCCTTCTAACTGC	790
QY	121	GlnProCysLeuAspCysGlyAlaLeuHisIrrHisIrrIrrGluLeuCysSerArgArg	1400
Db	791	CACCATGCTTACACTGCTGGGGGCCCTGCACGCCACACAGCGCTACCTCTTCCCGCAGA	850
QY	141	AspIrrAspCysGlyTrrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSer	1600
Db	851	GATACTGACTGTGGGACCTGCGCTGCTTCAATGAAACATGGCGATGGCTGCGGTCTCC	910
QY	161	CysProIrrSerIrrLeuGlySerCysAspProGlnArgCysAlaIaValCysGlyTrrArg	1800
Db	911	TGCCCCACAGTAATTCTCA-----GCTGCGTGGGATGGAGG	946
QY	181	Gln 181	
Db	947	GAA 949	

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 2003
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1577
LENGTH: 10797
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-847-1577

Alignment Scores:
Pred. No.: 2,366-68 Length: 10797
Score: 767.00 Matches: 167
Percent Similarity: 40.988 Conservative: 1
Best Local Similarity: 40.738 Mismatches: 5
Query Match: 69.668 Indels: 239
Gaps: 4

US-09-993-234-6_COPY_19_204 (1-186) x US-09-764-847-1577 (1-10797)

QY 1 LeuLeuGlyAlaAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
|||||
Db 5250 CTGCTGGGGGGCCCGGGCCAGGGGCGACACTGAGCCCGGCTGTGACTGTGCCGGTGAC 5309
/

QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAla----- 35
|||||
Db 5310 TTCACACAGACAGATGTGTCTGTTTGTGTGACAGAGGCTGCCACCGGGTAAAGTGGCCACAG 5369

QY 35 ----- 35
Db 5370 GGGTGGAGAGCATGTGGCGAGGCGCTGAGAGGTGGCGGGCAGGCCGGAGGTAA 5429

QY 35 ----- 35
Db 5430 GAGGAGCTGGGAGGGAGGTAGGGTAGGCTGACAGAGATGAGGAGCTGGAGAGAA 5489

QY 35 ----- 35
Db 5490 GAGGGAGGAGGCGAGGTGGAAAGCAGGTGGGGGCTGTGGGCGAGCCCTCGCTGC 5549

QY 36 -----GlyHisTyrLeuLysAlaProCysThrGluProCysG 48
|||||
Db 5550 CTGACCCCTGGCTGTTCCACAGGGCAGCTACGGAAGGCCCTTGCAGGAGGCCCTGCGG 5609

QY 48 yAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHisAs 68
|||||
Db 5610 CAACCTCCACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5669

QY 68 nSerGluCysAlaArgCysGlnAlaCysAspGlu----- 79
|||||
Db 5670 TTCTGAATGTGCCCCGCTGCGAGGCTGTGATGAGCAGAGGCTGAGGGGCTTCTCAGTGTGTG 5729

QY 79 ----- 79
Db 5730 GCAGGAGTTCCTAAGGACAGGCTTTCGAAGGAAGTGCTGGCTGGGGCCAAACTTG 5789

QY 79 ----- 79
Db 5790 GGGTGTGAGGGTCTGCACCCACCTTGCAGAAACCTCCACCCCTGATCCTTCAGGG 5849

QY 79 ----- 79
Db 5850 TGGCCCTTGGCCCTTCTCTCTTCTCTGGTGAACCTTCCATCTCTCAGTGTGCTTGGCTCT 5909

QY 79 ----- 79
Db 5910 GGTGGGCTTAATCTCTGAGCTCTCTCTTTTAAAGGTAGCCCTGACTGTGTCTT 5969

QY 79 ----- 79

Db 5970 TGGCTAATTTCTGTCTCATTACTTGTGGATATGCTTGCCTTCATGGAGGACCTTT 6029
QY 80 -----GlnAlaSerGlnValAl 85
|||||

Db 6030 GGGCTGTACTACTTCTCCTACTCCCATCTCCCTGCACCCCGACCGC-TGCCAGTGGC 6088
QY 85 aLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal 105
Db 6089 GCTGGAGAACTGTTCACAGACTGGCGGACACCGGCTGTGGCTGTAGAGCAGGCTGTGT 6148

QY 105 IGIuGlyGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAs 125
Db 6149 GGAATGCCAGTCAAGCCAAATGTGTACACAGTTCACCTTCTACTGCAACCATGCTTGA 6208

QY 125 pCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSer----- 138
Db 6209 CTGGGGGGCCCTGCACCGCCACACAGGCTACTGTGTGA-GTACCCCGACCGAGGCTCT 6267

QY 138 ----- 138
Db 6268 CTACTCCAGACCCCTTCTCCTGCTGACCCACCTCTGTCCTAGTGTGACGATGCT 6327

QY 139 -----ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTy 152
Db 6328 CTCTGGATTGACAGTTCCCGCAGAGATGACTGTGGGAGCTGCTGCTGCTTCTTA 6387

QY 152 rGluHisGlyAspGlyCysValSerCysProThrSerThrLeuGlySerCysProGluAr 172
Db 6388 TGAACATGGCGATGGCTGCGTGTCTTCTGCCCCCAGCTAATTCTTA----- 6430

QY 172 gCysAlaAlaValCysGlyTyrPargln 181
Db 6431 -----GCTGTGTGGATGAGAGGAA 6451

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GenCore version 5.1.4.p5.4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:19:54 ; Search time 1163.45 Seconds

(without alignments)
2589.161 Million cell updates/sec

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Perfect score: 1101

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Ygapop 10.0 , Ygapex 0.5
Fgapop 6.0 , Fgapex 7.0
Delop 6.0 , Delcxt 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blomumc2 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pic -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-WARN.TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELcxt=7

Database : EST:
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2: em_estlum:*
3: em_estlu:*
4: em_estlu:*
5: em_estlu:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
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16: em_estlum:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_hum:*
20: em_gss_hum:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1075	97.6	767 13 B1909448	B1909448 603065172
2	1072	97.4	698 9 A1807913	A1807913 wf52c03.x
3	1069	97.1	632 10 A268610	A268610 xy41b12.x
4	1049	95.3	688 9 A142836	A142836 tg19b08.x
5	1006	91.4	552 14 A1140043	A1140043 qae7a04.x
6	979	88.9	552 14 BM783972	BM783972 K-EST0062
7	979	88.9	585 14 BM517358	BM517358 xp3q02.x
8	970	88.1	565 14 BM744307	BM744307 K-EST0017
9	964	87.6	514 14 BM756372	BM756372 K-EST0034
10	964	87.6	514 14 BM783979	BM783979 K-EST0062
11	943	85.6	508 9 A1203624	A1203624 qe75f02.x
12	935	84.9	492 14 BM741016	BM741016 K-EST0013
13	920	83.6	488 14 BM70798	BM70798 K-EST0054
14	867	78.7	1010 14 B0068309	B0068309 AGENCOURT
15	825.5	75.0	478 10 AM002222	AM002222 w85c09.x
16	795	72.2	427 12 BE656572	BE656572 PM4-CT040
17	707	64.2	433 14 A1700459	A1700459 wd41b11.x
18	692	62.9	433 14 H41522	H41522 y90f012.s1
19	654	59.4	572 10 BE668836	BE668836 159213 MA
20	595	54.0	432 14 N71143	N71143 za80h09.s1
21	580.5	52.7	434 14 BM826048	BM826048 K-EST0098
22	521	47.3	345 9 AA934992	AA934992 op33h05.s
23	518.5	47.1	443 14 H46211	H46211 y014h09.r1
24	479	43.5	673 13 BM251737	BM251737 B07L01000
25	474.5	43.1	755 13 B1655045	B1655045 603282719
26	463	42.1	468 14 H46374	H46374 y012d07.r1
27	451.5	41.0	775 12 BG867742	BG867742 op23c01.s
28	424.5	38.6	322 9 AA971249	AA971249 6073c01.s
29	420	38.1	330 14 N71141	N71141 za80g11.s1
30	410.5	37.3	639 10 BB636341	BB636341 BB636341
31	407	37.0	316 14 H49675	H49675 y023d06.r1
32	391.5	35.6	393 14 H41851	H41851 y007f03.r1
33	360.5	32.7	418 14 H46662	H46662 y012e12.r1
34	325	29.5	397 14 H46378	H46378 y012f05.r1
35	296	26.9	246 14 H46424	H46424 y012e12.s1
36	294	26.7	246 14 H19739	H19739 y060h04.r1
37	283.5	25.7	368 10 BB872434	BB872434 BB872434
38	277.5	25.2	517 14 BM692368	BM692368 UT-E-CL1-
39	221	20.1	556 10 AV664984	AV664984 AV664984
40	214	19.4	252 9 BM695862	BM695862 UT-E-CL1-
41	213	19.3	779 9 A1119338	A1119338 u03d04.y
42	212	19.3	725 12 BG863025	BG863025 602796549
43	212	19.3	984 12 BF164835	BF164835 601777753
44	209.5	19.0	775 13 B1555040	B1555040 603236555
45	209	19.0	651 13 BM009354	BM009354 603629813

ALIGNMENTS

RESULT 1
LOCUS B1909448
DEFINITION 603065172F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214568 5',
ACCESSION B1909448
VERSION B1909448.1 GI:16172666
KEYWORDS
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 767)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT

Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: InCyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM1538 row: 0 column: 17
 High quality sequence stop: 754.

FEATURES

source

Location/Qualifiers
 1. .767

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5214568"
 /clone_1lb="NIH_MGC_118"
 /tissue_type="leukocyte"
 /lab_host="DH10B"
 /note="Vector: PCMW-SF00T6; Site_1: Not; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dt primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH MGC Library."

BASE COUNT 122 a 243 c 241 g 161 t
 ORIGIN

Alignment Scores:

Pred. No.: 1.46e-92 Length: 767
 Score: 1075.00 Matches: 186
 Percent Similarity: 98.94% Conservative: 0
 Best Local Similarity: 98.94% Mismatches: 0
 Query Match: 97.64% Indels: 2
 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x B1909448 (1-767)

QY 1 LeuLeuGlyAlaArg-AlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAs 20
 |||||||
 Db 90 CTGCTGGGGGCGCGGCCAGGCGCGACCTGCTACCCCGAGGTGTGCTGCGCGTGA 149
 QY 20 PheHisLysLysLleGlyLeuPheCysArgGlyCysProAla-GlyHisTyrLeu 40
 |||||||
 Db 150 CTTCACAAAGAGATGTGTGTGTGTGTGCAAGGCTGCGCGTGGGCGCTACTACTGA 209
 QY 40 ysaAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThr 60
 |||||||
 Db 210 AGGCCCCCTGCAGGAGCCCTGGGCACTCCACCTGTGTGTGTCCCAAGACACT 269
 QY 60 heLeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGlu 80
 |||||||
 Db 270 TCTTGCCCTGGGGAACCACTAATTCGAATGTGCCGCGCTGCGATGAGC 329
 QY 80 lAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCys 100
 |||||||
 Db 330 AGGCCCCAGGTGGCGCGTGGAGAACTGTTCAAGCTGGCCGACCCGCTGTGCTGA 389
 QY 100 ysaProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyr 120
 |||||||
 Db 390 ACCGAGGCTGGTTGTGTGAGTGCAGCTCAGCCAGTGTGCACTTCACTTACT 449
 QY 120 ysaGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArg 140
 |||||||
 Db 450 GCCAACCAATGCTAGACTCGGGGCGCTGACCGCACACAGCGCTACTGTTCGCCGA 509
 QY 140 rAspThrAspCysGlyTrpCysLeuProGlyPheTyrGlnHisGlyAspArgLysVal 160
 |||||||
 Db 510 GAGATCTGACTGTGGACCTGCTGCTGTCTATGAACATGGCGAGTGGCTGCTGT 569

QY 160 erCysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrp 180
 |||||||
 Db 570 CCGGCCCAAGACACACCTGGGAGCTGTCCAAAGGCGTGTGCTGTGAGTGA 629
 QY 180 rglMetPheTrpValGln 186
 |||||||
 Db 630 GGCAGATGTCTGGGTCCAG 649

RESULT 2

A1807913

LOCUS

DEFINITION

A1807913 698 bp mRNA linear EST 19-DEC-1999
 w52c03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
 IMAGE:2359204 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
 PRECURSOR ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Email: cgaabs-r@mail.nih.gov
 This clone is available royally-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert length: 1568 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 459.

FEATURES

source

Location/Qualifiers

1. .698

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2359204"

/clone_1lb="Soares_NFL_T_GBC_S1"

/lab_host="DH10B"

/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBHL19W, testis NHT, and B-cell
 NCI CGAP GCBI) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT 111 a 218 c 214 g 155 t
 ORIGIN

Alignment Scores:

Pred. No.: 2.47e-92 Length: 698
 Score: 1072.00 Matches: 182
 Percent Similarity: 97.85% Conservative: 0
 Best Local Similarity: 97.85% Mismatches: 4
 Query Match: 97.37% Indels: 0
 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x A1807913 (1-698)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
 |||||||
 Db 18 CTGCTGGGGGCGCGGCCAGGCGGCGTGTGATTCACAGGTGTGAGTGGCGGTGAC 77
 QY 21 PheHisLysLysLleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
 |||||||
 Db 78 TTCCCAAGAAAGATGTGTGTGTGTGTGCAAGGCTGCCACAGCGGCGCTACTGTAAG 137

was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 602632-607239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT	102 a	194 c	192 g	143 t	1 others
ORIGIN					

ORIGIN

Alignment Scores:

Pred. No.:	4.12e-92
Score:	1069.00
Percent Similarity:	98.39%
Best Local Similarity:	98.39%
Query Match:	97.09%
DB:	10 ⁶
	Gaps:
	Indels:
	Mismatches:
	Conservative:
	Matches:
	Length:
	6322
	1833

US-09-993-234-6_COPY_19_204 (1-186) x AW268610 (1-632)

Db	378	CACCATCCCTAGATCGGGGGCCCTGCACCGCACACAGCGCTACTCTGTCCCGCAGA	437	Oy	1	LeuLeuGluValAlaArgAlaGlnGlyLysIleThrArgSerProArgCysAspCysAlaGlyAsp	20
Oy	141	AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer	160	Db	9	CTGCTGGGGGGCCCCGGCCAGCGGCGACCTGTACCCTCCAGGTGTGACTGTCCGGTAC	68
Db	438	GATACTGACTGTGGGAACTGCTGCTTCTTATGACATGGCGATGGCTGCGCTGC	497	Oy	21	PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys	40
Oy	161	CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg	180	Db	69	TTCCACAGAAAGATTGGCTGTGTTGTTGGCAAGGCTGCCAGCGGGCGACACTCCGTGAAG	12
Db	498	TGCCCTACAGAGACCCCTGTGAGCTGTCCAGAGCGCTGTGCGCTGTGTGGCTGAGG	557	Oy	41	AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe	60
Oy	181	GlnMetPheThrPvalGln	186	Db	129	GCCCTTGCAGAGAGCCCTGCGGCAACTCCACTCTGTGTGTGTCTCCCAAGACACTTC	18
Db	558	CAGATGTTCTGGGTGCAG	575	Oy	61	LeuAlaTrrGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln	80

RESULT 3

LOCUS	632 bp	mRNA	linear	EST 03-JAN-2000
AM266610				
DEFINITION	xv41p12.x1 Soares_MFL_T-GBC_S1 Homo sapiens cDNA clone			

ACCESSION	IMAGE:2815679.3, similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
VERSION	PRECUSOR ;, mRNA sequence.
KEYWORDS	AW268610
SOURCE	AW268610.1 GI:6655640
	EST:
	human.

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

FEATURES	Location/Qualifiers
source	1. .632

LOCUS	A1424936	688 bp	mRNA	linear	EST 30-MAR-1999
DEFINITION	tg19b08.x1 NCI-CGAP CLL1 Homo sapiens cDNA clone IMAGE:2109207 3'				
DESCRIPTION	similar to RF:000276 000276 LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH				
FEATURES	2..111 mRNA sequence.				

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	GI
Al424936 Al424936.1 EST. human. Homo sapiens	GI:4270854
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 688) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	


```
|||||
Db 47 CTGCTGGGGGCGCCGAGCGGCGGCGCTGTAAGCCCGGAGGTGAGCTGTGGCGGTAC 106
Qy 21 PheHISLysLISlegLYLeuPheCysCysArgGLYcysProAlaGLYHISLysLeuLys 40
Db 107 TTCACAAAGAAAGATTGGCTCTTTTGTTCAGAGGCTCCAGCGGGGACTACTAG 166
Qy 41 AlaProCysThrGLUProCysGLYAsnSerThrCysLeuValcysProGLInAspThrPhe 60
Db 167 GCGCCCTTGACAGGAGCCCTCGGCAACTCCACCTGCTTGTGTGTCGCCAAGACACTTC 226
Qy 61 LeuAlaTrpGLUAsnHISAsnSerGLUcysAlaArgCysGLInAlaCysAspGLIn 80
Db 227 TTGGCGCTGGAGAACCAACCAATATTCGAATGTGCCCTCGCAGGCTGTGATGAGCAG 286
Qy 81 AlaSerGLInAlaLeuGLUAsnCysSerAlaValAlaAspThrArgCysGLYcysLys 100
Db 287 GCCCTCCAGGTGGCGGTGAGAACTGTTACAGACAGTGGCGGACACCGGCTGTGGCTGTAAG 346
Qy 101 ProGLYTrpPheValGLUcysGLInValSerGLInCysValSerSerProPheTrcys 120
Db 347 CCAGCGCTGGTTGTGAGTGTCCAGGTCCAGCAATGTGTCCACAGTTCACCTTCTACTGCG 406
Qy 121 GLNProCysLeuAspCysGLYAlaLeuHISArgHISThrArgLeuLeuCysSerArgArg 140
Db 407 CACCCATGCTAGACTGCGGGGCGGCGCTGACCGCACACAGCGCTACTCTGTCCCGCAGA 466
Qy 141 AspThrAspCysGLYThrCysLeuProGLYpHeTrpGLUHSGLYAspGLYcysValSer 160
Db 467 GATCTGACTGTGGAGACTGCTGCTGCTGTCTATGAACTGCGAGTGGCTGCTGCTGCC 526
Qy 161 CysProThrSerThrLeuGLYSerCysAspProGLUArg 172
Db 527 TGCCCAAGAGCACCCCTGNGAGCTGTTCAGAGCGC 562

RESULT 6
BM783972
LOCUS BM783972 552 bp mRNA linear EST 05-MAR-2002
DEFINITION K-EST0062019 S6SN0620 Homo sapiens cDNA clone S6SN0620-31-H06 5',
ACCESSION BM783972
VERSION BM783972.1 GI:19132204
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 552)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Chaong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
JOURNAL 21C Frontler Korean EST Project 2001
COMMENT Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsungemail.kr@db.re.kr
Plate: 31 row: H column: 06
High quality sequence stop: 552.
FEATURES
source
1..552
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SN0620-31-H06"
/clone_id="S6SN0620"
/sex="F"
/tissue_type="Ascites"
/cell_line="Scattering floating"
/lab_host="Top10F"
```

```
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
with tabacco acid pyrophosphatase (TAP). The deapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
```

BASE COUNT 92 a 172 c 173 g 115 t

ORIGIN

Alignment Scores:

Pred. NO.:	Length:	Matches:
Score: 1.32e-83	552	169
Percent Similarity: 979.00		
Best Local Similarity: 93.92%		
Query Match: 93.37%	Mismatches: 3	
	Indels: 8	
DB: 14	Gaps: 1	

US-09-993-234-6_copy_19_204 (1-186) x BM783972 (1-552)

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Qy 1 LeuLeuGLInAlaArgAlaGLInGLYGLYThrArgSerProArgCysAspCysAlaGLYAsp 20
Db 20 CTGCTGGGGGCGCCGAGCGGCGGCGGCGGCTGTAAGCCCGAGGTGAGCTGTGGCGGTAC 79
Qy 21 PheHISLysLISlegLYLeuPheCysCysArgGLYcysProAlaGLYHISLysLeuLys 40
Db 80 TTCACAAAGAAAGATTGGCTCTTTTGTTCAGAGGCTCCCGGCGGCTACTACTGTAAG 139
Qy 41 AlaProCysThrGLUProCysGLYAsnSerThrCysLeuValcysProGLInAspThrPhe 60
Db 140 GCCCTTGACAGGAGCCCTCGGCGCAACTCCACCTGCTGTGTGTCGCCAAGACACTTC 199
Qy 61 LeuAlaTrpGLUAsnHISAsnSerGLUcysAlaArgCysGLInAlaCysAspGLIn 80
Db 200 TTGGCTGAGAGAACCAACCAATATTCGAATGTGCCCGCTGCGAGGCTGTGATGAGCAG 259
Qy 81 AlaSerGLInAlaLeuGLUAsnCysSerAlaValAlaAspThrArgCysGLYcysLys 100
Db 260 GCGTCCAGGTGGCGCTGAGAACTGTTACAGAGTGGCGGACACCGGCTGTGGCTGTAAG 319
Qy 101 ProGLYTrpPheValGLUcysGLInValSerGLInCysValSerSerProPheTrcys 120
Db 320 CCAGGCTGTTGTGAGTGTCCAGGTCCAGCAATGTGTCCACAGTTCACCTTCTACTGCG 379
Qy 121 GLNProCysLeuAspCysGLYAlaLeuHISArgHISThrArgLeuLeuCysSerArgArg 140
Db 380 CACCCATGCTAGACTGCGGGGCGGCGGCGGCGGCGGCTGTTCTGTCCCGCAGA 439
Qy 141 AspThrAspCysGLYThrCysLeuProGLYpHeTrpGLUHSGLYAspGLYcysValSer 160
Db 440 GATCTGACTGTGGAGACTGCTGCTGCTGTCTATGAACTGCGAGTGGCTGCTGCTGCC 499
Qy 161 CysProThrSerThrLeuGLYSerCysAspProGLUArgCysAlaValcysGLYTrpArg 180
Db 500 TGCCCGACGTAATTCCTA-----CGTGTGCTGGAGTGGAGG 535
Qy 181 GLN 181
Db 536 GAA 538

RESULT 7
LOCUS AM517358 585 bp mRNA linear EST 03-MAR-2000
DEFINITION xp93902.x1 Soares_NHCE_cervix Homo sapiens cDNA clone IMAGE:2747954
```


ORIGIN

Alignment Scores:

Pred. No.: 9.88e-83 Length: 565
Score: 970.00 Matches: 168
Percent Similarity: 93.37% Conservative: 1
Best Local Similarity: 92.82% Mismatches: 4
Query Match: 88.10% Indels: 8
DB: 14 Gaps: 1

US-09-993-234-6_copy_19_204 (1-186) x BM744307 (1-565)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProAlaGlyAspCysAlaGlyasp 20
DB 20 TTGCTGGGGGGCCCGCCCACTGGCGACCTGTAACCCAGTGTGACTGTCGGGTAC 79
QY 21 PheHisLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 80 TTCCACAAAGAGATTGGCTGTGTTTGTTCAGAGAGCTGCCAGCGGGCACTACCTGAAG 139
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 140 GCCCTTCACAGAGACCTGGCGCACTGCTGTGTGTGTCCTCCCAAGACACTTC 199
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 200 TTGGCTGGGGAACCACTAATTCGTAATGTGCCCTGCCAGGCTGTGATGACGAG 259
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 260 GCTTCACAGGTTGGCGGTGAGAACCTGTTACAGACAGGCGCACCCGCTGTGGCTGAG 319
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
DB 320 CCAGGCTGTGTGGAGATGTCAGGTGACCAAGTGTGACAGTTCACCTTACTGTC 379
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 380 CAACCATCTAGACTGTGGGGCCCTGTCACCGCCACACACGCTACTGTTCCTCCGAGAG 439
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSer 160
DB 440 GATCTGACTGTGGACCTGCTGCTGCTGTCTTCTATGACATGGGAGATGGCTGCTGTC 499
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180
DB 500 TGCCCAAGATATTCCTA-----GCTGTGTGGAGATGAGAG 535
QY 181 Gln 181
DB 536 GAA 538

RESULT 9

BM756372

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BM756372 514 bp mRNA linear EST 04-MAR-2002
K-EST0034666 S6SNU620 Homo sapiens cDNA clone S6SNU620-27-G03 5',
mRNA sequence.
BM756372
BM756372.1 GI:19085987
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Kim, M.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409

Email: yongsung@mail.kr.ibm.re.kr
Plate: 27 row: G column: 03
High quality sequence stop: 514.
Location/Qualifiers

FEATURES

source

1. 514
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-27-G03"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNV-620"
/lab_host="Top10F"

/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
Site_2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
with tabacco acid pyrophosphatase (TAP). The deapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

BASE COUNT 86 a 166 c 153 g 109 t
ORIGIN

Alignment Scores:

Pred. No.: 3.21e-82 Length: 514
Score: 964.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 87.56% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_copy_19_204 (1-186) x BM756372 (1-514)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProAlaGlyAspCysAlaGlyasp 20
DB 20 TTGCTGGGGGGCCCGCCCACTGGCGACCTGTAACCCAGTGTGACTGTCGGGTAC 79
QY 21 PheHisLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 80 TTCCACAAAGAGATTGGCTGTGTTTGTTCAGAGAGCTGCCAGCGGGCACTACCTGAAG 139
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 140 GCCCTTCACAGAGACCTGGCGCACTGCTGTGTGTGTCCTCCCAAGACACTTC 199
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 200 TTGGCTGGGGAACCACTAATTCGTAATGTGCCCTGCCAGGCTGTGATGACGAG 259
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 260 GCTTCACAGGTTGGCGGTGAGAACCTGTTACAGACAGGCGCACCCGCTGTGGCTGAG 319
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
DB 320 CCAGGCTGTGTGGAGATGTCAGGTGACCAAGTGTGACAGTTCACCTTACTGTC 379
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 380 CAACCATCTAGACTGTGGGGCCCTGTCACCGCCACACACGCTACTGTTCCTCCGAGAG 439

QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrluHisGlyAspGlyCysValSer 160
 Db 440 GATACGACTGTGGAGCCTGCTGCTTATGAAATGCGATGCGCTGCTGCC 499
 QY 161 CysProThr 163
 Db 500 TGCCCCACG 508
 RESULT 10
 LOCUS BM783979 514 bp mRNA linear EST 05-MAR-2002
 DEFINITION K-EST0062030 S6SNU620 Homo sapiens CDNA clone S6SNU620-32-A05 5',
 mRNA sequence.
 ACCESSION BM783979
 VERSION BM783979.1 GI:19132211
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 514)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong, Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: Yongsung@email.kribb.re.kr
 Plate: 32 row: A column: 05
 High quality sequence stop: 514.
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 1. .514
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="S6SNU620-32-A05"
 /clone_1ib="S6SNU620"
 /sex="F"
 /tissue_type="Ascites"
 /cell_type="Scattering floating"
 /cell_line="SND-620"
 /lab_host="Top10F"
 /note="Organ: Stomach. Vector: pCNS. Site:1: EcoRI;
 Site:2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tabacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."
 BASE COUNT 86 a 166 c 153 g 109 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.21e-82 Length: 514
 Score: 964.00 Matches: 163
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 87.56% Indels: 0
 DB: 14 Gaps: 0

US-09-993-234-6_Copy_19_204 (1-186) x BM783979 (1-514)
 QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
 Db 20 CTGCTGGGGGCCCCGGGGCCAGGGCGGCACCTGTAGCCCCAGGTGTGCTGCCGGGTAG 79
 QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
 Db 80 TTCCACAGAGAAATTGGCTCTTTTGTTCAGAGGCTGCCCCAGGGGAGCTACCTGAAG 139
 QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
 Db 140 GCCCTTGACAGGAGGCCCTCGGCACACTCCACCTGCCTTGTGTCTCCCAAGACACTTC 139
 QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysAlaAcysAspGluGln 80
 Db 200 TTGGCTGGGAGAACACCACTAATCTGAAATGTGCCCGCTGCAGGCTGTGATGAGCAG 259
 QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
 Db 260 GCCTCCAGGTGGCGCTGGAGAACTGTTCAGAGTGGCCAGACCCGCTGTGCTGTAAG 319
 QY 101 ProGlyTyrPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
 Db 320 CCAGGCTGTTGTGGAGTGCAGGTCCAGGCAATGTGTGACAGCTTACACCTTCTACTGC 379
 QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
 Db 380 CAACCAATGCTTAAACGCGGGGCCCGCCACCGCCACACACGCGTACTCTGTTCCACAG 439
 QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrluHisGlyAspGlyCysValSer 160
 Db 440 GATACGACTGTGGAGCCTGCTGCTTATGAAATGCGATGCGCTGCTGCC 499
 QY 161 CysProThr 163
 Db 500 TGCCCCACG 508
 RESULT 11
 LOCUS AI203624 508 bp mRNA linear EST 29-OCT-1998
 DEFINITION ge75f02.x1 Soares-fetal_lung_NBHL19W Homo sapiens CDNA clone
 IMAGE:1744827 3' similar to SW:WSHL_HUMAN Q03038 WSL-1 PROTEIN
 PRECURSOR ; mRNA sequence.
 ACCESSION AI203624 GI:3756230
 VERSION AI203624.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 508)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert length: 1699 Std Error: 0.00
 Seq primer: -40UP from Glibco
 High quality sequence stop: 442.
 FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1744827"
 /clone_1ib="Soares fetal_lung_NBHL19W"
 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: lung; Vector: pTY73D (Pharmacia) with a

modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTCACCAATCTGACGTGGAGCGGCGGCAATTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library. Soares fetal heart NBH19W."

BASE COUNT 82 a 161 c 159 g 106 t
ORIGIN

Alignment Scores:

Score: 3.19e-80 Length: 508
943.00 Matches: 160
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.65% Indels: 0
Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x A1203624 (1-508)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20

Db 29 CTGCTGGGGGGCCCGCCAGCGCGCAGCTGTGAGCCCGCAGGTGTGAGTGTGCGGTGAC 88

QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40

Db 89 TTCACAAAGAAATGGTCTGTGTGTGACAGAGCTCCACAGCGGGGCGACTACTGTAG 148

QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60

Db 149 GCCCTTGGCAGGAGCCCTGGGCAACACACCTGCTGTGTGTCGCCAAGACACCTTC 208

QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80

Db 209 TTGGCTGGGAGAACACCATTAATTCGAAATGTGCCCGCTCCAGGCTGTGATGACGAG 268

QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100

Db 269 GCCCTCCAGGTGGGCTGGAGAACTGTTCACAGAGGCGGACACCCGGTGGCTGTAG 328

QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120

Db 329 CCAGGCGGTGTGTGAGAGTGCACAGGTGACCAATGTGTACAGATTCACCTCTTACATGC 388

QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140

Db 389 CACCATGCTCCAGACTGCGGCGCCCTGCACCGCACACACCGCTACTCTGTTCGGCAGA 448

QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSer 160

Db 449 GATCTACTGTGGAGACCTGCTGCTGTCTTATGAACATGGGAGTGGCTGTCTC 508

RESULT 12 492 bp mRNA linear EST 01-MAR-2002
BM741016

LOCUS K-EST0013376 S6SNU620 Homo sapiens cDNA clone S6SNU620-2-C03 5',
DEFINITION mRNA sequence.

ACCESSION BM741016 GI:19062345

VERSION .BM741016.1

KEYWORDS EST.

ORGANISM human.

REFERENCE

AUTHORS

TITLE

ZIC Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center

52 Korea Research Institute of Bioscience & Biotechnology

Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.krdb.re.kr

Plate: 2 row: C column: 03

High quality sequence stop: 492.

location/Qualifiers

1..492

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="S6SNU620-2-C03"

/clone_id="S6SNU620"

/sex="F"

/tissue_type="Ascites"

/cell_type="Scattering floating"

/cell_line="SNU-620"

/lab_host="Top10F"

/note="Organ: Stomach; Vector: pcms; Site_1: EcoRI;

Site_2: NotI; The poly (A)+ RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then deapped

with tabacco acid pyrophosphatase (TAP). The deapped

intact mRNA was ligated with DNA-RNA linker including EcoR

I site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized from oligo dt-selected mRNA by

priming with dt-tailed vector. The dt-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10F by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library."

BASE COUNT 85 a 157 c 146 g 104 t
ORIGIN

Alignment Scores:

Pred. No.: 1.77e-79 Length: 492
Score: 935.00 Matches: 161
Percent: 99.38% Conservative: 0
Best Local Similarity: 99.38% Mismatches: 1
Query Match: 84.92% Indels: 1
Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x BM741016 (1-492)

QY 2 LeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAspPhe 21

Db 2 CTGGGGGGCCCGGCCCA-GCGCGACACTGTGACAGGCTGTGAGTGTGCGGTACTTC 60

QY 22 HisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAla 41

Db 61 CACAAGAGATTTGCTGTGTGTGTCAGAGGCTCCACAGCGGCGACACTGAAGGCC 120

QY 42 ProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeu 61

Db 121 CTTTGCAGGAGCCCTGGGCAACTCCACTCTGTGTGTGTCGCCCAAGACACTTCTTG 180

QY 62 AlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAla 81

Db 181 GCCTGGAGAAACACCATTAATCTGATGTGCCCTGCGCAGGCTGTGATGACAGGCC 240

QY 82 SerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysPro 101

Db 241 TCCAGGTGGCGCTGGAAGACTGTTCACAGAGGCGCGACACCCGCTGTGAGTAAAGCA 300

QY 102 GlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGln 121

Db 301 GCGTGGTTTGTGAGTGTGACAGGTCCAAATGTGTACAGATTCACCTTCTACTGCAG 360

QY 122 ProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgasp 141
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 Db 361 CCATGCGCTAAGTACGCGGGCCCTGCACCGCCACACAGGCTACTCTGTCCCGAGAGAT 420
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 QY 142 ThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCys 161
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 Db 421 ACTGACTGTGGACCTGCTGCTGCTGTATGACATGCGATGGCGCTGCTGCTGCTG 480
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 QY 162 ProThr 163
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 Db 481 CCCACG 486
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 LOCUS BM770798
 DEFINITION K-EST0054419 S6SNU620s1 Homo sapiens cDNA clone S6SNU620s1-21-D12
 5' mRNA sequence.
 ACCESSION BM770798 GI:19100413
 VERSION BM770798
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 488)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kr.ibm.re.kr
 Plate: 21 row: D column: 12
 High quality sequence stop: 488.
 Location/Qualifiers
 1..488
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="S6SNU620s1-21-D12"
 /clone_1lb="S6SNU620s1"
 /sex="F"
 /tissue_type="Ascites"
 /cell_type="Scattering floating"
 /lab_host="Top10F"
 /note="Organ: Stomach; Vector: pcns; Site: 1: EcoRI;
 Site: 2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then deapped
 with tabacco acid pyrophosphatase (TAP). The deapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library. After analyzing and
 sequencing about 2,000 - 3,000 colonies in original cDNA
 library, the abundant cDNAs were selected and amplified by
 PCR reaction using vector region primer including 77
 promoter as 5' primer and N(dT)14 as 3' primer. The PCR
 products were used as template for synthesis of
 biotinylated single stranded RNA by in vitro transcription

reaction. The synthesized RNA probes were hybridized with
 antisense single stranded cDNAs prepared from original
 library and incubated with avidin gel. After removing
 DNA-RNA hybrids by centrifuge, the subtracted cDNA
 libraries were constructed by transformation of the
 remaining DNA into competent cells E. coli Top10F with
 electroporation method."

BASE COUNT 83 a 156 c 147 g 102 t
 ORIGIN

Alignment Scores:
 Pred. No.: 4.73e-78 Length: 488
 Score: 920.00 Matches: 156
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 83.56% Indels: 0
 DB: 14 Gaps: 0

US-09-993-234-6_Copy_19_204 (1-186) x BM770798 (1-488)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspAlaGlyAsp 20
 |||||
 Db 20 CTCCTGGGGCCCGGGCCAGGGCGGCGACTGTAAGCCAGGTGTACTGTGGGTGAC 79
 |||||
 QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlnHisTyrLeuLys 40
 |||||
 Db 80 TTCACAGAGAAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 139
 |||||
 QY 41 AlaProCysThrLysProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
 |||||
 Db 140 GCCCTTGGCAGGAGGCGCTGGCGCAACTCCACTGCTGTGTGTGTGTGTGTGTGTGT 199
 |||||
 QY 61 LeuAlaTProLysHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGln 80
 |||||
 Db 200 TTGGCTGGAGAGAACCAACCAATATTGTGAATGTGCCCTGCCAGGCTGTGTGTGAGCAG 259
 |||||
 QY 81 AlaSerGlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
 |||||
 Db 260 GCTCCAGAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCGGACCGCGGTGGCTGTAAAG 319
 |||||
 QY 101 ProGlyTyrPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
 |||||
 Db 320 CAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 379
 |||||
 QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
 |||||
 Db 380 CACACGCTAAGTACGCGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCAGAA 439
 |||||
 QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAsp 156
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 Db 440 GATGACTGACTGTGGACCTGCTGCTGCTGTATGACATGGCGAT 487
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 5' mRNA sequence.
 ACCESSION B0068309
 VERSION B0068309.1 GI:19897355
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 1010)
 NIH-MGC http://mhc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Life technologies, Inc.
 cDNA library preparation: Life technologies, Inc.
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)


```

Db      329  CCAGGCTGGTTTGGAGTCCAGGTCAGCCATGTCAGCAGTTCACCCCTTCTACTGC 388
QY      121  GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
          |||||
Db      389  CAACCATGCTTAGACTGCGGGCCCTGCACCGCCACAA-CGGCTACTCTGTTC-CGCAGA 446
QY      141  AspThrAspCysGlyThrCysLeuProGlyPhe 151
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Db      447  GATCT-GACTGTGGGACCTGCTGCTGCTTT 478

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GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:35:34 ; Search time 825.126 Seconds
(without alignments)
2504.221 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdt -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NOR=ext -HEA=SITE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0993234.@CGML_1.1.853_@runat_27032003.115455.15349 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-MARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXt=7

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2: gb_htg:.*
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15: em_ba:.*
16: em_fun:.*
17: em_hum:.*
18: em_in:.*
19: em_mu:.*
20: em_com:.*
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22: em_ov:.*
23: em_pat:.*
24: em_ph:.*
25: em_pl:.*
26: em_ro:.*
27: em_sts:.*
28: em_un:.*

29: em_vl:.*
30: em_htg_hum:.*
31: em_htg_inv:.*
32: em_htg_other:.*
33: em_htg_mus:.*
34: em_htg_pln:.*
35: em_htg_rtd:.*
36: em_htg_mam:.*
37: em_htg_vrt:.*
38: em_sy:.*
39: em_htg_hum:.*
40: em_htg_mus:.*
41: em_htg_other:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	368	100.0	705 9 HSU94508	U94508 Human lymph
2	368	100.0	838 9 HSU94507	U94507 Human lymph
3	368	100.0	952 9 HSU94506	U94506 Human lymph
4	368	100.0	1087 9 HSU94505	U94505 Human lymph
5	368	100.0	1119 9 HSU94509	U94509 Human lymph
6	368	100.0	1143 9 HSU94510	U94510 Human lymph
7	368	100.0	1198 9 HSU94504	U94504 Human lymph
8	368	100.0	1250 9 AX150176	AX150176 Sequence
9	368	100.0	1254 6 AR119657	AR119657 Sequence
10	368	100.0	1254 9 HSU72763	U72763 Human death
11	368	100.0	1254 9 HSU78029	U78029 Human death
12	368	100.0	1254 9 HSU94501	U94501 Human lymph
13	368	100.0	1257 9 HSU94502	U94502 Human lymph
14	368	100.0	1355 9 HSU94503	U94503 Human lymph
15	368	100.0	1528 9 HSU83597	U83597 Human death
16	368	100.0	1557 9 HSU75380	U75380 Human death
17	368	100.0	1581 9 AK094463	AK094463 Homo sapi
18	368	100.0	1634 9 HSU74611	U74611 Human Apo-3
19	368	100.0	1662 6 AX055442	AX055442 Sequence
20	368	100.0	1662 6 AX201344	AX201344 Sequence
21	368	100.0	1783 6 AR119656	AR119656 Sequence
22	368	100.0	2053 9 AK094488	AK094488 Homo sapi
23	368	100.0	4811 9 AB051851	AB051851 Homo sapi
24	368	100.0	4825 9 AB051850	AB051850 Homo sapi
25	368	100.0	53982 9 AL158217	AL158217 Homo sapi
26	356	96.7	1669 9 AF026070	AF026070 Homo sapi
27	356	96.7	1743 6 AX331947	AX331947 Sequence
28	356	96.7	1743 9 HSW5L1	Y09392 H. sapientis m
29	356	96.7	1763 9 AF026071	AF026071 Homo sapi
30	350	95.1	1619 10 BC017526	BC017526 Mus muscu
31	350	95.1	97483 2 AC118359	AC118359 Rattus no
32	350	95.1	196368 2 AL772240	AL772240 Mus muscu
33	344	93.5	1665 10 AF329969	AF329969 Mus muscu
34	309	84.0	18015 10 AF134858	AF134858 Mus muscu
35	278	75.5	523 11 G37503	G37503 SHGC-57889
36	161	43.8	1956 10 MUSTNFR2	M59377 Murine tumo
37	161	43.8	2004 4 SSU19994	U19994 Sus scrofa
38	161	43.8	2048 10 MUSWTNFR1	M60468 Mouse tumor
39	161	43.8	2063 10 MPM55R	X59238 Murine mRNA
40	161	43.8	2086 10 BC004599	BC004599 Mus muscu
41	161	43.8	2154 10 MUSTNFR5	L26349 Mus muscu
42	161	43.8	2179 10 MMTNFR5	X57796 Mouse mRNA
43	161	43.8	52858 2 AC115960	AC115960 Mus muscu
44	159	43.2	2171 4 AB051103	AB051103 Felis cat
45	157	42.7	2115 10 AF329976	AF329976 Rattus no

RESULT 1

ALIGNMENTS

HSU94508
LOCUS HSU94508 705 bp mRNA linear PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 7 mRNA, alternatively
spliced, complete cds.
ACCESSION U94508
VERSION U94508.1 GI:2071962
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 705)
McMichael, A.J., Xu, X.N., Olsen, A.L., Cowper, A.E., Tan, R.,
Screation, G.R., and Bell, J.I.
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 705)
Screation, G.R.
Direct Submission
Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source Location/Qualifiers
1..705
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..705
/function="mediates apoptosis"
/note="similar to Fas and TNF-R1; lacks transmembrane
domain; possibly soluble; LARD-6; LARD-7; NGFR family
member"
/codon_start=1
/product="lymphocyte associated receptor of death 7"
/protein_id="AAC5131.1"
/db_xref="GI:2071963"
/translation="MEORPGCAVAAYAAALVILGARAQGRSPRCDCADPFHKKIG
LFCGRGCPADAGMALTLPAPATHLSPIDSAHTLAPDSSEKICTYVLGNSRTPGY
PENCALCPQWTMSMDLPSPALRGAAPPTSPSPASPMAMQDPGLYDMQAVP
ARRKREYRTIGLRPAETLEAVELEIGRRDOQYELTKRWKQDPAGLAVYAALERMG
LDGCEVLDLSRLQKGP"
160..161
/note="deletion compared to LARD 1a, deposited in Genbank
Accession Number U94501, probable skipping of putative
exons 3, 4, 5, 6 and 7"
misc_feature
BASE COUNT 112 a 236 c 248 g 109 t
ORIGIN
Alignment Scores:
Pred. No.: 6.17e-32 Length: 705
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x HSU94508 (1-705)
QY 1 Metaspalavalproalargatrtprlysgluphevalargthrlengilyleuarglu 20
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Db 466 ATGACGCGGTCCAGCGCGGTGGAAGAGTTCGTGCGACGCTGGCGCTGGCGCAG 525
QY 21 Alaagullleaglualavalglualglutlleglargpheargaspglnglntyrqlumet 40
|||||
Db 526 GCAGGATCGAAGCGGTGAGGTGAGATCGGCCCTTCGAGACGACGACGACGAGATG 585
QY 41 Leuysaagrtparglinglncinproalagilyleugilyalavaltyralalaleu 60
|||||
Db 586 CTCAGCGCTGGCGCGACGACGCGCGCGCTCGAGACCGCTTTACGCGCGCTGGAG 645

QY 61 Argmetglyleuaspglycysvalgluaspleu 71
|||||
Db 646 CCATGGGCTGGACGCGCTCGTGGAGACTTG 678
RESULT 2
LOCUS HUS94507
DEFINITION HUS94507 838 bp mRNA linear PRI 15-MAY-1997
Human lymphocyte associated receptor of death 6 mRNA, alternatively
spliced, complete cds.
ACCESSION U94507
VERSION U94507.1 GI:2071960
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 838)
McMichael, A.J., Xu, X.N., Olsen, A.L., Cowper, A.E., Tan, R.,
Screation, G.R., and Bell, J.I.
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 838)
Screation, G.R.
Direct Submission
Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source Location/Qualifiers
1..838
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..831
/function="mediates apoptosis"
/note="similar to Fas and TNF-R1; truncated before the
transmembrane domain; possibly soluble; LARD-6"
/codon_start=1
/product="lymphocyte associated receptor of death 6"
/protein_id="AAC5131.1"
/db_xref="GI:2071961"
/translation="MEORPGCAVAAYAAALVILGARAQGRSPRCDCADPFHKKIG
LFCGRGCPAQAVALENCSAYADTRCGCKPQWVECOVSCVSSSPFYCPCPLCGAL
HKHRLDHPSTVTLGQRHPSTGS"
160..161
/note="deletion compared to LARD 1a, deposited in Genbank
Accession Number U94501, probably due to skipping of
putative exons 5, 6 and 7, leading to premature
transcriptional termination"
misc_feature
BASE COUNT 134 a 281 c 285 g 138 t
ORIGIN
Alignment Scores:
Pred. No.: 7.38e-32 Length: 838
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x HUS94507 (1-838)
QY 1 Metaspalavalproalargatrtprlysgluphevalargthrlengilyleuarglu 20
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Db 599 ATGACGCGGTCCAGCGCGGTGGAAGAGTTCGTGCGACGCTGGCGCTGGAG 658

QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlyTyrGluMet 40
DB 659 GCACAGATCGAAGCCGCGAGGTGGAGATCGCGCTTCCAGACACAGACTAGCATG 718
QY 41 LeuGlyArgTyrPArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
DB 719 CTCAGAGCGGTGGCCGACGACAGCCCGCGGCTTCGAGCGCTTTACGCGCCCTGGAG 778
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 779 CGCATGGGCTGAGCGCTGCTGGAGACTTG 811
RESULT 3
HSU94506 952 bp mRNA linear PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 5 mRNA, alternatively
DEFINITION spliced, complete cds.
ACCESSION U94506.1 GI:2071958
VERSION 094506.1
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 952)
Screaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL 97272273
MEDLINE 9114039
PUBMED 2 (bases 1 to 952)
Screaton,G.R.
AUTHORS Direct Submission
TITLE Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
JOURNAL Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source Location/Qualifiers
1.952
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1.411
/function="mediates apoptosis"
/note="LARD-5: similar to Fas and TNF-R1; possibly
soluble; truncated before the transmembrane domain"
/codon_start=1
/product="lymphocyte associated receptor of death 5"
/protein_id="AAC51311.1"
/db_xref="GI:2071959"
/translation="MEORPRGCAVAANAALLVLGARAAGGTRSPRCDAGDFHKRTG
LFCRCRPAASQVAALECNADVADTRCGCKRGMFVEQVSCVSSSFFTCPCIDCGAL
HNHRLGSRNDRDCTGLPGFEHGDGVCSTP"
160.161
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exon 3"
misc_feature
407..408
/note="deletion compared to LARD-1a, deposited in GenBank
Accession Number U94501, probably due to skipping of
putative exons 6 and 7, leading to premature
transcriptional termination"
BASE COUNT 154 a 317 c 319 g 162 t
ORIGIN
Alignment Scores:
Pred. No.: 8.42e-32 Length: 952
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x HSU94506 (1-952)
QY 1 MetSphAlaValProAlaArgTyrGlyGluPheValArgThrLeuGlyLeuArgGlu 20
DB 713 ATGACGGGGTCCAGCCGCGGCTGGAGAGTTCGCGCCACGCTGGCTGGCGAG 772
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlyTyrGluMet 40
DB 773 GCACAGATCGAAGCCGCGAGGTGGAGATCGCGCTTCCAGACACAGACTAGCATG 832
QY 41 LeuGlyArgTyrPArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
DB 833 CTCAGAGCGGTGGCCGACGACAGCCCGCGGCTTCGAGCGCTTTACGCGCCCTGGAG 892
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 893 CGCATGGGCTGAGCGCTGCTGGAGACTTG 925
RESULT 4
HSU94505 1087 bp mRNA linear PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 4 mRNA, alternatively
DEFINITION spliced, complete cds.
ACCESSION U94505
VERSION 094505.1 GI:2071956
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1087)
Screaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL 97272273
MEDLINE 9114039
PUBMED 2 (bases 1 to 1087)
Screaton,G.R.
AUTHORS Direct Submission
TITLE Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
JOURNAL Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source Location/Qualifiers
1.1087
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1.346
/function="mediates apoptosis"
/note="LARD-4: similar to Fas and TNF-R1; possibly
soluble; truncated before the transmembrane domain"
/codon_start=1
/product="lymphocyte associated receptor of death 4"
/protein_id="AAC51310.1"
/db_xref="GI:2071957"
/translation="MEORPRGCAVAANAALLVLGARAAGGTRSPRCDAGDFHKRTG
LFCRCRPAHYLKAPCTEPCGCTCIVCPDFFLAENHNHNSCARCAGCDQASQV
ALFNGSAVADTRCGCKRGMFVEQVSCVSSSFFTCPCIDCGALHNHRLGSRNDRD
DCTGCLPGFEHGDGVCSTP"
542..543
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exons 6 and 7 leading to premature transcriptional
termination"
BASE COUNT 180 a 363 c 355 g 189 t
ORIGIN

Alignment Scores:

Pred. No.: 9,65e-32 Length: 1087
 Score: 368.00 Matches: 71
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x HS094505 (1-1087)

QY 1 MetaspAlaValProAlaArgArGTpLySGluPheValArgThrLeuGlyLeuArgGlu 20
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 DB 848 ATGAGAGCGGCTCCACGCGCGCCCTGGAAGAGATTCTGCGCACGCTGGGGCTGGCGAG 907
 QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlyGluMet 40
 |||||
 DB 908 GCAGAGATCGAAGCCGTGGAGTGGAGATCGCGCTTCGAGACACAGAGTACGAGATG 967
 QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
 |||||
 DB 968 CTCACACGCTGGCGCGCAGCAGCAGCCGCGCGCTCGGAGCCGTTACGCGCCCTGGAG 1027
 QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
 |||||
 DB 1028 CGCATGGGCTGAGCGCGCTGCGTGGAGAACTTG 1060

RESULT 5 HS094509 1119 bp mRNA linear PRI 15-MAY-1997
 LOCUS HS094509 Human lymphocyte associated receptor of death 8 mRNA, alternatively
 DEFINITION spliced, complete cds.
 ACCESSION U94509
 VERSION U94509.1 GI:2071964

KEYWORDS

SOURCE

Organism Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 1119)
 Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
 McMichael,A.J. and Bell,J.I.
 LARD: a new lymphoid-specific death domain containing receptor
 regulated by alternative pre-mRNA splicing
 Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)

TITLE LARD: a new lymphoid-specific death domain containing receptor
 regulated by alternative pre-mRNA splicing
 Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)

JOURNAL 97272273
 MEDLINE 9114039
 PUBMED 2 (bases 1 to 1119)
 Screation,G.R.
 DIRECT SUBMISSION
 TITLE Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
 Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
 JOURNAL 9DU, UK

FEATURES
 source
 1..1119
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_line="Hela"
 /cell_type="lymphocyte"
 1..1119
 /function="mediates apoptosis"
 /note="LARD-8; NGFR family member; similar to Fas and
 TNF-R1"

CDS
 /codon_start=1
 /product="lymphocyte associated receptor of death 8"
 /protein_id="AAC51314.1"
 /db_xref="GI:2071965"
 /translation="MEORRGCAVVAALLVILGARGAGGSRPRCDADFHKKIG
 LFCRGCPAAQVALENCASAVADTRCGCKPGEFVECVQSYQCVSSPFYQPCQLDGLAL
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 LLAGLVPLILGATLTYYRRCWPKPKPLTADDEAGMEALTPPPATHLSPLDSAHHTLA
 PDSSEKICTVQVLGNSWTPGYPETQELACQVTVMSMDLPSRALGPAAAPTLSPESP
 AGSPAMMLOPQPOLYVDVDAVARMRKEFVRLIGIREAIEAIVEIEIGRFRDQYEMT
 KRMROQDPAGIGAVYALMERGLDGCVEDLSRLQKRP"

misc-feature

160..161
 /note="deletion compared to LARD 1a, deposited in GenBank
 Accession Number U94501, probable skipping of putative
 exon 3"
 BASE COUNT 175 a 374 c 371 g 199 t
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Alignment Scores:

Pred. No.: 9.94e-32 Length: 1119
 Score: 368.00 Matches: 71
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x HS094509 (1-1119)

QY 1 MetaspAlaValProAlaArgArGTpLySGluPheValArgThrLeuGlyLeuArgGlu 20
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 DB 880 ATGAGAGCGGCTCCACGCGCGCCCTGGAAGAGATTCTGCGCACGCTGGGGCTGGCGAG 939
 QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlyGluMet 40
 |||||
 DB 940 GCAGAGATCGAAGCCGTGGAGTGGAGATCGCGCTTCGAGACACAGAGTACGAGATG 999
 QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
 |||||
 DB 1000 CTCACACGCTGGCGCGCAGCAGCAGCCGCGCGCTCGGAGCCGTTACGCGCCCTGGAG 1059
 QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
 |||||
 DB 1060 CGCATGGGCTGAGCGCGCTGCGTGGAGAACTTG 1092

RESULT 6 HS094510 1143 bp mRNA linear PRI 15-MAY-1997
 LOCUS HS094510 Human lymphocyte associated receptor of death 9 mRNA, alternatively
 DEFINITION spliced, complete cds.
 ACCESSION U94510
 VERSION U94510.1 GI:2071966

KEYWORDS
 SOURCE

Organism Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 1143)
 Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
 McMichael,A.J. and Bell,J.I.
 LARD: a new lymphoid-specific death domain containing receptor
 regulated by alternative pre-mRNA splicing
 Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)

TITLE LARD: a new lymphoid-specific death domain containing receptor
 regulated by alternative pre-mRNA splicing
 Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)

JOURNAL 97272273
 MEDLINE 9114039
 PUBMED 2 (bases 1 to 1143)
 Screation,G.R.
 DIRECT SUBMISSION
 TITLE Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
 Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
 JOURNAL 9DU, UK

FEATURES
 source
 1..1143
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_line="Hela"
 /cell_type="lymphocyte"
 1..1143
 /function="mediates apoptosis"
 /note="LARD-9; NGFR family member; similar to Fas and
 TNF-R1"

CDS
 /codon_start=1
 /product="lymphocyte associated receptor of death 9"
 /protein_id="AAC51315.1"
 /db_xref="GI:2071967"

VERSION U78029.1 GI:1778763
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1254)
AUTHORS Degli-Esposti, M.A., Din, W.S., Cosman, D., Smith, C.A. and Goodwin, R.G.
TITLE A Novel Member of the TNF Receptor Family, Is a Strong Inducer of Apoptosis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1254)
AUTHORS Degli-Esposti, M.A. and Goodwin, R.G.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1996) Biochemistry, Immunex Corporation, 51 University St., Seattle, WA 98101, USA
FEATURES
source
1. 1254
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1pter"
/cell_type="peripheral blood T-cells"
1. 1254
/product="apoptosis inducing receptor AIR"
/protein_id="AAB40918.1"
/db_xref="GI:1778764"
/translation="MEGRPRGCAVAANAALLVLLGARAGCGTSPRDCACDDEPKKIG
LFRCRCRPAHGYLAKPCTEPCNGSTLCVCPDPTFLAENHNHNSCARCQACDEASOV
ALENCASAVADPTGRCGKPGWVEQVSCVSSPPYCPCLDCGALHRTLLSLRRT
DCGTCCLPGEYEHGDCVSCPTSLGSCPERCAAVCGRORHFWVOLLGAVPLLLGA
TLVYTYRHCWPHKPLVTADAGMEALPPPATLSPDASHLLAPDSSKICTVOL
VGNSTPGYETOEALCPQYTWMDQLPSRALGPAAPTLSPSPAGSPAMMIOPGPO
LYDMDAVPARARKERYRTIGLRAEIEAVEVEIGRRDQOTEMLKRRQDPAGLGA
VYALERMGLDGEVEDLSRLQRP"
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN
Alignment Scores:
Pred. No.: 1.12e-31 Length: 1254
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x HSU78029 (1-1254)
QY 1 Metaspalavalprolaaargatrgtrpysgluphevalargthrleuglyleuarglu 20
Db 1015 ATGAGCGCGGCTCCAGCGCGGCTGAGAGAGTTCGCGCCACGAGCTGGCGCGAG 1074
QY 21 Alaclullleglualavalglualgluileglyarpgheargaspnglntyrclumet 40
Db 1075 GCAGAGATCGAAGCGGTGAGGTGAGATCGCGCTCCAGACGACAGTACGAGATG 1134
QY 41 Leuysaragtrparagnglnglnprolaaglyleuglyalavaltyrralalaleuclu 60
Db 1135 CTCAAGCGCTGGCGCCAGCAGCGCCGCGGCTCGGAGCGCTTTCAGCGCGCTGGAG 1194
QY 61 Argmetcglyleuaspglycyvaigluaspleu 71
Db 1195 CGCATGGGCTGGAGCGCTGCTGGAGACTTG 1227
RESULT 12
LOCUS HSU94501 1254 bp mRNA linear PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 1a mRNA, complete cds.
ACCESSION U94501
VERSION U94501.1 GI:2071948

KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1254)
AUTHORS McMichael, A.J., Xu, X.N., Olsen, A.L., Cowper, A.E., Tan, R., LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL 9114039
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1254)
AUTHORS Sreteron, G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK
FEATURES
source
1. 1254
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1. 1254
/function="mediates apoptosis"
/note="LARD-1a; membrane protein; similar to Fas and TNF-RI, contains a death domain"
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/product="lymphocyte associated receptor of death 1a"
/protein_id="AAC51306.1"
/db_xref="GI:2071949"
/translation="MEGRPRGCAVAANAALLVLLGARAGCGTSPRDCACDDEPKKIG
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ALENCASAVADPTGRCGKPGWVEQVSCVSSPPYCPCLDCGALHRTLLSLRRT
DCGTCCLPGEYEHGDCVSCPTSLGSCPERCAAVCGRORHFWVOLLGAVPLLLGA
TLVYTYRHCWPHKPLVTADAGMEALPPPATLSPDASHLLAPDSSKICTVOL
VGNSTPGYETOEALCPQYTWMDQLPSRALGPAAPTLSPSPAGSPAMMIOPGPO
LYDMDAVPARARKERYRTIGLRAEIEAVEVEIGRRDQOTEMLKRRQDPAGLGA
VYALERMGLDGEVEDLSRLQRP"
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN
Alignment Scores:
Pred. No.: 1.12e-31 Length: 1254
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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Db 1015 ATGAGCGCGGCTCCAGCGCGGCTGAGAGAGTTCGCGCCACGAGCTGGCGCGAG 1074
QY 21 Alaclullleglualavalglualgluileglyarpgheargaspnglntyrclumet 40
Db 1075 GCAGAGATCGAAGCGGTGAGGTGAGATCGCGCTCCAGACGACAGTACGAGATG 1134
QY 41 Leuysaragtrparagnglnglnprolaaglyleuglyalavaltyrralalaleuclu 60
Db 1135 CTCAAGCGCTGGCGCCAGCAGCGCCGCGGCTCGGAGCGCTTTCAGCGCGCTGGAG 1194
QY 61 Argmetcglyleuaspglycyvaigluaspleu 71
Db 1195 CGCATGGGCTGGAGCGCTGCTGGAGACTTG 1227
RESULT 13
LOCUS HSU94502 1257 bp mRNA linear PRI 15-MAY-1997

DEFINITION Human lymphocyte associated receptor of death 1b mRNA,
alternatively spliced, complete cds.

ACCESSION U94502
VERSION U94502.1 GI:2071950

KEYWORDS

SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1257)

REFERENCE
AUTHORS Sreeton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
2 (bases 1 to 1257)

REFERENCE
AUTHORS Sreeton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="Lymphocyte"
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/function="mediates apoptosis"
/note="LARD-1b; membrane protein; similar to Fas and
TNF-R1; contains a death domain"
/codon_start=1
/product="Lymphocyte associated receptor of death 1b"
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/db_xref="GI:2071951"
/translation="MEORPRGCAAAVALLVLLGARAAGTRSPRCDCAGPFHKIG
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DCGTCLEPFEYHGDGCVSCPTSLGSCPERCAVCGMRQMFVQVLLAVPLILGA
TLTYTRHGMKPLVTADENAGMALPPTATHLSPIDSAHTLLAPDSSKICQV
LYGNSWTPGYPTFOALCPQVYMSDOLSRALGPAAPTLSPESPAGSPAMMLDGP
OLYVDADAVPARMKREYVETGLREAFETAVEIGRFRDQVEMLKRRQQDPAGLS
AYAALEHMGDLGCVEDLRSRGRGP"
708..711
/note="Insertion compared to LARD-1a, deposited in Genbank
Accession Number U94501, probably represents alternative
3' splice site"

BASE COUNT 202 a 421 c 408 g 226 t

ORIGIN

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/note="Insertion compared to LARD-1a, deposited in Genbank
Accession Number U94501, probably represents alternative
3' splice site"

Alignment Scores:
Pred. No.: 1,12e-31 Length: 1257
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x HSU94502 (1-1257)

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DB 1018 ATGGACGGCGCTCCACGGCGCGCTGGAAGAGTTCGTCGACGCTGGCGCTGCCGCGAG 1077
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OY 21 AlaGluIleGluAlaValGluIleGluArgPheArgAspGlnIntYrGluMet 40
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DB 1078 GCAGAGATCGAAGCCGTGGAGATGAGCCGCTTCCGACAGACAGATGAGATG 1137
|||||

OY 41 LeuArgArGTrpArgGlnGlnInProAlaGlyLeuGlyAlaValYrAlaAlaLeuGlu 60
|||||
DB 1138 CTCAGGCGCTGGCGCGACGACGCGCGGCGCTCGAGCGCTTACGCGCCCTGGAG 1197
|||||

OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
DB 1198 CGCATGGGCGCTCGACGCGCTGCTGGAAGACTTTC 1230
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RESULT 14
HSU94503
LOCUS 1355 bp mRNA linear PRI 15-MAY-1997

DEFINITION Human lymphocyte associated receptor of death 2 mRNA, alternatively
spliced, complete cds.

ACCESSION U94503
VERSION U94503.1 GI:2071952

KEYWORDS

SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1355)

REFERENCE
AUTHORS Sreeton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
2 (bases 1 to 1355)

REFERENCE
AUTHORS Sreeton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

FEATURES
source Location/Qualifiers
1..1355
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="Lymphocyte"
1..762
/function="mediates apoptosis"
/note="LARD-2; similar to Fas and TNF-R1; possibly
soluble; truncated before the transmembrane domain"
/codon_start=1
/product="Lymphocyte associated receptor of death 2"
/protein_id="AAC51308.1"
/db_xref="GI:2071953"
/translation="MEORPRGCAAAVALLVLLGARAAGTRSPRCDCAGPFHKIG
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ALENCSAVADTRCGCKPMFWPBCOVSSQVSSPFYQPCLDGALHRTLRILCSRDT
DCGTCLEPFEYHGDGCVSCPTSLGSCPERCAVCGMRQMFVQVLLAVPLILGA
GEEGNNHPTPTSCFCQSGSRSWALWSPSCIGPP"
599..700
/note="Insertion compared to LARD 1a, deposited in Genbank
Accession Number U94501, probable retained intron leading
to premature transcriptional termination"

BASE COUNT 223 a 441 c 451 g 240 t

ORIGIN

misc_feature
599..700
/note="Insertion compared to LARD 1a, deposited in Genbank
Accession Number U94501, probable retained intron leading
to premature transcriptional termination"

Alignment Scores:
Pred. No.: 1,21e-31 Length: 1355
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x HSU94503 (1-1355)

OY 1 MetaspAlaValProAlaArgArGTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
DB 1116 ATGGACGGCGCTCCACGGCGCGCTGGAAGAGTTCGTCGACGCTGGCGCTGCCGAG 1175
|||||

OY 21 AlaGluIleGluAlaValGluIleGluArgPheArgAspGlnIntYrGluMet 40
|||||

Db 1176 GCAGAGATCGAAGCCGTGAGATGCGCCCTCCAGACACAGTACGATG 1235

QY 41 LeuysArgTPArgGInGInProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
Db 1236 CTCAAGCCCTGGCGCGACAGACAGCCCGCGGCGCTCGAGCGCTTACGGCGCCTGGAG 1295

QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
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Db 1296 CGCATGGGCTGAGACGCTGCTGGAGAGACTTG 1328

RESULT 15
HSU83597 1528 bp mRNA linear PRI 27-JAN-1997
LOCUS Human death domain receptor 3 (DDR3) mRNA, partial cds.
DEFINITION U83597
ACCESSION U83597.1 GI:1800292
VERSION U83597.1
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1528)
AUTHORS Chaudhary, P.M. and Hood, L.E.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-1997) Molecular Biotechnology, University of
Washington, 1705 NE Pacific Street, HSB-K360, Seattle, WA 98195,
USA

FEATURES
source location/Qualifiers
1..1528
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/db_xref="taxon:9606"
/chromosome="1"
/map="1p36"
1..1528
/gene="DDR3"
<1..1238
/gene="DDR3"
/function="mediates apoptosis when cross-linked"
/note="A TNFR1-related death-domain containing receptor;
DR3, WSL-LR, Apo-3, TRAMP; transmembrane form; similar to
human EST clone 298913, GenBank accession Number N71143"
/codon_start=3
/product="death domain receptor 3"
/protein_id="AAB41432.1"
/db_xref="GI:1800293"
/translation="GCAAAVALILVLIGARAQGTSPRCDCAGDFPKKIGLFCRG
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AYADTRCGCKRPFVEECQVSCVSSSPFCPCIDCGALHNRHLCSKRDTCGTCI
LGFYEHGDCVSCPTSLGSCPERCAAVCGMFMWQVLLAGLVPLILGATLTYTY
RHCMPPKPLVTADAGMEALTPPATLSPIDSAHLLAPPDSEKICTVOLVNSWT
PGYETQDALCPQVTMSDQLPSRALGPAAAPLSPSPAGSPAMMLOPGPOLYDND
AVPARRKEFEVRTGLREAEIENAVEIEIGRRDQYEMLRKWRQDPAGAGVYAALE
RMGLDCVEELRSRLORCP"

BASE COUNT 280 a 496 c 470 g 282 t
ORIGIN

Alignment Scores:
Pred. No.: 1.37e-31 Length: 1528
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 9

US-09-993-234-6_COPY_339_409 (1-71) x HSU83597 (1-1528)

QY 1 MetAspAlaValProAlaArgArgTTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
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Db 999 ATGACGCGGCTCCAGCGCGCGGGAAGAGTCTGCGCACGCTGGGCTGGCGAG 1058,
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
Db 1059 GCAGATCGAAGCCGTGAGATGCGCCCTCCAGACACAGTACGAGATG 1118

QY 41 LeuysArgTPArgGInGInProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
Db 1119 CTCAAGCCCTGGCGCGACAGACAGCCCGCGGCGCTCGAGCGCTTACGGCGCCTGGAG 1178

QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
Db 1179 CGCATGGGCTGAGACGCTGCTGGAGAGACTTG 1211

Search completed: April 6, 2003, 21:08:13
Job time : 829.126 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Comphen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:33:09 ; Search time 66.109 Seconds

(without alignments)
2418.610 Million cell updates/sec

Title: US-09-993-234-6_COPY_339_409

Perfect score: 368
Sequence: 1 MDVAPRRKKEFVRLTGLRE.....LGAVYAAALERMGLDGCVEDL 71

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-DB=N.Geneseq.101002 -OPMT=fastap -SUFFIX=ing -MINMATCH=0.1 -LOOPECL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdl
-LIST=45 -DOCALLIGN=200 -THR_SCORE=ptc -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-NARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Database: N.Geneseq.101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	368	100.0	1250	22	AAE83770	Nucleotide sequence
2	368	100.0	1254	18	AAE89427	Death domain conta
3	368	100.0	1254	20	AAE89925	Death domain conta
4	368	100.0	1254	21	AAE68777	Human death domain
5	368	100.0	1634	18	AAE91180	Human apoptosis pr
6	368	100.0	1634	22	AAH27782	Human genomic DNA
7	368	100.0	1634	22	AAH47186	Human rheumatoid a
8	368	100.0	1662	22	AAE91477	Human PRO779 CDNA
9	368	100.0	1662	18	AAE89426	CDNA encoding huma
10	368	100.0	1783	20	AAE00924	Death domain conta
11	368	100.0	1783	21	AAE68776	Human death domain
12	368	100.0	1783	21	AAE68776	Human death domain
13	368	100.0	1847	19	AAV28700	Human apoptosis in
14	368	100.0	4825	24	AAH47185	Human DR3 gene ass
15	368	100.0	10797	23	ABK42690	Genomic sequence #
16	356	96.7	1743	24	ABH64119	Breast cancer rela
17	350	95.1	1251	19	AAE28701	Mouse apoptosis in
18	278	75.5	511	24	ABQ47530	Oligonucleotide to
19	278	75.5	511	24	ABQ47531	Oligonucleotide to
20	205	55.7	511	24	ABQ47532	Oligonucleotide to
21	205	55.7	511	24	ABQ47533	Oligonucleotide to
22	157	42.7	2130	24	ABK63694	Rat Tumour Necrosi
23	157	42.7	2173	11	AAO06284	Partial human TNFR
24	151	41.0	1368	14	AAO49932	Lambda-derived TNF
25	151	41.0	1368	21	AAE95105	Human TNFR1 coding
26	151	41.0	2062	13	AAO20973	TNF-alpha binding
27	151	41.0	2062	13	AAO24440	Encodes TNF-alpha
28	151	41.0	2088	12	AAO10883	30kD TNF inhibitor
29	151	41.0	2088	22	AAE83946	Human 30 kDa TNF-1
30	151	41.0	2111	12	AAO10955	Encodes human 55kD
31	151	41.0	2111	20	AAO209170	Human tumour necro
32	151	41.0	2111	22	AAH48859	Human TNF-beta associ
33	151	41.0	2111	24	AAH84039	Human CDNA differe
34	151	41.0	2111	24	ABN95862	Gene #2360 used to
35	151	41.0	2141	11	AAO06285	Human Tumour Necro
36	151	41.0	2161	21	AAE48475	Human Tumour necro
37	151	41.0	2161	21	ABK13194	Human tumour necro
38	151	41.0	2170	14	AAO50870	p55 Tumour necrosi
39	151	41.0	2175	16	AAO90513	Human TNF-R gene. H
40	151	41.0	2176	12	AAO12215	Type I TNF recepto
41	151	41.0	2254	21	AAE95104	Partial human TNFR
42	98	26.6	441	22	AAH86826	Human polynucleoti
43	94	25.5	1062	22	AAE63095	Human TR6 partial
44	94	25.5	1062	22	AAE84744	Partial nucleotide
45	94	25.5	1236	20	AAE23721	Human killer adria

ALIGNMENTS

RESULT 1
AAE83770
ID AAE83770 standard; DNA: 1250 BP.

AC AAE83770;

DT 06-AUG-2001 (first entry)

DE Nucleotide sequence of human TR3 gene.

XX TR3; cell proliferation; leukemia; immunosuppressive; cytostatic;

XX dermatological; antidiabetic; neuroprotective; cardiant;

XX antithyroid; antiinflammatory; antiatherogenic; T-cell-inhibitor; ds.

Key CDS Location/Qualifiers
I..1250

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FT      /note= "this codon has an apparent 1 nucleotide
FT      deletion which alters the reading frame"
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FT      deletion which alters the reading frame"
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FT      deletion which alters the reading frame"
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FT      /note= "this codon has an apparent 1 nucleotide
FT      deletion which alters the reading frame"
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FT      1..72
FT      /tag= b
FT      mat_peptide
FT      73..1247
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FT      PD
FT      25-MAY-2001.
FT      XX
FT      17-NOV-2000; 2000MO-US31692.
FT      PF
FT      19-NOV-1999; 990US-0166583.
FT      PR
FT      (TITL/) TITTLE T V.
FT      PA (WEGM/) WEGMANN K W.
FT      XX
FT      PI Tittle TV, Wegmann KW;
FT      XX
FT      DR WPI: 2001-343711/36.
FT      DR P-PSDB: AAB84941.
FT      PT Composition for treatment of T-cell mediated disease e.g. arthritis,
FT      cancer comprises a biologically active TR3-specific binding agent
FT      especially a monoclonal antibody -
FT      PT
FT      PS Disclosure: Page 72; 77pp; English.
FT      XX
FT      CC The invention relates to a composition comprising a biologically active
FT      TR3-specific binding agent (I) that binds to TR3 and inhibits the
FT      CC proliferation of cells expressing TR3. (I) identified by the methods are
FT      CC useful for treating a subject suspected of having a disease associated
FT      CC with a proliferation of cells expressing TR3 especially leukemias or
FT      CC lymphomas or a T-cell mediated disease especially autoimmune diseases
FT      CC such as myasthenia gravis, systemic lupus erythematosus, rheumatoid
FT      CC arthritis, diabetes, multiple sclerosis, sarcoidosis, myocarditis,
FT      CC thyroiditis and tumours. (I) is also useful for treating a subject
FT      CC suspected of having graft-versus-host disease, rejection of a
FT      CC transplanted organ such as heart, liver, lung, kidney, pancreas, bowel,
FT      CC skin or an appendage, or inflammatory diseases, allergies and contact
FT      CC dermatitis. The present sequence represents the nucleotide sequence of
FT      CC human TR3 gene.
FT      XX
FT      SQ Sequence 1250 BP; 201 A; 419 C; 406 G; 224 T; 0 other;

Alignment Scores:
Pred. No.: 2.23e-40 Length: 1250
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x AAF83770 (1-1250)
OY 1 MetaspalavalProalargArgtrpLysgluPhevalArgthLeuclyleuArgglu 20
DB 1011 ATGGACGGCGTCCAGCGCGGTGGAAGAGTTCGTGCGACGCTGGGCGCGGAG 1070
OY 21 AlagullleGluAlaValGluValGluLeuGluArgpHeaArgAspGlnInTyrtGluwet 40

```

```

DB 1071 GCAGATCGAAGCCGTGGAGTGTGAGATCGCCGCTTCGAGACCAGAGTACGAGATG 1130
OY 41 leuLysArgTrpArgGlnGlnInProAlaGlyLeuGlyAlaValtyrMAaAlaLeuGlu 60
DB 1131 CTCAGCGCTGGGCGCCAGACAGCCCGGGCTCGGAGCGCTTTACCGGCCCTGGAG 1190
OY 61 ArgmetGlyLeuAspGlyCysValGluAspLeu 71
DB 1191 CGCATGGGCGTGGAGCGCTGCGTGGAAAGACTTG 1223

RESULT 2
AAT89427
ID AAT89427 standard; cDNA; 1254 BP.
AC
AC AAT89427;
XX
DT 02-MAR-1998 (first entry)
XX
DE Death domain containing receptor DR3 cDNA.
XX
KW Death domain containing receptor; DR3; human; apoptosis;
XX inflammation; NF-kappaB; ds.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FH 1..72
XX FT sig_peptide /tag= a
XX FT 73..1251
XX FT mat_peptide /tag= b
XX FT
XX WO9733904-A1.
XX PD
XX 18-SEP-1997.
XX
XX 17-OCT-1996; 96WO-US16849.
XX PF
XX 12-MAR-1996; 96US-0013285.
XX PR
XX (HUMA-) HUMAN GENOME SCI INC.
XX PA (UNMI) UNIV MICHIGAN.
XX PA
XX Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
XX PI
XX WPI: 1997-470812/43.
XX DR P-PSDB: AAW31517.
XX
XX Death domain containing receptor polypeptide(s) DR3 and DR3-V1
XX for activation of apoptosis and NF-kappaB, antagonists can be used
XX to treat inflammatory diseases
XX
XX Claim 6; Page 75-77; 108pp; English.
XX
XX This cDNA clone codes for human death domain containing receptor
XX DR3 (see AAW31517), a novel member of the tumour necrosis factor
XX receptor family. It was isolated from a HUVEC cDNA library.
XX CC Related death domain containing receptor DR3-V1 cDNA (see AAT89426)
XX have also been identified in cDNA libraries of foetal liver,
XX foetal brain, tonsil and leukocyte. Nucleic acids encoding full-
XX length or mature DR3, or the extracellular, transmembrane,
XX intracellular or especially the death domain of DR3, can be used to
XX CC produce recombinant polypeptides in transformed host cells. These
XX polypeptides can be used to treat diseases and disorders associated
XX with the inhibition of apoptosis. Antagonists can be used to treat
XX diseases and disorders associated with increased apoptosis and for
XX treating inflammatory diseases and disorders.
XX
XX SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:
Pred. No.: 2.24e-40 Length: 1254
Score: 368.00 Matches: 71

```

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 18 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x AAT89427 (1-1254)

QY 1 MetaspalavalProalaArgarTrrpLysGluPheValArgThrLeuArgGlu 20
 |||||
 DB 1015 ATGAGCCGGTCCAGCCGGCGCTGGAGAGATTCTGCGCACGCTGGGCTGGCGAG 1074
 QY 21 AlaGluIleGluAlaValaGluValaGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
 |||||
 DB 1075 GCAGAGATCGAAGCCGTGGAGGTGGAGATCGCCGCTTCCAGACACAGACTACAGATG 1134
 QY 41 LeuysArgrTPArGInGInGInProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
 |||||
 DB 1135 CTCAAGCGCTGGCGCCAGCACAGCCCGCGGCTCGAGACCGCTTACGCGCCCTGGAG 1194
 QY 61 ArgMetGlyLeuAspGlyCysValaGluAspLeu 71
 |||||
 DB 1195 CGCATGGGCGCTGGAGCGCTGGAGACTTG 1227

RESULT 3
 AAX00925 standard; cDNA; 1254 BP.

AC AAX00925;

DT 25-MAR-1999 (first entry)

DE Death domain containing receptor polypeptide (DR3) encoding cDNA.

KM Death domain; receptor; DR3-V1; DR3; recombinant; ds.

XX Homo sapiens.

OS Homo sapiens.

FN Key Location/Qualifiers

FT CDS 1..1254

FT sig_peptide 1..72

FT mat_peptide 73..1251

FT /*tag- a

FT /*tag- b

FT /*tag- c

PN JF11000170-A.

XX 06-JAN-1999.

XX 12-MAR-1997; 97JP-0057503.

XX 06-FEB-1997; 97US-0037341.

XX 12-MAR-1996; 96US-0013285.

XX 17-OCT-1996; 96US-0028711.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (UNMI) UNIV MICHIGAN.

XX WPI: 1999-124390/11.

XX P-PSDB: AAW95538.

XX New death domain containing receptor and recombinant vector -

XX optionally comprising leader sequence

XX Claim 6; Fig 3; 50pp; Japanese.

XX The invention provides nucleotide sequences encoding death domain

XX containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone

XX is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is

XX contained in ATCC deposition No. 97577. Recombinant vectors comprising

XX the nucleic acid sequences and optionally the leader sequences are

XX used for the recombinant production of the proteins. The present

CC sequence represents a cDNA encoding the death domain containing
 CC receptor polypeptide (DR3).
 XX
 SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:

Pred. No.: 2,24e-40 Length: 1254
 Score: 368.00 Matches: 71
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x AAX00925 (1-1254)

QY 1 MetaspalavalProalaArgarTrrpLysGluPheValArgThrLeuArgGlu 20
 |||||
 DB 1015 ATGAGCCGGTCCAGCCGGCGCTGGAGAGATTCTGCGCACGCTGGGCTGGCGAG 1074
 QY 21 AlaGluIleGluAlaValaGluValaGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
 |||||
 DB 1075 GCAGAGATCGAAGCCGTGGAGGTGGAGATCGCCGCTTCCAGACACAGACTACAGATG 1134
 QY 41 LeuysArgrTPArGInGInGInProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
 |||||
 DB 1135 CTCAAGCGCTGGCGCCAGCACAGCCCGCGGCTCGAGACCGCTTACGCGCCCTGGAG 1194
 QY 61 ArgMetGlyLeuAspGlyCysValaGluAspLeu 71
 |||||
 DB 1195 CGCATGGGCGCTGGAGCGCTGGAGACTTG 1227

RESULT 4
 AAC68777 standard; cDNA; 1254 BP.

AC AAC68777;

DT 20-FEB-2001 (first entry)

DE Human death domain containing receptor DR3 coding sequence.

KM Human; death domain containing receptor; DR3; cancer;

KW autoimmune disorder; inflammation; cardiovascular disorder; infection;

KW neurodegenerative disease; angiogenesis; ss.

XX Homo sapiens.

XX WO200064465-A1.

XX 02-NOV-2000.

XX 21-APR-2000; 2000WO-US10741.

XX 22-APR-1999; 99US-0130488.

XX 28-MAY-1999; 99US-0136741.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (UNMI) UNIV MICHIGAN.

XX (YUGG/) YU G.

XX (NIJ/) NI J.

XX (GENTZ/) GENTZ R L.

XX (DILLON/) DILLON P J.

XX (DIXIT/) DIXIT V M.

XX YU G, NI J, Gentz RL, Dillon PJ, Dixit VM;

XX WPI: 2000-687263/67.

XX P-PSDB: AAB36265.

XX Treating graft-versus-host disease, cancer, immunodeficiency or an

XX autoimmune disease comprising administering an antibody to Death Domain

XX Containing Receptor proteins and a second therapeutic agent -

FT	XX	/product= "Rheumatoid arthritis associated protein"
FN	XX	
PD	XX	W0200132921-A2.
PD	XX	10-MAY-2001.
PF	XX	01-NOV-2000; 2000WO-JP07690.
PR	XX	01-NOV-1999; 99JP-0310805.
PA	XX	(SHIO/) SHIOZAWA S.
PI	XX	Shiozawa S, Konishi Y;
DR	XX	WPI; 2001-308750/32.
DR	XX	P-PSDB; AAB97370.
PT	XX	Diagnosing rheumatoid arthritis by probing digested human genomic DNA
PT	XX	or comparing expression of mRNA or polypeptide of a region of
PT	XX	transmembrane protein
PS	XX	Claim 1; Page 14-18; 21pp; Japanese.
CC	XX	This invention relates to a method of diagnosing chronic rheumatoid
CC	XX	arthritis by digesting human genomic DNA with EcoRI and hybridising it
CC	XX	with a probe containing a fragment of the present sequence which
CC	XX	represents DNA encoding a transmembrane protein. The method is used for
CC	XX	the diagnosis of chronic rheumatoid arthritis, and for developing new
CC	XX	treatments.
SO	XX	Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;
Alignment Scores:		
Pred. NO.:	3,11e-40	Length: 1634
Score:	368.00	Matches: 71
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	22	Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x AAN27782 (1-1634)		
OY	1	MethsapaIaValProAlaArgArGTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
Db	1103	ATGCACGCGGTCCACGCCGCGCTGGAAGAGTTCTGTGCGCAGCTGGCGCTGGCGGAG 1162
OY	21	AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIleTyrluMet 40
Db	1163	GCAGGATCCGAAGCCGTGTGAGGTGGAAGATCGGCCCTTCCGAGACAGCAGTACGAGATG 1222
OY	41	LeuLysATGTTPARGlInGlnIleProAlaGlyLeuGlyAlaValTyrAlaIleLeuGlu 60
Db	1223	CTCAAGCGCTGTGGCCGACAGCAGCAGCCCGCGGCTTCGAGGCCGTTTACCGGCGCTGGAG 1282
OY	61	ArgMetGlyLeuAspGlyCysValGluAspLeu 71
Db	1283	CGCATGGGGCTGGACGCGCTGCGTGAAGACTTG 1315
RESULT 7		
AA147186		
ID	AA147186	standard; cDNA; 1634 BP.
XX	AA147186;	
XX	22-AUG-2002	(first entry)
XX	Human	rheumatoid arthritis associated DR3 gene related cDNA #1.
XX	Human: DR3;	rheumatoid arthritis; antirheumatic; antiarthritic;
XX	gene therapy;	gene; ss.
XX	Homo sapiens.	
XX		

FH	Key	Location/Qualifiers
FT	CDS	89..1342 /*tag= a /product= "AA017879"
XX		
PN	WO200234912-A1.	
XX		
PD	02-MAY-2002.	
XX		
PF	24-OCT-2001; 2001WO-JP09313.	
XX		
PR	24-OCT-2000; 2000JP-0324286. 27-MAR-2001; 2001JP-0090346. 30-MAR-2001; 2001JP-0099990.	
XX		
PPA	(NEWI-) NEW IND RES ORG.	
XX	(SHIO/) SHIOZAWA S.	
PI	Shiozawa S, Konishi Y;	
XX		
DR	WPI; 2002-417133/44.	
XX	P-PSDB; AA017879.	
PT	Genomes, particularly DR3 genomic DNA, participating in rheumatoid arthritis via mutation, useful in evaluating disease onset and its possibility and providing therapy and remedies -	
XX		
PS	Example 1; Page 66-69; 84pp; Japanese.	
CC	The present invention relates to the human DR3 gene, which is associated with rheumatoid arthritis. Certain mutations in the gene can be linked to the disease. The sequences can be used to evaluate disease onset and its possibility and to provide therapy and remedies. The present sequence is a coding sequence described in the exemplification of the invention.	
XX		
SQ	Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;	
	Alignment Scores:	
	Pred. No.: 3,11e-40 Length: 1634	
	Score: 368.00 Matches: 71	
	Percent Similarity: 100.00% Conservative: 0	
	Best Local Similarity: 100.00% Mismatches: 0	
	Query Match: 100.00% Indels: 0	
	DB: 24 Gaps: 0	
US-09-993-234-6_COPY_339_409 (1-71) x AAL47186 (1-1634)		
OY	1 MetAspAlaValProAlaArgArgTrpLysGluPhenValArqThrLeuGlyLeuArgGlu 20	
Db	1103 ATGGAGCGGGGTGCCAGCGCGCGTGTGAAGAAGATGTGTGGCAGACGCTGGCGCTGCAGAG 1162	
OY	21 AlaGluIleGluAlaValGluValIleGlyArqPheArqAspGlnIntyrGluMet 40	
Db	1163 GCAGGATCGAAGCCGTGGAGGTGTGAATGAGCGCTTCGGAACACAGCAGTACGAGATG 1222	
OY	41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValArqAlaLeuGlu 60	
Db	1223 CTCAGGCGCTGGCCCCAGCACACCACCCGCGGCGCTCGAACCTTTACGGCGCGCTGGAG 1282	
OY	61 ArgMetGlyLeuAspGlyLysValGluAspLeu 71	
Db	1283 CGCATGGGCGCTGGAGCGGCTGTGTGAAGACTTG 1315	
RESULT 8		
XX	AAC91477	
XX	ID AAC91477 standard; cDNA; 1662 bp.	
XX	AC AAC91477;	
XX	DT 21-MAR-2001 (first entry)	
XX	DE Human PRO779 cDNA.	
XX		

Human; PRO: antiinflammatory; dermatological; antiarthritic;
antirheumatic; cardiac; antianaemic; immunosuppressive; antithyroid;
antidiabetic; nocitropic; neuroprotective; hepatotropic; virucide;
antiallergic; antiasthmatic; immune related disorder;
hepatobiliary disease; autoimmune disease; allergy; ss.
XX
OS Homo sapiens.
XX
PN WO200073452-A2.
XX
PD 07-DEC-2000.
XX
XX 02-JUN-2000; 2000WO-US15264.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 20-JUL-1999; 99US-0144732.
PR 20-JUL-1999; 99US-0144758.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28634.
PR 09-DEC-1999; 99US-0170262.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
XX
PA (GENTH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;
PI Wood WT;
PI WPI: 2001-025253/03.
DR P-PSDB: AAB50918.
XX
XX Thirty three nucleic acids encoding PRO polypeptides which are useful
PT in the diagnosis and treatment of immune related disorders, e.g.
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
PT thyroiditis and diabetes mellitus -
XX
PS Claim 48; Fig 33; 218pp; English.
XX
XX The present sequence is one of thirty three nucleic acids encoding PRO
CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
CC antagonists are useful for treating and diagnosing immune related
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases
CC (such as infectious, autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC disease, autoimmune or immune-mediated skin diseases (such as bullous
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),

CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC food hypersensitivity and urticaria), immunological diseases of the
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
CC and hypersensitivity pneumonitis), transplantation associated diseases
CC including graft rejection and graft-versus-host diseases.
XX
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;
XX
Alignment Scores:
Pred. No.: 3,18e-40 Length: 1662
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x AAC91477 (1-1662)
QY 1 MetAspAlaValProAlaArgArGTrPlysGluPheValArgThrLeuGlyLeuArgGlu 20
DB 1117 ATGAGCGCGGTCCACGCGCGCGCTGGAAGAGACTTGTGGCGACGGTGGCGCGAG 1176
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
DB 1177 GCAGAGATCGAAGCGGTGGAGGTGGAGATCGCGCTTCGAGACGACGATCGAGATG 1236
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyValAlaValTyrAlaIleArgGlu 60
DB 1237 CTCAGCGCTGGCGCGCGACGACGCGCGCGCTGGAGACCTTTACCGCGCGCTGGAG 1296
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1297 CGCATGGGCTGGAGCGCGCTGGAGAACTTG 1329
RESULT 9
ID ABRK40265 standard; cDNA: 1662 BP.
XX
AC ABRK40265;
XX
DT 15-JUL-2002 (first entry)
XX
XX cDNA encoding human PRO779 polypeptide.
DE
XX Human; PRO: benign tumour; malignant tumour; lymphoid malignancy;
KW Leukemia; neuronal disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder;
KW gene therapy; cytostatic; neuroprotective; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200153486-A1.
PN 26-JUL-2001.
XX
XX 11-FEB-2000; 2000WO-US03565.
PF
XX
XX 08-MAR-1999; 99WO-US05028.
PR 11-MAR-1999; 99US-123972P.
PR 11-MAY-1999; 99US-133459P.
PR 02-JUN-1999; 99WO-US12252.
PR 22-JUN-1999; 99US-140650P.
PR 22-JUN-1999; 99US-140653P.
PR 20-JUL-1999; 99US-144758P.
PR 26-JUL-1999; 99US-145698P.
PR 28-JUL-1999; 99US-146222P.
PR 17-AUG-1999; 99US-149395P.
PR 31-AUG-1999; 99US-151689P.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.


```
PR 05-JAN-2000; 2000MO-US00219.
XX
XX (GETH ) GENENTECH INC.
PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX
XX WPI; 2002-205567/26.
DR P-PSDB: AAB86139.
XX
XX Thirty five nucleic acids encoding PRO polypeptides, useful for
PT treating benign or malignant tumours, leukaemias and lymphoid
PT malignancies, inflammatory, angiogenic and immunologic disorders -
XX
PS Claim 50; Fig 23; 302pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The
CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
CC useful for treating benign or malignant tumours (e.g. renal, kidney,
CC bladder, breast, etc), leukaemias and lymphoid malignancies, other
CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
CC macrophagal, stromal and blastocellic disorders, inflammatory, immune
CC and angiogenic disorders. The polynucleotide sequences are also
CC useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
CC polypeptides of the invention.
XX
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;

Alignment Scores:
Pred. No: 3.18e-40 Length: 1662
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 24

US-09-993-234-6_COPY_339_409 (1-71) x ABK40265 (1-1662)
OY 1 Metasp1aValProAlaArgArGTrrpysglupheValArgThrLeuGlyLeuAArglu 20
DB 1117 ATGGACGGGGTCCAGCCGGCGCTGGGAAGAGTTCTGCGCCAGCTGGGCTGGCGGAG 1176
OY 21 AlaGlulIleGluAlaValAlGluValIleGlyArGpheaArAspGlnGlnTyrGluMet 40
DB 1177 GCAAGATCGAAGCCGTGGAGGTGAGATCGCCGCTTCCAGACACAGATACGAGATG 1236
OY 41 LeuysArGTrrpArGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
DB 1237 CTCAGGCGCTGGCGCCAGACAGCCCGGGGCTCGGAGCGCTTACGGCGCCTGGAG 1296
OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1297 CGCATGGGGCTGAGCGCTCGCTCGTGAAGACTTG 1329

RESULT 10
AAT89426
ID AAT89426 standard; cDNA; 1783 BP.
XX
XX AAT89426;
AC
XX
XX 02-MAR-1998 (first entry)
DT
XX
XX Death domain containing receptor DR3-VI cDNA.
DE
XX
XX Death domain containing receptor; DR3-VI; human; apoptosis;
KW
XX
XX Inflammation; NF-kappaB; ds.
OS
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH CDS 198..1484
```

```
FT FT sig_peptide /*tag= a
FT 198..302
FT mat_peptide /*tag= b
FT 304..1481
FT c /*tag= c
XX
XX W09733904-A1.
XX
XX 18-SEP-1997.
XX
XX 17-OCT-1996; 96WO-US16849.
XX
XX 12-MAR-1996; 96US-0013285.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI ) UNIV MICHIGAN.
XX
XX Dillon PJ, Dixit VM, Gentz RL, M1 J, Yu G;
XX
XX WPI; 1997-470812/43.
XX P-PSDB; AAW31516.
XX
XX Death domain containing receptor polypeptide(s) DR3 and DR3-VI -
PT for activation of apoptosis and NF-kappaB, antagonists can be used
PT to treat inflammatory diseases
XX
PS Claim 2; Page 71-73; 108pp; English.
XX
CC This cDNA clone, deposited as ATCC 97456, codes for human death
CC domain containing receptor DR3-VI (see AAW31516), a novel member of
CC the tumour necrosis factor receptor family. It was isolated from a
CC cDNA library derived from cells of a human testis tumour. Related
CC death domain containing receptor DR3 cDNA (see AAT89427) was isolated
CC from a HUVEC cDNA library. The genes have also been identified in
CC cDNA libraries of foetal liver, foetal brain, tonsil and leukocyte.
CC Nucleic acids encoding full-length or mature DR3-VI can be used to
CC produce recombinant polypeptides in transformed host cells. These
CC polypeptides can be used to treat diseases and disorders associated
CC with the inhibition of apoptosis. Antagonists, such as antibodies
CC raised against DR3-VI, can be used to treat diseases and disorders
CC associated with increased apoptosis and for treating inflammatory
CC diseases and disorders.
XX
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Alignment Scores:
Pred. No: 3.47e-40 Length: 1783
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 18

US-09-993-234-6_COPY_339_409 (1-71) x AAT89426 (1-1783)
OY 1 Metasp1aValProAlaArgArGTrrpysglupheValArgThrLeuGlyLeuAArglu 20
DB 1245 ATGGACGGGGTCCAGCCGGCGCTGGGAAGAGTTCTGCGCCAGCTGGGCTGGCGGAG 1304
OY 21 AlaGlulIleGluAlaValAlGluValIleGlyArGpheaArAspGlnGlnTyrGluMet 40
DB 1305 GCAGAGATCGAAGCCGTGGAGGTGAGATCGCCGCTTCCAGACACAGATACGAGATG 1364
OY 41 LeuysArGTrrpArGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
DB 1365 CTCAGGCGCTGGCGCCAGACAGCCCGGGGCTCGGAGCGCTTACGGCGCCTGGAG 1424
OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1425 CGCATGGGGCTGAGCGCTCGCTCGTGAAGACTTG 1457

RESULT 11
AAK00924
```

ID AAX00924 standard; cDNA; 1783 BP.
AC AAX00924;
XX
XX
DT 25-MAR-1999 (first entry)
XX
DE Death domain containing receptor polypeptide (DR3-V1) encoding cDNA.
XX
KM Death domain; receptor; DR3-V1; DR3; recombinant; ds.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS /tag= a
FT /product= "Death domain containing receptor DR3-V1"
FT sig_peptide /tag= b
FT mat_peptide /tag= c
FT /tag= c
XX
XX JP11000170-A.
XX
XX PD 06-JAN-1999.
XX
XX PF 12-MAR-1997; 97JP-0057503.
XX
XX PR 06-FEB-1997; 97US-0037341.
XX PR 12-MAR-1996; 96US-0013285.
XX PR 17-OCT-1996; 96US-0028711.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI) UNIV MICHIGAN.
XX
XX DR WPI: 1999-124390/11.
XX P-PSDB; AAM95537.
XX
XX PT New death domain containing receptor and recombinant vector -
XX optionally comprising leader sequence
XX
XX PS Claim 2; Fig 1, 2; 50pp; Japanese.
XX
XX CC The invention provides nucleotide sequences encoding death domain
XX containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
XX is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
XX contained in ATCC deposition No. 97757. Recombinant vectors comprising
XX the nucleic acid sequences and optionally the leader sequences are
XX used for the recombinant production of the proteins. The present
XX sequence represents a cDNA encoding the death domain containing
XX receptor polypeptide (DR3-V1).
XX
SQ Sequence 1783 BP; 330 A; 562 C; 327 T; 0 other;
XX
Alignment Scores:
Pred. No.: 3 47e-40 Length: 1783
Score: 368.00 Matches: 71
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OY 1 MetaspalaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
DB 1245 ATGAGCGCGGTCCACGCGCGCTGGAGAGATTGTCGACGCTGGGCTGCGCGAG 1304
OY 21 AlagluilegluAlaValGluValGluilegluArgPheArgAspGlnIntyrGluMet 40
DB 1305 GCAGAGATCGAAGCGGTGGAGTGGAGTCCGCTCCGAGACGACGATACGAGATG 1364
OY 41 LeuysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaLeuGlu 60
|||||

DB 1365 CTCAGCGCTGGCGCAGCAGACCCGCGCTGGAGCGCTTTACGCGCCCTGGAG 1424
OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1425 CGCATGGGCTGGACGCGCTGGAGACTTG 1457
RESULT 12
AAC68776
ID AAC68776 standard; cDNA; 1783 BP.
XX
AC AAC68776;
XX
XX DT 20-FEB-2001 (first entry)
XX
DE Human death domain containing receptor DR3-V1 coding sequence.
XX
XX KM Human; death domain containing receptor; DR3-V1; cancer;
XX autoimmune disorder; inflammation; cardiovascular disorder; infection;
XX neurodegenerative disease; angiogenesis; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200064465-A1.
XX
XX PD 02-NOV-2000.
XX
XX PF 21-APR-2000; 2000MO-US10741.
XX
XX PR 22-APR-1999; 99US-0130488.
XX PR 28-MAY-1999; 99US-0136741.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI) UNIV MICHIGAN.
XX (YUGG/) YU G.
XX (NIJ/) NI J.
XX (GENT/) GENTZ R L.
XX (DILL/) DILLON P J.
XX (DIXI/) DIXIT V M.
XX
XX PI Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;
XX
XX DR WPI: 2000-687263/67.
XX P-PSDB; AAB36264.
XX
XX PT Treating graft-versus-host disease, cancer, immunodeficiency or an
XX autoimmune disease comprising administering an antibody to Death Domain
XX Containing Receptor proteins and a second therapeutic agent -
XX
XX PS Example 1; Fig 1; 273pp; English.
XX
XX CC The present invention provides the protein and coding sequences for two
XX death domain containing receptors, designated DR3 and DR3-V1. These
XX receptors are involved in apoptosis, and the sequences given can be used
XX in the treatment of cancers, infections, cardiovascular disorders such as
XX arrhythmias, ischemia, aneurysms, arterial occlusive diseases, embolisms
XX and congenital heart defects, neurodegenerative diseases including
XX Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
XX sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
XX and to promote angiogenesis and wound healing.
XX
SQ Sequence 1783 BP; 330 A; 562 C; 327 T; 0 other;
XX
Alignment Scores:
Pred. No.: 3 47e-40 Length: 1783
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
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PN      02-MAY-2002.
XX      24-OCT-2001; 2001WO-JP09313.
XX      24-OCT-2000; 2000JP-0324296.
PR      27-MAR-2001; 2001JP-0090546.
PR      30-MAR-2001; 2001JP-0099990.
XX      (NEWI-) NEW IND RES ORG.
XX      (SHIO/) SHIOZAWA S.
XX      SHIOZAWA S, Konishi Y;
PI      WPI; 2002-417132/44.
XX      DR      WPI; 2002-417132/44.
XX      PT      Genomes, particularly DR3 genomic DNA, participating in rheumatoid
XX      PT      arthritis via mutation, useful in evaluating disease onset and its
XX      PT      possibility and providing therapy and remedies
XX      PS      Claim 1; Page 64-66; 84pp; Japanese.
XX      CC      The present invention relates to the human DR3 gene, which is associated
XX      CC      with rheumatoid arthritis. Certain mutations in the gene can be linked to
XX      CC      the disease. The sequences can be used to evaluate disease onset and its
XX      CC      possibility and to provide therapy and remedies. The present sequence is
XX      CC      the gene of the invention.
XX      SQ      Sequence 4825 BP; 921 A; 1378 C; 1521 G; 1005 T; 0 other;

Alignment Scores:
Pred. No.:      1.21e-39      Length:      4825
Score:      368.00      Matches:      71
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
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DB      4523 ATGCAGCCGCGCCAGCGCGCTGGAGAGAGTTCTGCGCCAGCTGGGCGCTCGCGAG 4582
OY      21 ALaGluIleGluAlaGluValGluIleGlyArgPheArgAspGlnGlyTyrGluMet 40
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DB      4583 GCAGAGATCGAAGCCGCTGAGGTGAGATCGCCGCTCCGAGACCAGTACGAGATG 4642
OY      41 LeuLYArgTrpArgGlnGlnInProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
DB      4643 CTCACGCGCTGCGCCAGAGAGAGAGCCCGCGGCGCTTGAGAGCGCTTTACCGCGCCCTGGAG 4702
OY      61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB      4703 CGCATGGGCTGAGCGGCTGCGTGGAGAGACTTG 4735

RESULT 15
ABK42690
ID      ABK42690 standard; DNA; 10797 BP.
XX      AC      ABK42690;
XX      DT      21-MAY-2002 (first entry)
XX      DE      Genomic sequence #589 encoding novel human connective tissue polypeptide.
XX      KW      Human; connective tissue related disorder; cancer; gene therapy;
XX      KW      cytosstatic; gene; ds.
XX      OS      Homo sapiens.
XX      PN      WO200155343-A1.
XX      PD      02-AUG-2001.
XX      PE      17-JAN-2001; 2001WO-US01322.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-565190/63.
XX
XX Nucleic acid encoding novel connective tissue associated polypeptides,
PT used in diagnosing, preventing, treating or ameliorating a disorder
XX such as cancer or rheumatoid arthritis -
XX
XX Disclosure; SEQ ID No 1577; 673pp; English.
PS
XX
CC The present invention relates to the isolation of novel human connective
CC tissue related polypeptides (A086435-A086923) and the polynucleotide
CC (CDNA and genomic) sequences encoding them. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of diseases associated with connective tissue(s), including
CC cancer. The polynucleotide sequences of the invention are also useful
CC in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding
CC the novel human connective tissue related polypeptides.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 10797 BP; 2003 A; 3215 C; 3378 G; 2201 T; 0 other;
Alignment Scores:
Pred. No.: 3,31e-39 Length: 10797
Score: 368.00 Matches: 71
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Best Local Similarity: 100.00% Mismatches: 0
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QY 21 AlaGluIleGluAlaValGluValGluIleGluArgPheArgAspGlnGlyTyrGluMet 40
Db 9182 GCAGAGATCGAAGCCGTGGAGGTGAGATCGCGCTTCCAGACACAGACAGATG 9241
QY 41 LeuysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValAlaAlaLeuGlu 60
Db 9242 CTCACGCGCTGGCCGACACACAGCCCGCGCTCGAGCGCTTACGCGCCCTGAG 9301
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
Db 9302 CGCATGGGCTGGACGCGCTGCTGGAAGACTTG 9334

Mon Apr 7 09:25:11 2003

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Page 12

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SUMMARIES

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5	161	43.8	1956	2	US-08-762-308-10
6	156	42.4	2440	4	US-09-513-007-1
7	151	41.0	427	4	US-09-397-787-236
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15	151	41.0	2175	1	US-08-054-970-1	Sequence 1, Appl
16	94	25.5	1062	4	US-09-333-593A-3	Sequence 3, Appl
17	94	25.5	1236	4	US-09-134-618-1	Sequence 1, Appl
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19	94	25.5	1799	4	US-09-329-633A-1	Sequence 1, Appl
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31	70.5	19.2	606	4	US-09-328-111-495	Sequence 1, Appl
32	70.5	19.2	2016	4	US-09-132-118-1	Sequence 1, Appl
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41	63	17.1	1878	4	US-09-732-025-1	Sequence 1, Appl
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43	62	16.8	35060	3	US-08-814-095-7	Sequence 7, Appl
44	61.5	16.7	12127	3	US-08-444-644-32	Sequence 32, Appl
45	61.5	16.7	12127	4	US-08-232-246A-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-08-815-469-3
Sequence 3, Application US/08815469
Patent No. 6153402

GENERAL INFORMATION:

APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Geotz, Retner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HERewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285

FILED DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Stefie, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-08-815-469-3

Alignment Scores:
Pred. No.: 3,63e-43 Length: 1254
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x US-08-815-469-3 (1-1254)

QY 1 MetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
DB 1015 ATGAGCGCGGTCCACGCGGCGGTGGAAGAGTTGTCGCGACGCTGGGGCTGCGCGAG 1074

QY 21 AlaGluIleGluAlaValAlaGluValIleGlyArgPheArgAspGlnInTyrgIuMet 40
DB 1075 GCAGAGATCGAAGCCGTGGAGGTGAGATCGCGCCGCTTCGAGACACAGAGTACGAGATG 1134

QY 41 LeuLysArgTrpArgGlnGlnGlnInProAlaGlyLeuGlyAlaValTyrrAlaLeuGlu 60
DB 1135 CTCACCGCTGGCGCGACGAGCAGCGCGGCGGCTTGAGCCGTTACCGCGCCCTGGAG 1194

QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1195 CGCATGGGCGTGGACGCGCTGCTGGAGAACTTG 1227

RESULT 2
US-08-928-069-11
Sequence 11, Application US/08928069
Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996

ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-928-069-11

Alignment Scores:
Pred. No.: 5,16e-43 Length: 1634
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x US-08-928-069-11 (1-1634)

QY 1 MetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
DB 1103 ATGAGCGCGGTCCACGCGGCGGTGGAAGAGTTGTCGCGACGCTGGGGCTGCGCGAG 1162

QY 21 AlaGluIleGluAlaValAlaGluValIleGlyArgPheArgAspGlnInTyrgIuMet 40
DB 1163 GCAGAGATCGAAGCCGTGGAGGTGAGATCGCGCCGCTTCGAGACACAGAGTACGAGATG 1222

QY 41 LeuLysArgTrpArgGlnGlnGlnInProAlaGlyLeuGlyAlaValTyrrAlaLeuGlu 60
DB 1223 CTCACCGCTGGCGCGACGAGCAGCGCGGCGCTGCGAGCCGTTACCGCGCCCTGGAG 1282

QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1283 CGCATGGGCGTGGACGCGCTGCTGGAGAACTTG 1315

RESULT 3
US-08-828-683A-9
Sequence 9, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-828-683A-9

Alignment Scores:
Pred. No.: 5.16e-43 Length: 1634
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x US-08-828-683A-9 (1-1634)

QY 1 MetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
Db 1103 ATGAGACCGGCTCCAGCGCGCGCTGGAGAGAGTTCTGCGCAGCGTGGCGGAG 1162
QY 21 AlagluilegluaIaValaIgluValaIgluIleGlyArgPheArgAspGlnIntyrGluMet 40
Db 1163 GCAGAGATCGAAGCCGCGGAGGTGAGATGCGCCGCTCCGAGCCGACGATGAGATG 1222
QY 41 LeuLysArgTrpArgGlnGlnInProAlaGlyLeuGlyValaValTyrAlaAlaLeuGlu 60
Db 1223 CTCAGAGCGTGGCGCCAGCAGACCGCGGCGCTCGAGCGCTTTCAGCGGCGCTGAG 1282
QY 61 ArgMetClyLeuAspGlyCysValaIgluAspLeu 71
Db 1283 CGCATGGGCGTGGAGCGGCTGCTGAGACTTG 1315

RESULT 4
US-08-815-469-1
Sequence 1, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488-0310003/EKS/RM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 198..1481
US-08-815-469-1

Alignment Scores:
Pred. No.: 5.79e-43 Length: 1783
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x US-08-815-469-1 (1-1783)

QY 1 MetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
Db 1245 ATGAGACCGGCTCCAGCGCGCGCTGGAGAGAGTTCTGCGCAGCGTGGCGGAG 1304
QY 21 AlagluilegluaIaValaIgluValaIgluIleGlyArgPheArgAspGlnIntyrGluMet 40
Db 1305 GCAGAGATCGAAGCCGCGGAGGTGAGATGCGCGCTCCGAGCCGACGATGAGATG 1364
QY 41 LeuLysArgTrpArgGlnGlnInProAlaGlyLeuGlyValaValTyrAlaAlaLeuGlu 60
Db 1365 CTCAGAGCGTGGCGCCAGCAGACCGCGGCGCTCGAGCGCTTTCAGCGGCGCTGAG 1424
QY 61 ArgMetGlyLeuAspGlyCysValaIgluAspLeu 71
Db 1425 CGCATGGGCGTGGAGCGGCTGCTGAGACTTG 1457

RESULT 5
US-08-762-308-10
Sequence 10, Application US/08762308
Patent No. 5925548
GENERAL INFORMATION:
APPLICANT: Beutler, Bruce A.
APPLICANT: Bazzoni, Flavia M.
TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,308
FILING DATE: 09-DEC-1996

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/224,593
FILING DATE: 05-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: US-08-762-308-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 418-3000
TELEFAX: 474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-762-308-10

Alignment Scores:
Pred. No.: 1 75e-13 Length: 1956
Score: 161.00 Matches: 34
Percent Similarity: 64.00% Conservative: 14
Best Local Similarity: 45.33% Mismatches: 23
Query Match: 43.75% Indels: 4
DB: 2 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-08-762-308-10 (1-1956)

OY 1 MetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
DB 1182 GTGGATGGCTGCTCCACGCGCTGGAAGAGATTATCGCTTCGAGGCGTACGACGAG 1241
OY 21 AlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnIleArgGlu 39
DB 1242 CACGAGATCGAAGCGCTGAGATGACGAGACGGCGCTGCTGCGGAGGCTCAGTACAC 1301
OY 40 MetLeuLysArgTrpArgGlnGlnGlnProAla-----GlyLeuGlyAlaValIleArg 56
DB 1302 ATGCTGGAGCGCTGGCGCGCGACGCGCGCCACGACGACACGCTGAGAGTGTGGCG 1361
OY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1362 CCGGCTCTCCAGATGACACTGGCTGGCTGCTGAGAAATATC 1406

RESULT 6
US-09-513-007-1
Sequence 1, Application US/09513007
Patent No. 6406907
GENERAL INFORMATION:
APPLICANT: Taylor, J. Michael
APPLICANT: Kehli, Jr., Marcus
APPLICANT: Lee, Eun-Kyung
APPLICANT: Mwangi, Simon
TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
FILE REFERENCE: 08411-018001
CURRENT APPLICATION NUMBER: US/09/513_007
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 60/122,156
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2440
TYPE: DNA
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: CDS
LOCATION: (294)...(1706)
US-09-513-007-1

Alignment Scores:

Pred. No.: 1 21e-12 Length: 2440
Score: 156.00 Matches: 36
Percent Similarity: 61.33% Conservative: 10
Best Local Similarity: 48.00% Mismatches: 25
Query Match: 42.39% Indels: 4
DB: 2 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-09-513-007-1 (1-2440)

OY 1 MetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
DB 1428 GTGGAGCGCTGCCCCGCTGCGCTGGAAGAGATTGCTGCGGCTGAGGCTGAGCAG 1487
OY 21 AlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnIleArgGlu 39
DB 1488 CACGAGATCGAAGCGCTGAGAGCGGAGAACGGCGCCACTGCGCGACGCGACATACAC 1547
OY 40 MetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaValIleArg 56
DB 1548 ATGCTGGCGCGCTGGCGCGCGCACGCGCGCCGACGACGCTGAGCTGTGGCG 1607
OY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1608 CCGGCTCTCAGGACATGACCTGCTGGGTGCTGGAACATA 1652

RESULT 7
US-09-397-787-236
Sequence 236, Application US/09397787
Patent No. 6468758
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Lodes, Michael J.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
FILE REFERENCE: 210121.466C2
CURRENT APPLICATION NUMBER: US/09/397,787
PRIOR FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 236
LENGTH: 427
TYPE: DNA
ORGANISM: Homo sapien
US-09-397-787-236

Alignment Scores:
Pred. No.: 6 17e-13 Length: 427
Score: 151.00 Matches: 34
Percent Similarity: 62.67% Conservative: 13
Best Local Similarity: 45.33% Mismatches: 24
Query Match: 41.03% Indels: 4
DB: 2 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-09-397-787-236 (1-427)

OY 1 MetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
DB 56 GTGGAGACGTCGCCCTGCTGCGCTGGAAGAGATTGCTGCGGCTGAGGCTGAGCAG 115
OY 21 AlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnIleArgGlu 39
DB 116 CACGAGATCGAAGCGCTGAGAGCTGAGAACGGCGCTGCTGCGGAGCGCCCAATACAC 175
OY 40 MetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaValIleArg 56
DB 176 ATGCTGGAGCTGAGCGCGCGCACGCGCGCGGAGCAGCCTGAGACTGCTGTGGA 235
OY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 236 CCGGCTCTCCGACATGACCTGCTGGGCTGCTGAGAGACATC 280

NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1620
US-08-321-668-1

Alignment Scores:
Pred. No.: 5.32e-12 Length: 2175
Score: 151.00 Matches: 34
Percent Similarity: 62.67% Conservative: 13
Best Local Similarity: 45.33% Mismatches: 24
Query Match: 41.03% Indels: 4
DB: 1 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-08-321-668-1 (1-2175)

QY 1 MetaspalaValProAlaArgTrpLysGluPheValArgThrLeuArgGlu 20
DB 1342 GTGAGAACGCGCCCGCTGCGTGGAGAAATTCGTCGCGCCCTAGCGCAC 1401

QY 21 AlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyrglu 39
DB 1402 CACGAGATCGATCGCGCTGCGAGCTGCAGAACGCGCGCTCCCGCCGAGCCCAATACAC 1461

QY 40 MetLeuysArgTrpArgGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
DB 1462 ATGCTGCGAGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGGGA 1521

QY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1522 CGCGTGTCCGCGCAGATGAGCTGCTGGGCTGCTGAGGAGACATC 1566

RESULT 13
US-08-837-941-1
Sequence 1, Application US/08837941
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
APPLICANT: VARPOLOMEY, Eugene
APPLICANT: BARKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,941
FILING DATE: 28-APR-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/321,668
FILING DATE: 12-OCT-1994
APPLICATION NUMBER: IL 107268
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1620
US-08-837-941-1

Alignment Scores:
Pred. No.: 5.32e-12 Length: 2175
Score: 151.00 Matches: 34
Percent Similarity: 62.67% Conservative: 13
Best Local Similarity: 45.33% Mismatches: 24
Query Match: 41.03% Indels: 4
DB: 1 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-08-837-941-1 (1-2175)

QY 1 MetaspalaValProAlaArgTrpLysGluPheValArgThrLeuArgGlu 20
DB 1342 GTGAGAACGCGCCCGCTGCGTGGAGAAATTCGTCGCGCGCTGAGCGCAC 1401

QY 21 AlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyrglu 39
DB 1402 CACGAGATCGATCGCGCTGCGAGCTGCAGAACGCGCGCTCCCGCCGAGCCCAATACAC 1461

QY 40 MetLeuysArgTrpArgGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
DB 1462 ATGCTGCGAGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGGGA 1521

QY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1522 CGCGTGTCCGCGCAGATGAGCTGCTGGGCTGCTGAGGAGACATC 1566

RESULT 14
US-08-126-016-1
Sequence 1, Application US/08126016
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: NOPHAR, YARON
APPLICANT: KEMPER, OLIVER
APPLICANT: ENGELMANN, HARTMUT
APPLICANT: BRAKEBUSCH, CORD
APPLICANT: ADERKA, DAN
TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TBP-I)
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/126,016
  FILING DATE: 24-SEP-1993
  CLASSIFICATION: 435
  PRIORITY APPLICATION DATA:
    APPLICATION NUMBER: US 07/625668
    FILING DATE: 13-DEC-1990
  ATTORNEY/AGENT INFORMATION:
    NAME: BROWDY, ROGER L.
    REGISTRATION NUMBER: 25,618
    REFERENCE/DOCKET NUMBER: WALLACH4
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 202-628-5197
      TELEFAX: 202-737-3528
  TELEX: 248633
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 2175 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 256..1620
      NAME/KEY: mat_peptide
      LOCATION: 319..1620
US-08-126-016-1

Alignment Scores:
Pred. No.: 5,32e-12 Length: 2175
Score: 151.00 Matches: 34
Percent Similarity: 62.67% Conservative: 13
Best Local Similarity: 45.33% Mismatches: 24
Query Match: 41.03% Indels: 4
DB: 1 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-08-126-016-1 (1-2175)
QY 1 MetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
DB 1342 GTGAGAGACGTGCCCGCGTGGCTGGAAGAAATTCGTGGCGGCGCTAGGCGTGAACGAC 1401
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyrGlu 39
DB 1402 CACGAGATCATGCTGCGTGGAGCTGCAGAACGGGCGCTGCGCGCGAGGCGCAATACAGC 1461
QY 40 MetLeuLysArgTrpArgGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
DB 1462 ATGCTGGCAGCTGGAGGCGCGACGCCGCGGCGGAGGCGCACGCTGAGACTGTGGGA 1521
QY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1522 CGCGTCTCCGCGACATGACCTGCTGGCTGAGAGACATC 1566

RESULT 15
US-08-054-970-1
; Sequence 1, Application US/08054970
; Patent No. 6395267
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
```

```

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/054,970
  FILING DATE: 03-MAY-1993
  CLASSIFICATION: 435
  ATTORNEY/AGENT INFORMATION:
    NAME: Townsend, Kevin G.
    REGISTRATION NUMBER: 34,033
    REFERENCE/DOCKET NUMBER: WALLACH-9
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 202-628-5197
      TELEFAX: 202-737-3528
  TELEX: 248633
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 2175 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 256..1620
US-08-054-970-1

Alignment Scores:
Pred. No.: 5,32e-12 Length: 2175
Score: 151.00 Matches: 34
Percent Similarity: 62.67% Conservative: 13
Best Local Similarity: 45.33% Mismatches: 24
Query Match: 41.03% Indels: 4
DB: 4 Gaps: 2

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DB 1342 GTGAGAGACGTGCCCGCGTGGCTGGAAGAAATTCGTGGCGGCGCTAGGCGTGAACGAC 1401
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyrGlu 39
DB 1402 CACGAGATCATGCTGCGTGGAGCTGCAGAACGGGCGCTGCGCGCGAGGCGCAATACAGC 1461
QY 40 MetLeuLysArgTrpArgGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
DB 1462 ATGCTGGCAGCTGGAGGCGCGACGCCGCGGCGGAGGCGCACGCTGAGACTGTGGGA 1521
QY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1522 CGCGTCTCCGCGACATGACCTGCTGGCTGAGAGACATC 1566
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Search completed: April 6, 2003, 23:30:04
Job time : 17.9856 secs

GenCore version 5.1.4-p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 21:08:18 ; Search time 27.0348 Seconds
(without alignments)
2303.655 Million cell updates/sec

Title: US-09-993-234-6_COPY-339_409
Perfect score: 368
Sequence: 1 MAAVPAARRRKEFVRLGLRE.....LGAVALERMGIDGVEDL 71

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 593429 segs, 438583890 residues
Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published.Applications_NA.QEFT-fastcap.SUFFIX-rmpb.MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT-bits -START=1 -END=1 -MATRIX=bl0sum62
-TRANS=human40.ccl -LIST=45 -DOCALIGN=200 -THR_SCORE=pcr -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MALEN=200000000 -USER=US0993334.GCGN.1.1.249 &runat_27032003_115459_15466
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published.Applications_NA:*
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12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	368	100.0	1254	10 US-09-333-966-3	Sequence 3, Appl1
2	368	100.0	1634	9 US-10-081-280-9	Sequence 9, Appl1
3	368	100.0	1634	9 US-10-112-793-9	Sequence 9, Appl1
4	368	100.0	1634	9 US-10-112-193-11	Sequence 11, Appl1

5	368	100.0	1634	10 US-09-993-234-9	Sequence 9, Appl1
6	368	100.0	1783	10 US-09-333-966-1	Sequence 1, Appl1
7	368	100.0	10797	9 US-10-092-154-1577	Sequence 1577, Ap
8	368	100.0	10797	10 US-09-764-847-1577	Sequence 1577, Ap
9	356	96.7	1743	9 US-09-954-531-1389	Sequence 1389, Ap
10	356	96.7	2130	10 US-09-917-800A-1601	Sequence 1601, Ap
11	157	42.7	2130	10 US-09-898-234-14	Sequence 14, Appl
12	157	42.7	2173	9 US-09-899-429A-24	Sequence 24, Appl
13	157	42.7	2173	9 US-09-792-356-14	Sequence 14, Appl
14	157	42.7	2173	10 US-09-899-429A-26	Sequence 14, Appl
15	156	42.4	2440	10 US-09-970-352-1	Sequence 1, Appl1
16	151	41.0	427	10 US-09-876-889-236	Sequence 236, App
17	151	41.0	479	9 US-10-043-487-100	Sequence 100, App
18	151	41.0	1368	9 US-09-898-234-1	Sequence 1, Appl1
19	151	41.0	1368	9 US-09-899-429A-1	Sequence 1, Appl1
20	151	41.0	1368	9 US-09-792-356-1	Sequence 1, Appl1
21	151	41.0	1368	10 US-09-899-422-1	Sequence 1, Appl1
22	151	41.0	2111	10 US-09-880-107-2360	Sequence 2360, Ap
23	151	41.0	2141	9 US-09-898-234-16	Sequence 24, Appl
24	151	41.0	2141	9 US-09-899-429A-26	Sequence 26, Appl
25	151	41.0	2141	9 US-09-792-356-16	Sequence 16, Appl
26	151	41.0	2141	10 US-09-899-422-16	Sequence 16, Appl
27	151	41.0	2175	12 US-10-120-397-1	Sequence 1, Appl1
28	94	25.5	1062	8 US-08-916-625B-3	Sequence 3, Appl1
29	94	25.5	1236	9 US-10-076-754-1	Sequence 1, Appl1
30	94	25.5	1236	9 US-10-076-773-1	Sequence 1, Appl1
31	94	25.5	1236	12 US-10-067-615-1	Sequence 1, Appl1
32	94	25.5	1600	10 US-09-874-138-1	Sequence 1, Appl1
33	94	25.5	1600	12 US-10-005-842-1	Sequence 1, Appl1
34	94	25.5	1799	9 US-09-992-964-10	Sequence 10, Appl1
35	94	25.5	1799	10 US-09-828-739-1	Sequence 1, Appl1
36	94	25.5	1799	10 US-09-887-879-10	Sequence 10, Appl1
37	94	25.5	1799	12 US-10-052-798-2	Sequence 2, Appl1
38	94	25.5	3881	8 US-08-916-625B-1	Sequence 1, Appl1
39	94	25.5	3964	9 US-08-811-088-5	Sequence 5, Appl1
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41	94	25.5	4051	9 US-09-811-088-3	Sequence 3, Appl1
42	94	25.5	4051	10 US-09-757-421-1	Sequence 1, Appl1
43	76	20.7	2040	9 US-09-991-496-5	Sequence 5, Appl1
44	76	20.7	2040	10 US-09-874-923-5	Sequence 5, Appl1
45	76	20.7	4233	9 US-09-991-496-99	Sequence 99, Appl1

ALIGNMENTS

RESULT 1
US-09-333-966-3
Sequence 3, Application US/09333966
Patent No. US2002009773A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE:
; APPLICATION NUMBER: No. US2002009773A1 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1251
;
US-09-333-966-3
;
Alignment Scores:
Pred. No.: 3.73e-45 Length: 1254
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

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QY 1 MetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
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QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIleTyrGluMet 40
DB 1075 GCAGAGATCGAAGCCGTGGAGGTGAGATCGGCCCTCCGAGACGACGATCGAGATG 1134
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaIleLeuGlu 60
DB 1135 CTCAGCGCTGGCGGCGACGACGACCGCGGCGCTGGAGCCGTTACGCGGCGCTGGAG 1194
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1195 CGCATGGGCGCTGGAGCGCTGCGTGGAGACTTG 1227

RESULT 2
US-10-081-280-9
; Sequence 9, Application US/10081280
; Patent No. US20020165157A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/081,280
; FILING DATE: 21-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,270
; FILING DATE: 31-Mar-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1634 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-081-280-9
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Alignment Scores:
Pred. No.: 5.15e-45 Length: 1634
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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QY 1 MetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
DB 1103 ATGGAGCGCGTCCACGCGGCGCTGGAAAGAGTTGTCGCGCAGCTGGGCGCGAG 1162
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIleTyrGluMet 40
DB 1163 GCAGAGATCGAAGCCGTGGAGGTGAGATCGGCCCTCCGAGACGACGATCGAGATG 1222
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaIleLeuGlu 60
DB 1223 CTCAGCGCTGGCGGCGACGACGACCGCGGCGCTGGAGCCGTTACGCGGCGCTGGAG 1282
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1283 CGCATGGGCGCTGGAGCGCTGCGTGGAGACTTG 1315

RESULT 3
US-10-112-793-9
; Sequence 9, Application US/10112793
; Publication No. US20020192729A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,193
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/938,069
FILING DATE: 11-Sep-1997
APPLICATION NUMBER: 60/026943
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-112-193-11

Alignment Scores:
Pred. No.: 5.15e-45 Length: 1634
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

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QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnIntArgLsuMet 40
Db 1163 GCAAGATTCGAGCGCCGTGGAGGTGGAGATGCGCGCTTCGAGACACGACAGTACGACATG 1222Z
QY 41 LeuLysArgTPrParGngIngInGluProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
Db 1223 CTCAGAGCGCTGGCGCCAGCAGACGCCCGCGGCGCTCGAGCGCTTACGCGGCGCTGGAG 1282Z
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
Db 1283 CGCATGGCGCTGGACGCGCTCGTGGAAAGACTTG 1315

RESULT 5
US-09-993-234-9
Sequence 9, Application US/09993234
Patent No. US2002014678A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/993,234

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FILING DATE: 19-NO. US20020146768A1-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,683
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-993-234-9

Alignment Scores:
Pred. No.: 5,15e-45 Length: 1634
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x US-09-993-234-9 (1-1634)

QY 1 Metaspalalavalprolaararartrpysgluphevalarqthrleuglyleuarglu 20
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QY 21 Alaagutleuglualavalgluvalgluileglarqphearqaspglnglntyglunet 40
DB 1163 GCAAGATCGAAGCGCTGAGGTGAGATCGCGCTTCCGAGACACAGTACGAGATG 1222
QY 41 Leuysarqtrparqnglnglprolaaglyleuglylavaltyrvalalalenglu 60
DB 1223 CTCAGCGCTGGCGGACAGACAGCCCGGCGCTCGGAGCGCTTACGCGCGCTGGAG 1282
QY 61 Argmetglyleuaspglycysvalgluaspheu 71
DB 1283 CGCATGGGGCTGAGCGGCTGCTGGAAGACTTG 1315

RESULT 6

US-09-333-966-1
Sequence 1, Application US/09333966
Patent No. US2002009773A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
APPLICATION NUMBER: No. US2002009773A1 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 198..1481
US-09-333-966-1

Alignment Scores:
Pred. No.: 5.73e-45 Length: 1783
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x US-09-333-966-1 (1-1783)

QY 1 Metaspalalavalprolaararartrpysgluphevalarqthrleuglyleuarglu 20
DB 1245 ATGAGCGGGTCCGAGCGCGCTGGAAGAGTTCGTGCGAGCGCTGGGCTGGCGAG 1304
QY 21 Alaagutleuglualavalgluvalgluileglarqphearqaspglnglntyglunet 40
DB 1305 GCAGATCGAAGCGCTGAGGTGAGATCGCGCTTCCGAGACACAGTACGAGATG 1364
QY 41 Leuysarqtrparqnglnglprolaaglyleuglylavaltyrvalalalenglu 60
DB 1365 CTCAGCGCTGGCGGACAGACAGCCCGGCGCTCGGAGCGCTTACGCGCGCTGGAG 1424
QY 61 Argmetglyleuaspglycysvalgluaspheu 71
DB 1425 CGCATGGGGCTGAGCGGCTGCTGGAAGACTTG 1457

RESULT 7

US-10-092-154-1577
Sequence 1577, Application US/10092154
Publication No. US20030054375A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See file wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1577

LENGTH: 10797
TYPE: DNA
ORGANISM: Homo sapiens
US-10-092-154-1577

Alignment Scores:

Pred. No.:	5.17e-44	Length:	10797
Score:	368.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-993-234-6_COPY_339_409 (1-71) x US-10-092-154-1577 (1-10797)

OY 1 MetaspalavalprolaaragatgtrpbysgluPhevalArghrleuglyleuarglu 20
|||||
DB 9122 ATGAGACGGCTCCACGCGCGCTCGAAGAGTTCCTGCCACGCTGGGGCTGCCGAG 9181
OY 21 AlagluileglualavalgluValgluileglyArghrleuglyleuarglu 40
|||||
DB 9182 GCAGAGATCGAAGCCGTGGAGGTGAGATCGCGCTTCGAGACGACGAGTACGAGATG 9241
OY 41 LeuysArgrtrpargnginglnproalaglyleuglylavaltyrralaaleuglu 60
|||||
DB 9242 CTCAGACGGCTGGCGCAGCAGACGCGCGCTCGAGACCGCTTTACGCGCGCTGGAG 9301
OY 61 Argmetglyleuaspglycysvalgluasplleu 71
|||||
DB 9302 CGCATGGGCTGAGCGGCTGCTCGAAGACTTG 9334

RESULT 8
US-09-764-847-1577
Sequence 1577, Application US/09764847
Patent No. US20020132767A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 2003
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 1577
LENGTH: 10797
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-847-1577

Alignment Scores:

Pred. No.:	5.17e-44	Length:	10797
Score:	368.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-993-234-6_COPY_339_409 (1-71) x US-09-764-847-1577 (1-10797)

OY 1 MetaspalavalprolaaragatgtrpbysgluPhevalArghrleuglyleuarglu 20
|||||
DB 9122 ATGAGACGGCTCCACGCGCGCTCGAAGAGTTCCTGCCACGCTGGGGCTGCCGAG 9181
OY 21 AlagluileglualavalgluValgluileglyArghrleuglyleuarglu 40
|||||
DB 9182 GCAGAGATCGAAGCCGTGGAGGTGAGATCGCGCTTCGAGACGACGAGTACGAGATG 9241
OY 41 LeuysArgrtrpargnginglnproalaglyleuglylavaltyrralaaleuglu 60
|||||
DB 9242 CTCAGACGGCTGGCGCAGCAGACGCGCGCTCGAGACCGCTTTACGCGCGCTGGAG 9301
OY 61 Argmetglyleuaspglycysvalgluasplleu 71

|||||
DB 9302 CGCATGGGCTGAGCGGCTGCTCGAAGACTTG 9334

RESULT 9
US-09-954-531-1389

Sequence 1389, Application US/09954531
Patent No. US20020165180A1
GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
SOFTWARE: Patentln version 3.0
SEQ ID NO 1389
LENGTH: 1743
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-531-1389

Alignment Scores:

Pred. No.:	3.29e-43	Length:	1743
Score:	356.00	Matches:	69
Percent Similarity:	97.18%	Conservative:	0
Best Local Similarity:	97.18%	Mismatches:	2
Query Match:	96.74%	Indels:	0
DB:	9	Gaps:	0

US-09-993-234-6_COPY_339_409 (1-71) x US-09-954-531-1389 (1-1743)

OY 1 MetaspalavalprolaaragatgtrpbysgluPhevalArghrleuglyleuarglu 20
|||||
DB 1184 ATGAGACGGCTCCACGCGCGCTCGAAGAGTTCCTGCCACGCTGGGGCTGCCGAG 1243
OY 21 AlagluileglualavalgluValgluileglyArghrleuglyleuarglu 40
|||||
DB 1244 GCAGAGATCGAAGCCGTGGAGGTGAGATCGCTCTCCGAGACGACGAGTACGAGATG 1303
OY 41 LeuysArgrtrpargnginglnproalaglyleuglylavaltyrralaaleuglu 60
|||||
DB 1304 CTCAGACGCTGGCGCAGCAGACGCGCGCTCGAGACCGCTTTACGCGCGCTGGAG 1363
OY 61 Argmetglyleuaspglycysvalgluasplleu 71
DB 1364 CGCATGGGCTGAGCGGCTGCTCGAAGACTTG 1396

RESULT 10

US-09-917-800A-1601
Sequence 1601, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Gene Logic, Inc.
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31

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: PRIOR APPLICATION NUMBER: US 60/222,040
: PRIOR FILING DATE: 2000-07-31
: PRIOR APPLICATION NUMBER: US 60/222,880
: PRIOR FILING DATE: 2000-11-02
: PRIOR APPLICATION NUMBER: US 60/290,029
: PRIOR FILING DATE: 2001-05-11
: PRIOR APPLICATION NUMBER: US 60/290,645
: PRIOR FILING DATE: 2001-05-15
: PRIOR APPLICATION NUMBER: US 60/292,336
: PRIOR FILING DATE: 2001-05-22
: PRIOR APPLICATION NUMBER: US 60/295,798
: PRIOR FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: US 60/297,457
: PRIOR FILING DATE: 2001-06-13
: PRIOR APPLICATION NUMBER: US 60/298,884
: PRIOR FILING DATE: 2001-06-19
: PRIOR APPLICATION NUMBER: US 60/303,459
: PRIOR FILING DATE: 2001-07-09
: NUMBER OF SEQ ID NOS: 1740
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1601
: LENGTH: 2130
: TYPE: DNA
: ORGANISM: Rattus norvegicus
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_013091
US-09-917-800A-1601

Alignment Scores:
Pred. No.: 1,01e-13 Length: 2130
Score: 157.00 Matches: 35
Percent Similarity: 62.67% Conservative: 12
Best Local Similarity: 46.67% Mismatches: 24
Query Match: 42.66% Indels: 4
DB: 10 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-09-917-800A-1601 (1-2130)
QY 1 Metaspalalavalproalargtrparysgluphevalargthleuglyleuarglu 20
Db 1345 GTGGATGGCGCTCCGACACGCTGGAAGAGTTCATGCGGCTCGTGGAGCGAG 1404
QY 21 Alaaliuileglualavalgluvalgluileglyarg---PheArGAspGlnGlnItyrGlu 39
Db 1405 CACGAGATCGAGCGGCTGCGACGAGCGGCGTCCCTCCGCGAGCGCTCATTAACAC 1464
QY 40 MetleuLysArGTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
Db 1465 ATGCTGGAAGCTGGCGCGCGCGACACCGCGACGAGCGCCAGCTGAGCTAGTGGGC 1524
QY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
Db 1525 CGCGTCTTTCGACATGACCTGCGTGGCTGCGTGGAGAACATC 1569

RESULT 11
US-09-898-234-14
: Sequence 14, Application US/09898234
: Patent No. US2002015112A1
: GENERAL INFORMATION:
: APPLICANT: Hauptmann, Rudolph
: APPLICANT: Hummer, Adolph
: APPLICANT: Maurer-Fogy, Ingrid
: APPLICANT: Stratowa, Christian
: TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
: FILE REFERENCE: 98,385-1
: CURRENT APPLICATION NUMBER: US/09/898,234
: PRIOR APPLICATION NUMBER: 09/525,998
: PRIOR FILING DATE: 2000-03-15
: PRIOR APPLICATION NUMBER: 08/383,676
: PRIOR FILING DATE: 1995-02-01
: PRIOR APPLICATION NUMBER: 08/153,287
```

```

: PRIOR FILING DATE: 1993-11-17
: PRIOR APPLICATION NUMBER: 07/821,750
: PRIOR FILING DATE: 1992-01-02
: PRIOR APPLICATION NUMBER: 07/511,430
: PRIOR FILING DATE: 1990-04-20
: NUMBER OF SEQ ID NOS: 87
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 14
: LENGTH: 2173
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (245)..(1630)
: OTHER INFORMATION: Description of Artificial Sequence: ratTNF-R8
US-09-898-234-14

Alignment Scores:
Pred. No.: 1,03e-13 Length: 2173
Score: 157.00 Matches: 35
Percent Similarity: 62.67% Conservative: 12
Best Local Similarity: 46.67% Mismatches: 24
Query Match: 42.66% Indels: 4
DB: 9 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-09-898-234-14 (1-2173)
QY 1 Metaspalalavalproalargtrparysgluphevalargthleuglyleuarglu 20
Db 1352 GTGGATGGCGCTCCGACACGCTGGAAGAGTTCATGCGGCTCGTGGAGCGAG 1411
QY 21 Alaaliuileglualavalgluvalgluileglyarg---PheArGAspGlnGlnItyrGlu 39
Db 1412 CACGAGATCGAGCGGCTGCGACGAGCGGCGTCCCTCCGCGAGCGCTCATTAACAC 1471
QY 40 MetleuLysArGTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
Db 1472 ATGCTGGAAGCTGGCGCGCGCGACACCGCGACGAGCGCCAGCTGAGCTAGTGGGC 1531
QY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
Db 1532 CGCGTCTTTCGACATGACCTGCGTGGCTGCGTGGAGAACATC 1576

RESULT 12
US-09-899-429A-24
: Sequence 24, Application US/09899429A
: Patent No. US20020169118A1
: GENERAL INFORMATION:
: APPLICANT: Hauptmann, Rudolph
: APPLICANT: Hummer, Adolph
: APPLICANT: Maurer-Fogy, Ingrid
: APPLICANT: Stratowa, Christian
: TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
: FILE REFERENCE: 98-385-J
: CURRENT APPLICATION NUMBER: US/09/899,429A
: PRIOR APPLICATION NUMBER: 09/792,356
: PRIOR FILING DATE: 2000-02-23
: PRIOR APPLICATION NUMBER: 08/477,639
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: 08/383,676
: PRIOR FILING DATE: 1995-02-01
: PRIOR APPLICATION NUMBER: 08/153,287
: PRIOR FILING DATE: 1993-11-17
: PRIOR APPLICATION NUMBER: 07/821,750
: PRIOR FILING DATE: 1992-01-02
: PRIOR APPLICATION NUMBER: 07/511,430
: PRIOR FILING DATE: 1990-04-20
: NUMBER OF SEQ ID NOS: 97
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 24
: LENGTH: 2173
```

```

: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: ratNF-R8
: NAME/KEY: CDS
: LOCATION: (245)..(1627)
US-09-899-429A-24

Alignment Scores:
Pred. NO.: 1.03e-13 Length: 2173
Score: 157.00 Matches: 35
Percent Similarity: 62.67% Conservative: 12
Best Local Similarity: 46.67% Mismatches: 24
Query Match: 42.66% Indels: 4
DB: 9 Gaps: 2

US-09-993-224-6_COPY_339_409 (1-71) x US-09-899-429A-24 (1-2173)
OY 1 MetaspAlaValProAlaIarGArGrTpyrGluPhaValaIgrHrIeuGlyLeuArgGlu 20
Db 1352 GGGAGATGGCGTCCCTCCGACACGCTGGAAGAGATTCATGCGCTCCGGGGCTGAGCGAG 1411
OY 21 AlaGluIeGluAlaValaGluValaGluIeGlyArg---PheaArgspGInGIntyrGlu 39
Db 1412 CACGAGATCGACGCGGTGTGAGCGTGCAGAAAGCGCGTTCCTCCGCGAGGCTCATTAACG 1471
OY 40 MetLeuLysArGrTrpArgGInGInGInPro-----AlaGlyLeuGlyAlaValTyr 56
Db 1472 ATGCTGGAAGCCTGGCGCGCGCCGACACCGCGACACGAGCGCACGCGTGCAGTAgTGGCG 1531
OY 57 AlaAlaIeUGluArgMetGlyLeuAspGlyCysValaGluAspLeu 71
Db 1532 CGCGTCTTGGCGACATGAACTCGCGTGCCTGCTGGAGAATGC 1576

RESULT 13
US-09-792-356-14
: Sequence 14, Application US/09792356
: Publication NO. US20020183485A1
: GENERAL INFORMATION:
: APPLICANT: Hauptmann, Rudolph
: APPLICANT: Himmler, Adolph
: APPLICANT: Maurer-Fogy, Ingrid
: APPLICANT: Stratowa, Christian
: TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
: FILE REFERENCE: 98, 385-G
: CURRENT APPLICATION NUMBER: US/09/792,356
PRIOR APPLICATION NUMBER: 2001-08-17
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/383,676
PRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR FILING DATE: 1992-01-02
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 2173
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (245)..(1630)
OTHER INFORMATION: Description of Artificial Sequence: ratNF-R8
US-09-792-356-14

Alignment Scores:
Pred. No.: 1.03e-13 Length: 2173
Score: 157.00 Matches: 35
Mismatches: 24
Indels: 4
Gaps: 2

```

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Oy      21 AlagluileglualvalgluValguilegluYarg---PheArqAspInglntYrglu 39
          |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1412 CACGAGATTCAGCGGGCTTGGAGCTGCAGAAACGGGGCTTGCCCTCCGGAGGCTCATTAACG 1471
Oy      40 MetLeuysArgrTPrAArgIngInglInPro-----AlaglyLeuglyAlaValTYr 56
          |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1472 ATGCTGGAAACCTGGGGGGGCCGCAACACCGACACAGAGAGCACCCTGTGAAGTAGTGGGC 1531
Oy      57 AlaAlaleuGluarYmetgLyLeuAspglyCytsValgluaSpleu 71
          |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1532 CGCGTGGCTTTGGCAGACnGAACCTGGTGGCTGCTCGAGAGAACATTC 1576

RESULT 15
US-09-970-532-1
; Sequence 1' Application US/09970532
; Patient No. US20020076765X1
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael
; APPLICANT: Kehrl, Jr., Marcus
; APPLICANT: Lee, Eun-Kyung
; APPLICANT: Mwangl, Simon
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 08411-018001
; CURRENT APPLICATION NUMBER: US/09/970_532
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 09/513_007
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2440
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (294)..(1706)
US-09-970-532-1

Alignment Scores:
Pred. No.: 1.67e-13 Length: 2440
Score: 156.00 Matches: 36
Percent Similarity: 61.33% Conservative: 10
Best Local Similarity: 48.00% Mismatches: 25
Query Match: 42.39% Indels: 4
DB: Gaps: 2

US-09-993-234_6_COPY_339_409 (1-71) x US-09-970-532-1 (1-2440)
Oy      1 MetaspAlaValProAlaArgrTPRlygluPhueValArgrThrlenglyleuArglu 20
          |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1428 GTGGAGCGGGCCCCCGCTCGCGCTGGAAAGATTGGTGTCCGGCGGTGGGACTGAGCGAG 1487
Oy      21 AlaguileglualvalgluValguilegluYarg---PheArqAspInglntYrglu 39
          |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1488 CACGAGATTCAGCGGGCTTGGAGCTGCAGAAACGGGGCGCACCTGCGGAGCGGACGATTAACG 1547
Oy      40 MetLeuysArgrTPrAArgIngInglInPro-----AlaglyLeuglyAlaValTYr 56
          |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1548 ATGCTGGCGGCTGGCGGGCGCGACGCCCGCGGAGGCCACCGCTGAGAGCTGCTGGGC 1607
Oy      57 AlaAlaleuGluarYmetgLyLeuAspglyCytsValgluaSpleu 71
          |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1608 CGCGTGGCTAGCGAGACnTGAACCTGCTGGTGGCTCGGAAAACAATA 1652
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Search completed: April 7, 2003, 03:59:22
Job time : 36.0348 secs

150


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/db_xref="taxon:3606"
/clone="IMAGE:2815679"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NDHL19W, testis NH7, and B-cell
NCI-GAP-GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
T.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729098-731359. Subtraction by Bento
Soares and M. Fatima Bonaldo."

```

Query Match	Similarity	Score	547.6	DB 10	Length	632
Best Local	Similarity	99.1%	Pred.	No. 2.1e-135		
Matches	550	Conservative	0	Mismatches	5	Indels
						Gaps
						0
QY	1	CTGGGGCCCCGGGCCCCAGGCGCGCACCTGCTGAGCCCGCAGGTGTGACTGTGGCGGTACTTC	60			
Db	12	CTGGGGGGCCCCGGGCCCCAGGCGCGCACCTGCTGAGCCCGCAGGTGTGACTGTGGCGGTACTTC	71			
QY	61	CACAGAGAGATTGGTCTGTTTGTTCAGAGGCTGCCAGCGGGGACCTACCTGAGAGCC	120			
Db	72	CACAGAGAGATTGGTCTGTTTGTTCAGAGGCTGCCAGCGGGGACCTACCTGAGAGCC	131			
QY	121	CCCTGACGAGGAGCCCTGGCGGCACTCCACTGCTGCTGTGTGTCCTCCAAAGACACTTCTTG	180			
Db	132	CCCTGACGAGGAGCCCTGGCGGCACTCCACTGCTGTGTGTGTCCTCCAAAGACACTTCTTG	191			
QY	181	GCCTGGGAGAACCCACCATTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC	240			
Db	192	GCCTGGGAGAACCCACCATTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC	251			
QY	241	TCCAGAGTGGCGCTGGAGAACTGTTAGCAAGTGGCGGACACCCGCTGTGCTGTAAGCCA	300			
Db	252	TCCAGAGTGGCGCTGGAGAACTGTTAGCAAGTGGCGGACACCCGCTGTGCTGTAAGCCA	311			
QY	301	GGCTGGTTTGTGGAGTGGCCAGGTGACGCAATGTGTGACAGTTCACCCCTTACTGTGCCAA	360			
Db	312	GGCTGGTTTGTGGAGTGGCCAGGTGACGCAATGTGTGACAGTTCACCCCTTACTGTGCCAA	371			
QY	361	CCATGCGCTAGACGCGCGGGGCCCTGCACCGGCACACAGCGCTACTCTTTCCCGAGAGAT	420			
Db	372	CCATGCGCTAGACGCGCGGGGCCCTGCACCGGCACACAGCGCTACTCTTTCCCGAGAGAT	431			
QY	421	ACTGACTGTGGACACTGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC	480			
Db	432	ACTGACTGTGGACACTGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC	491			
QY	481	CCCACAGACACCTGTGGGAGACTGTCCAGAGCGCTGTGCCGTGTCTGTGGCTGAGGACG	540			
Db	492	CCCACAGACACCTGTGGGAGACTGTGTGAGAGCGCTGTGCCGTGTCTGTGGCTGAGGACG	551			
QY	541	ATGTTCTGGGTCCAG	555			
Db	552	ATGTTCTGGGTCCAG	566			

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.
AUTHORS	1 (bases 1 to 698)
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgaps@remail.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (infoimage.llnl.gov) for further information. Insert length: 1568 Std Error: 0.00 Seq primer: ~40UP from Gibco High quality sequence stop: 459.
FEATURES	Location/Qualifiers
Source	1..698

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/db.xref="taxon:9606"
/clone.lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/notes="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBLH19W, testis NHT, and B-cell NLT0.CGAH.GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687339, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bernaldo."
BASE COUNT      111 a      218 c      214 g      155 t
ORIGIN
Query Match      98.0%; Score 543.8; DB 9; Length 698:
Best Local Similarity 98.7%; Pred. No. 2.3e-134;
Matches 548; Conservative 0; Mismatches 7; Indels 0; Gaps 0:
OY      1 CTGGGGGGCCCCGGCCAGGCGGCACTGCTGATCCCGAGGTGACGTGCGCGGTGACTTC 60
DB      21 CTGGGGGGCCCCGGCCAGGCGGCGGCTGTATCCCGAGGTGACTGTGCCGCTGACTTC 80
OY      61 CACAAGAGATGTGCTGTTTGTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 120
DB      81 CACAAGAGATGTGCTGTTTGTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 140
OY      121 CCTTCACAGGAGCCCTCGCGGCACTCCACTGCTTGTGTGTGCCAGACACTTCTTG 180
DB      141 CCTTCACAGGAGCCCTCGCGGCACTCCACTGCTTGTGTGTGCCAGACACTTCTTG 200
OY      181 GCGTGGGAGAACCCACCATTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATAGAGGCC 240
DB      201 GCGTGGGAGAACCCACCATTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATAGAGGCC 260
OY      241 TCCCAAGTGGGCGCTGGAGAACTGTTACAGAGTGGCGGACACCCGCTGTGGCTGAAGCA 300
DB      261 TCCCAAGTGGGCGCTGGAGAACTGTTACAGAGTGGCGGACACCCGCTGTGGCTGAAGCA 320
OY      301 GCGTGGTGTGTGAGATGCCAGGTCAAGCCAAATGTGTACAGAGTTCAACCCCTTACTGCCAA 360
DB      321 GCGTGGTGTGTGAGATGCCAGGTCAAGCCAAATGTGTACAGAGTTCAACCCCTTACTGCCAA 380
OY      361 CCATGCGTAGACTGCGGGGCGCTGCACCGCCACACAGGCTACTGTTGCCGACAGAT 420
DB      381 CCATGCGTAGACTGCGGGGCGCTGCACCGCCACACAGGCTACTGTTGCCGACAGAT 440
OY      421 ACTGACTGTGGGAACTGCGCTGCGCTGCTTCTATGAACAATGGGATGGCTGCGCTGTCTGC 480
DB      441 ACTGACTGTGGGAACTGCGCTGCGCTGCTTCTATGAACAATGGGATGGCTGCGCTGTCTGC 500

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[illegible]

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FEATURES
source
    1.767
    Location/Qualifiers
    High quality sequence stop: 754.
    plate: LRAM1538 row: 0 column: 17
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    clone distribution: MGC clone distribution information can be
    DNA Sequencing by: Incyte Genomics, Inc.
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    CDNA Library Preparation: Life Technologies, Inc.
    tissue Procurement: Life Technologies, Inc.

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5214568"
/clone_1lb="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/notice="Vector: PCWY-SPORT6; Site_1: NotI; Site_2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned. (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
BASE COUNT      122 a      243 c      241 g      161 t
ORIGIN

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Query Match	Similarity	96.5%	Score	535.6	DB	13	Length	767
Best Local	Similarity	99.1%	Pred	No.3	8e-132			
Matches	549	Conservative	0	Mismatches	4	Indels	1	Gaps
QY	3	GGGGCCCCGGCCACAGGGGGCAGCTCGTAGCCCCACAGGTGTGACTGTCGGCGGACTTTC	CA	62				
DB	96	GGGGCCCCGGTCCACAGGGGGCCAGCTGTAGCCCCACAGGTGTGACTGTCGGCGGACTTTC	CA	155				
QY	63	CAAGAAGATTGTCCTGTTTTCAGAGAGGCTGCCAGC-GGGGCACTACCTGAAAGCCCC		121				
DB	156	CAGAAGATTGTCCTGTTTTCAGAGAGGCTGCCAGCTGGGGGCACTACCTGAAAGCCCC		215				
QY	122	CTTGACGGAGGCCGCGGCACTCACCTGCCTGTGTGTCCCAAGACACTTCTTGG		181				
DB	216	CTTGACGGAGGCCCTGCGGCACTCACCTGCCTGTGTGTCCCAAGACACTTCTTGG		275				

QY	182	CCTGGGAAACACCATTAATTCGAATGTGCGCCGTGCAGGCGTGTATGAGCAGGCGCT	241
Db	276	CCTGGGAAACACCATTAATTCGAATGTGCGCCGTGCAGGCGTGTATGAGCAGGCGCT	335
QY	242	CCCAAGTGGCGCTGGAGAACTGTTTCAGCAGTGGCGGCAGACCCCGCTGTGGCTGTAAAGCCAG	301
Db	336	CCCAAGTGGCGCTGGAGAACTGTTTCAGCAGTGGCGGCAGACCCCGCTGTGGCTGTAAAGCCAG	395
QY	302	GCTGGTTTGTGGAGTGCACAGGTCAACCAATGTGTAGCAGTTCAACCTTTCTACTGCCAAC	361
Db	396	GCTGGTTTGTGGAGTGCACAGGTCAACCAATGTGTAGCAGTTCAACCTTTCTACTGCCAAC	455
QY	362	CATGGCTTAGACCTGGCGGGGCCCTGCACCCGACACACAGGCTACTGTTTCCGAGAGATA	421
Db	456	CATGGCTTAGACCTGGCGGGGCCCTGCACCCGACACACAGGCTACTGTTTCCGAGAGATA	515
QY	422	CTGACTGTGGAGACCTGCCTGCCTTGACTTCTATGAACATGGGATGGCTGCCTGCTCC	481
Db	516	CTGACTGTGGAGACCTGCCTGCCTTGACTTCTATGAACATGGGATGGCTGCCTGCTCC	575
QY	482	CCACGAGACACCTGGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGGAGGACAGA	541
Db	576	CCACGAGACACCTGGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGGAGGACAGA	635
QY	542	TGTTCTGGGTCGAG	555
Db	636	TGTTCTGGGTCGAG	649

RESULT 4	688 bp	mRNA	linear	EST 30-MAR-1999
AI124936	tg19b08.x1	NCI CGAP CLL1	Homo sapiens	cDNA clone IMAGE:2109207.3
LOCUS	similar to TR:000276	000276	LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH	
DEFINITION	2 ; mRNA sequence.			
ACCESSION	AI124936			
VERSION	AI124936.1	GI:4270854		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 688)	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap .		
		National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
		Tumor Gene Index		
		Unpublished (1997)		
		Contact: Robert Strausberg, Ph.D.		
		Email: cgapb-remail.nih.gov		
		Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,		
		M.D., Louis M. Staudt, M.D., Ph.D.		
		CDNA Library Preparation: M. Bento Soares, Ph.D.		
		CDNA Library Arrayed by: Greg Lennon, Ph.D.		
		DNA Sequencing by: Washington University Genome Sequencing Center		
		Clone distribution: NCI-CGAP clone distribution information can be		
		found through the I.M.A.G.E. Consortium/URL at:		
		www-bio.llnl.gov/bhrp/image/image.html		
		Insert Length: 2028 Std Error: 0.00		
		Seq primer: -40UP from GIDCO		
		High quality sequence stop: 445.		
FEATURES	source	location/Qualifiers		
		1..688		

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2109207"
/clone_id="NCL CGAP CLL1"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH108"
/note="vector: pR73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dt) primer [5',
TGGTACCAATCTGTGAAGTGGAGCGCGCCGACATGCTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI

```

adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento

BASE COUNT	113 a	208 c	229 g	138 t
ORIGIN				

Query Match	533	DB 9	length 688
Best Local Similarity	98.2%	Pred. No.	1.7e-131
Matches 539	Conservative	0	Mismatches 10; Indels 0; Gaps 0;

QY	1	CTGGGGGGCCCCGGCCAGGGGGGGGCACTGCTGACCCAGGTGTGACGTGGCCGGTACATTC	60
Db	50	CTGGGGGGCCCCGGGGGGGGGGGGGCACTGCTGACCCAGGTGTGACGTGGCCGGTACATTC	109
QY	61	CACAAGAAAGATTGTCTGTTGTTTGTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAAGGC	120
Db	110	CACAAGAAAGATTGTCTGTTGTTTGTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAAGGC	169
QY	121	CCTTGCACGGAGCCCTTGGCGGCACTGCACCTGCTTTGTGTGTGCCAAGACACCTTCTTG	180
Db	170	CCTTGCACGGAGCCCTTGGCGGCACTGCACCTGCTTTGTGTGTGCCAAGACACCTTCTTG	229
QY	181	GCCTGGGAAGAACCCACCATTAATCTGAATGTGCCCGCTGCCAGAGCCGTGATAGCAGGCG	240
Db	230	GCCTGGGAAGAACCCACCATTAATCTGAATGTGCCCGCTGCCAGAGCCGTGATAGCAGGCG	289
QY	241	TCCCAGAGTGGCGGTGAGAACTGTTAGCAGAGTGGCCGACACCGCGCTGTGGCTGAAGCCA	300
Db	290	TCCCAGAGTGGCGGTGAGAACTGTTAGCAGAGTGGCCGACACCGCGCTGTGGCTGAAGCCA	349
QY	301	GGCTGGTTTTGTGGAGTGCACAGGTCAAGCCAAATGTTGACGACATTTACCTTTACTGCCAA	360
Db	350	GGCTGGTTTTGTGGAGTGCACAGGTCAAGCCAAATGTTGACGACATTTACCTTTACTGCCAA	409
QY	361	CCATGGCTTAGACTGCGGGGGCCCTGCACCGCCCAACACAGGCTACTGTGTTCCCGCAGAGAT	420
Db	410	CCATGGCTTAGACTGCGGGGGCCCTGCACCGCCCAACACAGGCTACTGTGTTCCCGCAGAGAT	469
QY	421	ACTGACTGTGGGACTGCTGCTGCTGACTTATGAACATGGCGATGGCTGCGTGTCTGC	480
Db	470	ACTGACTGTGGGACTGCTGCTGCTGACTTATGAACATGGCGATGGCTGCGTGTCTGC	529
QY	481	CCCAAGAGACACCTTGGGGAGCTGTCCAGAGCGCTGTGCCGTCTCTGTGGCTGGAGGCA	540
Db	530	CCCAAGAGACACCTTGGGGAGCTGTCCAGAGCGCTGTGCCGTCTCTGTGGCTGGAGGCA	589
QY	541	ATGTTCTGG 549	
Db	590	AGTAAGTGG 598	

RESULT 5
A1140043

IMAGE:1693710 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECURSOR ;, mRNA sequence.

ACCESSION	AI140043	GI:36475000
VERSION	AI140043.1	
KEYWORDS	EST.	
SOURCE	human.	

ORGANISM

REFERENCE
AUTHORS
Mukherjya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 562)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE	Author	Journal	Year
National Cancer Institute			
Tumor Gene Index			
Transcribed (1987)			

JOURNAL
unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.lnl.gov) for further information
Insert Length: 1640 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 494.

FEATURES	Location/Qualifiers
source	1. .562

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/organism="Homo sapiens"  
/db_xref="taxon:9606"  
/clone="IMAGE:1693710"  
/clone_lib="Scars_fetal_heart_NbNH19W"  
/sex="unknown"
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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: heart; Vector: pF713D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
TGTTCACATCTGTAAGGAGGAGCGCCGACATCTTTTTTTTTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pF713 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHL19W."
BASE COUNT      88 a      182 c      180 g      111 t      1 others
ORIGIN

```

Query Match	92.3%	Score 512	DB 9	length 563
Best Local Similarity	99.8%	Pred. No.	6.2e-126	
Matches 512; Conservative	0	Mismatches	1	Indels 0; Gaps 0

QY	1	CTGGGGGCCCGGGCCAGAGGGGGCACTGTATGCCAGGTGTGACTGTGGCGGTACTTC	60
Db	50	CTGGGGGGCCCCGGGCCAGAGGGGGCACTGTATGCCAGGTGTGACTGTGGCGGTACTTC	109
QY	61	CACAAAGAAATTGGTCTGTGTTTGTGGAGAGGCTGCCAGCGGGGCACTACCTGAAAGGC	120
Db	110	CACAAAGAAATTGGTCTGTGTTTGTGGAGAGGCTGCCAGCGGGGCACTACCTGAAAGGC	169
QY	121	CCATTGACGAGACCCCTGGCGGCACTGCACCTGCTTGTGTGCCAAGACACTTCTTG	180
Db	170	CCATTGACGAGACCCCTGGCGGCACTGCACCTGCTTGTGTGCCAAGACACTTCTTG	229
QY	181	GCCTTGGAGAAACCAACCATATTTCTGAATTTGCCCGTGGCAGAGCCCTGTATAGCAGGCG	240
Db	230	GCCTTGGAGAAACCAACCATATTTCTGAATTTGCCCGTGGCAGAGCCCTGTATAGCAGGCG	289
QY	241	TCCCAAGTGGGCGCTGGAGAACTGTTACGAGAGTGGCCGACACCGCGCTGTGGCTGAAGCA	300
Db	290	TCCCAAGTGGGCGCTGGAGAACTGTTACGAGAGTGGCCGACACCGCGCTGTGGCTGAAGCA	349
QY	301	GGCTGTTTGTGGAGTGGCCAGGTGCACCCAAATGTGCAGCAGTTTACCCCTTACTGCCAA	360
Db	350	GGCTGTTTGTGGAGTGGCCAGGTGCACCCAAATGTGCAGCAGTTTACCCCTTACTGCCAA	409
QY	361	CCATGCGTATGACTGGGGGGCCCTGCACCGCCACACAGGCTACTCTGTTTCCCGAAGAT	420
Db	410	CCATGCGTATGACTGGGGGGCCCTGCACCGCCACACAGGCTACTCTGTTTCCCGAAGAT	469
QY	421	ACTGAACTGGGAAACCTGGCTGGCTGGCTTCTAATGAACATGGGAGTGGCGGTGCTCG	480
Db	470	ACTGAACTGGGAAACCTGGCTGGCTGGCTTCTAATGAACATGGGAGTGGCGGTGCTCG	529
QY	481	CCCAAGACACCTGGGGAGCTGCCAGAGCG	513
Db	530	CCCAAGACACCTGGGGAGCTGCCAGAGCG	562

RESULT 6					
BM783972					
LOCUS	552 bp	mRNA	linear	EST 05-MAR-2002	
DEFINITION	K-EST0062019	S6SNU620	Homo sapiens cDNA clone S6SNU620-31-H06 5'		

ACCESSION	BM783972	mrna sequence.
VERSION	BM783972.1	GI:19132204
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
AUTHORS	1 (bases 1 to 552)	
	Kim,M.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.	
	Oh,K.Y., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and	
	Kim,Y.S.	
TITLE	21C Frontier Korean EST Project 2001	
JOURNAL	Unpublished (2002)	
COMMENT	Contact: Kim YS	
	Genome Research Center	
	Korea Research Institute of Bioscience & Biotechnology	
	52 Eoeun-Gong Yuseong-gu, Daejeon 305-333, South Korea	
	Tel: +82-42-860-4470	
	Fax: +82-42-860-4409	
	Email: yongsungemail.kr@kribb.re.kr	
	Plate: 31 row: H column: 06	
	High quality sequence stop: 552.	
FEATURES	Location/Qualifiers	

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FEATURES
SOURCE
    location/Qualifiers
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            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="S6SN0620-31-H06"
            /clone_id="S6SN0620"
            /sex="F"
            /tissue_type="Asclites"
            /cell_type="Scattering floating"
            /cell_line="SNU-620"
            /lab_host="Top10F"
            /note="Organ: Stomach; Vector: pCNS; Site:1: EcoRI;
            Site:2: NotI; The poly (A)+ RNA was dephosphorylated with
            bacterial alkaline phosphatase (BAP) and then deprotected
            with tobacco acid pyrophosphatase (TAP). The deprotected
            intact mRNA was ligated with DNA-RNA linker including EcoRI
            I site by treatment of T4 RNA ligase and the first strand
            cDNA was synthesized from oligo dt-selected mRNA by
            priming with dt-tailed vector. The dt-tailed vector was
            adjusted to have about 60nt. The cDNA vector was
            circularized with E. coli DNA ligase after digestion of
            EcoRI which site is also included in vector. An RNA strand
            converted to a DNA strand by Okayama-Berg method. The
            obtained cDNA vectors were used for transformation of
            competent cells E. coli Top10F by electroporation method.
            The cDNA libraries constructed by this method are
            full-length enriched cDNA library."
2 a 172 c 173 g 115 t

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Query Match	87.68;	Score 486.4;	DB 14;	Length 552;
Best Local Similarity	98.88;	Pred. No. 4.2e-119;		
Matches 490;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;

QY	1	CTGGGGGCGCGGGCCAGAGGGCGGACCTGTAGGCCCGAGGTGTACACTGTGCGGGTGAATTTC	60
Db	23	CTGGGGGCGCGGGCCAGAGGGCGGACCTGTAGGCCCGAGGTGTACACTGTGCGGGTGAATTTC	82
QY	61	CACAAGAGATTGGTCTGTTTGTGTTCAGAGAGGCTGCCACCGGGGCACTACCTCGAAGAGCC	120
Db	83	CACAAGAGATTGGTCTGTTTGTGTTCAGAGAGGCTGCCACCGGGGCACTACCTCGAAGAGCC	142
QY	121	CCTTTCACGAGAGCCCTCGGGCAATCCACACTGCCCTTGTGTGTCCGCCAAGACACTTCTTTG	180
Db	143	CCTTTCACGAGAGCCCTCGGGCAATCCACACTGCCCTTGTGTGTCCGCCAAGACACTTCTTTG	202
QY	181	GCGTCGGAGAACCAACATTAATTCTGATGATGTGCCGGCGCCAGGCGTGTGATGAGCAGGCC	240
Db	203	GCGTCGGAGAACCAACATTAATTCTGATGATGTGCCGGCGCCAGGCGTGTGATGAGCAGGCC	262

Oy	241	TCCAGGATGGGCGTGGAGAACTGTTACAGAGTGGCCGACACCCGCTGGCTGTAAAGCA	300
Dd	263	TCCAGATGGGCGCTGGAGAACTGTTACAGACTGGCCGACACCCGCTGGCTGTAAAGCA	322
Oy	301	GCGTGGTTTGTGTGGAGTGCAGAGTCAGCCAAATGTGTACAGATTCACCTTCTACTGCCAA	360
Dd	323	GCGTGGTTTGTGTGGAGTGCAGAGTCAGCCAAATGTGTACAGATTCACCTTCTACTGCCAA	382
Oy	361	CCATGCTTAGACTGCGGGGGCCCTGCACCGGCACACAGGGCTACTCTGTCCGACAGAT	420
Dd	383	CCATGCTTAGACTGCGGGGGCCCTGCACCGGCACACAGGGCTACTCTGTCCGACAGAT	442
Oy	421	ACTGACTGTGGAGACTGCGCTGCCTGTGTATGAAACATGGCGATGGCTGCTGCTCG	480
Dd	443	ACTGACTGTGGAGACTGCGCTGCCTGTGTATGAAACATGGCGATGGCTGCTGCTCG	502
Oy	481	CCGACGAGACCCCTGG	496
Dd	503	CCGACGATATTCCTAG	518

RESULT 7	LOCUS	DEFINITION
AM517358	585 bp	linear
AM517358	mp3q92.x1 Soares_NHCE cervix Homo sapiens CDNA IMAGE:27479954	EST 03-MAR-2000
	3' similar to TR:000276 000276 LYMPHOCYTE ASSOCIATED RECEPTOR OF	
	DEATH 2. ;, mRNA sequence.	

ACCESSION	AW517358	
VERSION	AW517358.1	GI:7155440
KEYWORDS	EST.	
SOURCE	human.	

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 585)
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 489.

FEATURES	Location/Qualifiers
source	1. .585

BASE COUNT
ORIGIN

94 a 181 c 193 g 117 t

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1fb="IMAGE:2747934"
/clone_1lb="Soares_NHCE_cervix"
/lab_host="DH10B (phage-resistant)"
/note="Organ: cervix; Vector: pF73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGGAGCGCGGCGCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pF73 vector.
Library is normalized; constructed by Bento Soares and
M.Felina Bonaldo."
```

Query Match	87.6%	Score 486.4	DB 10	Length 585
Best Local Similarity	98.8%	Pred. No. 4.3e-119		
Matches 490; Conservative	0	Mismatches 6	Indels 0	Gaps 0

OY 1 CTGGGCCCCCGGCCAGGCGGCACATCTGTAGCCCAAGTGTACTGTGCCGGTGAATTTC 60
 |||||||
D8 50 CTGGGCCCCCGGCCAGGCGGCACATCTGTAGCCCAAGTGTACTGTGCCGGTGAATTTC 109

QY 61 CACAAGAGATTGTCCTGTTTGTGTCAGAGGCTCCAGCGGGGCACTACCTGAAGGCC 120
 Db 110 CACAAGAGATTGTCCTGTTTGTGTCAGAGGCTCCAGCGGGGCACTACCTGAAGGCC 169
 QY 121 CCTTGACAGGAGCCCTGGGGCACTCCACCTGCTTGTGTGTGCCAAGACACTTTTG 180
 Db 170 CCTTGACAGGAGCCCTGGGGCACTCCACCTGCTTGTGTGTGCCAAGACACTTTTG 229
 QY 181 GCTTGAGAGAACCCATTAATCTGAATGTGCCCTGACAGGCTGTGATGAGAGGCC 240
 Db 230 GCTTGAGAGAACCCATTAATCTGAATGTGCCCTGACAGGCTGTGATGAGAGGCC 289
 QY 241 TCCAGAGTGGGCTGGAGAACTGTCACAGTGGCCGACACCCGCTGTGCTGAAGCCA 300
 Db 290 TCCAGAGTGGGCTGGAGAACTGTCACAGTGGCCGACACCCGCTGTGCTGAAGCCA 349
 QY 301 GCTTGAGTGTGAGTGCAGAGTGCAGCAATGTGCACAGTTCACCTTACAGCCAA 360
 Db 350 GCTTGAGTGTGAGTGCAGAGTGCAGCAATGTGCACAGTTCACCTTACAGCCAA 409
 QY 361 CCATGCTAGACTGCGGGGCTGCGACCGCCACACAGGCTACTGTTCCCGCAGAGAT 420
 Db 410 CCATGCTAGACTGCGGGGCTGCGACCGCCACACAGGCTACTGTTCCCGCAGAGAT 469
 QY 421 ACTGACTGTGGACCTGCTGCTGCTTCTATGAAACATGGCGATGGCTGCTGCTGC 480
 Db 470 ACTGACTGTGGACCTGCTGCTGCTTCTATGAAACATGGCGATGGCTGCTGCTGC 529
 QY 481 CCCAGAGACCCCTGG 496
 Db 530 CCCAGTAACTTCTGAG 545

RESULT 8
 BM756372 514 bp mRNA linear EST_04-MAR-2002
 LOCUS K-EST0034666 S6SNU620 Homo sapiens cDNA clone S6SNU620-27-G03 5'
 DEFINITION mRNA sequence.
 ACCESSION BM756372
 VERSION BM756372.1 GI:19085987
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 514)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 TITLE Unpublished (2002)
 JOURNAL Contact: Kim YS
 COMMENT Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@kribb.re.kr
 Plate: 27 row: G column: 03
 High quality sequence stop: 514.
 FEATURES
 Location/Qualifiers
 1..514
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="S6SNU620-27-G03"
 /clone_lib="S6SNU620"
 /sex="F"
 /tissue_type="Ascites"
 /cell_type="Scattering floating"
 /cell_line="SNU-620"
 /lab_host="Top10F"
 /note="Organ: Stomach; Vector: pcMS; Site:1: EcoRI;

QY 61 CACAAGAGATTGTCCTGTTTGTGTCAGAGGCTCCAGCGGGGCACTACCTGAAGGCC 120
 Db 110 CACAAGAGATTGTCCTGTTTGTGTCAGAGGCTCCAGCGGGGCACTACCTGAAGGCC 169
 QY 121 CCTTGACAGGAGCCCTGGGGCACTCCACCTGCTTGTGTGTGCCAAGACACTTTTG 180
 Db 170 CCTTGACAGGAGCCCTGGGGCACTCCACCTGCTTGTGTGTGCCAAGACACTTTTG 229
 QY 181 GCTTGAGAGAACCCATTAATCTGAATGTGCCCTGACAGGCTGTGATGAGAGGCC 240
 Db 230 GCTTGAGAGAACCCATTAATCTGAATGTGCCCTGACAGGCTGTGATGAGAGGCC 289
 QY 241 TCCAGAGTGGGCTGGAGAACTGTCACAGTGGCCGACACCCGCTGTGCTGAAGCCA 300
 Db 290 TCCAGAGTGGGCTGGAGAACTGTCACAGTGGCCGACACCCGCTGTGCTGAAGCCA 349
 QY 301 GCTTGAGTGTGAGTGCAGAGTGCAGCAATGTGCACAGTTCACCTTACAGCCAA 360
 Db 350 GCTTGAGTGTGAGTGCAGAGTGCAGCAATGTGCACAGTTCACCTTACAGCCAA 409
 QY 361 CCATGCTAGACTGCGGGGCTGCGACCGCCACACAGGCTACTGTTCCCGCAGAGAT 420
 Db 410 CCATGCTAGACTGCGGGGCTGCGACCGCCACACAGGCTACTGTTCCCGCAGAGAT 469
 QY 421 ACTGACTGTGGACCTGCTGCTGCTTCTATGAAACATGGCGATGGCTGCTGCTGC 480
 Db 470 ACTGACTGTGGACCTGCTGCTGCTTCTATGAAACATGGCGATGGCTGCTGCTGC 529
 QY 481 CCCAGAGACCCCTGG 496
 Db 530 CCCAGTAACTTCTGAG 545

Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 86 a 166 c 153 g 109 t
 ORIGIN
 Query Match 87.6%; Score 486; DB 14; Length 514;
 Best Local Similarity 100.0%; Pred. No. 5,1e-119;
 Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGGGGCGGGGCGCCAGGCGGCACTGTGAGCCAGGTGACTGTGCGGTGATTC 60
 Db 23 CTGGGGGCGGGGCGCCAGGCGGCACTGTGAGCCAGGTGACTGTGCGGTGATTC 82
 QY 61 CACAAGAGATTGTCCTGTTTGTGTCAGAGGCTCCAGCGGGGCACTACCTGAAGGCC 120
 Db 83 CACAAGAGATTGTCCTGTTTGTGTCAGAGGCTCCAGCGGGGCACTACCTGAAGGCC 142
 QY 121 CCTTGACAGGAGCCCTGGGGCACTCCACCTGCTTGTGTGTGCCAAGACACTTTTG 180
 Db 143 CCTTGACAGGAGCCCTGGGGCACTCCACCTGCTTGTGTGTGCCAAGACACTTTTG 202
 QY 181 GCTTGAGAGAACCCATTAATCTGAATGTGCCCTGACAGGCTGTGATGAGAGGCC 240
 Db 203 GCTTGAGAGAACCCATTAATCTGAATGTGCCCTGACAGGCTGTGATGAGAGGCC 262
 QY 241 TCCAGAGTGGGCTGGAGAACTGTCACAGTGGCCGACACCCGCTGTGCTGAAGCCA 300
 Db 263 TCCAGAGTGGGCTGGAGAACTGTCACAGTGGCCGACACCCGCTGTGCTGAAGCCA 322
 QY 301 GCTTGAGTGTGAGTGCAGAGTGCAGCAATGTGCACAGTTCACCTTACAGCCAA 360
 Db 333 GCTTGAGTGTGAGTGCAGAGTGCAGCAATGTGCACAGTTCACCTTACAGCCAA 382
 QY 361 CCATGCTAGACTGCGGGGCTGCGACCGCCACACAGGCTACTGTTCCCGCAGAGAT 420
 Db 383 CCATGCTAGACTGCGGGGCTGCGACCGCCACACAGGCTACTGTTCCCGCAGAGAT 442
 QY 421 ACTGACTGTGGACCTGCTGCTGCTTCTATGAAACATGGCGATGGCTGCTGCTGC 480
 Db 443 ACTGACTGTGGACCTGCTGCTGCTTCTATGAAACATGGCGATGGCTGCTGCTGC 502
 QY 481 CCCAGC 486
 Db 503 CCCAGC 508

RESULT 9
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 LOCUS K-EST0062030 S6SNU620 Homo sapiens cDNA clone S6SNU620-32-A05 5'
 DEFINITION mRNA sequence.
 ACCESSION BM783979
 VERSION BM783979.1 GI:19132211
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 514)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,


```

|||||
Db 23 CTGGGGCCCCGGCCAGTGGCGGCACTGTGTAACCCAGAGTGTGACTGTGCCGTACTTC 82
QY 61 CACAAGAAATTTGTCCTGTTTGTTCAGAGGCTCCAGCGGGGCACTACTGAAGGCC 120
Db 83 CACAAGAAATTTGTCCTGTTTGTTCAGAGGCTCCAGCGGGGCACTACTGAAGGCC 142
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QY 181 GCGTGGAGAACACCAATTAATCTGAATGTGCCCTGCCAGAGCCCTGTGATGAGAGGCC 240
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QY 301 GCGTGGTGTGGAGTGGCCAGGTGACGCCAATGTGTCAGAGTTCACCCCTTCTACTGCCAA 360
Db 323 GCGTGGTGTGGAGTGGCCAGGTGACGCCAATGTGTCAGAGTTCACCCCTTCTACTGCCAA 382
QY 361 CCATGCTAGACTGGCGGGCCCTGCAACGCCACACAGGCTACTGTTCGCCAGAGAT 420
Db 383 CCATGCTAGACTGGCGGGCCCTGCAACGCCACACAGGCTACTGTTCGCCAGAGAT 442
QY 421 ACTGACTGTGGAGACCTGCTGCTGCTTCTATGAACATGGGAGTGGCTGTCCCTGC 480
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QY 481 CCCAGCAGCACCCCTGG 496
Db 503 CCCAGCTAATTCCTAG 518

RESULT 11
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LOCUS ge7f02.x1 Soares fetal_lung_NBHL19W Homo sapiens cDNA clone
DEFINITION IMAGE:1744827, 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECUSOR ; mRNA sequence.
ACCESSION AI203624
VERSION AI203624.1 GI:3756230
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 508)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1699 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 442.
Location/Qualifiers
1. 508
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1744827"
/clone_1lb="Soares_fetal_lung_NBHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/Note="Organ: Lung; Vector: pT73D (Pharmacia) with a
modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTCAAGTGGAGCGGCCCAATTTTTTTTTTTTTTTT-3']"
```

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double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NBHL19W."

BASE COUNT      82 a      161 c      159 g      106 t

Query Match      85.9%; Score 477; DB 9; Length 508;
Best Local Similarity 100.0%; Pred. No. 1,3e-116;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CACAAGAAATTTGTCCTGTTTGTTCAGAGGCTCCAGCGGGGCACTACTGAAGGCC 120
Db 92 CACAAGAAATTTGTCCTGTTTGTTCAGAGGCTCCAGCGGGGCACTACTGAAGGCC 151
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Db 152 CCTTCAGAGGAGCCCTGGGCGCACTCCAGCTCCCTGTGTGTGCCAAGACCTTCTTG 211
QY 181 GCGTGGAGAACACCAATTAATCTGAATGTGCCGCTGCCAGAGCCCTGTGATGAGAGGCC 240
Db 212 GCGTGGAGAACACCAATTAATCTGAATGTGCCGCTGCCAGAGCCCTGTGATGAGAGGCC 271
QY 241 TCCCAAGTGGCGCTGGAGAACTGTTCAGAGTGGCCGACACCCGCTGTGSGCTTAAGCA 300
Db 272 TCCCAAGTGGCGCTGGAGAACTGTTCAGAGTGGCCGACACCCGCTGTGSGCTTAAGCA 331
QY 301 GCGTGGTGTGGAGTGGCCAGGTGACGCCAATGTGTCAGAGTTCACCCCTTCTACTGCCAA 360
Db 332 GCGTGGTGTGGAGTGGCCAGGTGACGCCAATGTGTCAGAGTTCACCCCTTCTACTGCCAA 391
QY 361 CCATGCTAGACTGGCGGGCCCTGCAACGCCACACAGGCTACTGTTCGCCAGAGAT 420
Db 392 CCATGCTAGACTGGCGGGCCCTGCAACGCCACACAGGCTACTGTTCGCCAGAGAT 451
QY 421 ACTGACTGTGGAGACCTGCTGCTGCTTCTATGAACATGGGAGTGGCTGTCCCTGC 477
Db 452 ACTGACTGTGGAGACCTGCTGCTGCTTCTATGAACATGGGAGTGGCTGTCCCTGC 508

RESULT 12
BM741016 492 bp mRNA linear EST 01-MAR-2002
LOCUS K-EST0013376 S6SNU620 Homo sapiens cDNA clone S6SNU620-2-C03 5',
DEFINITION mRNA sequence.
ACCESSION BM741016
VERSION BM741016.1 GI:19062345
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 492)
Oh,K.J., Cheong,J.E., Sohn,H.Y., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Kim,Y.S.,
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong, Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: Yongsung@mail.kribb.re.kr
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GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 6, 2003, 15:03:59 ; Search time 111 Seconds
(without alignments)
4385.839 Million cell updates/sec

Title: US-09-993-234-9_COPY_146_700

Perfect score: 555
Sequence: 1 CCGGGGGCCCCGGCCAGGG.....GGCAGATGTTGTCGACAG 555

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 593429 segs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA.*

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	100.0	1254	10	US-09-333-966-3
2	555	100.0	1634	9	US-10-081-280-9
3	555	100.0	1634	9	US-10-112-793-9
4	555	100.0	1634	9	US-10-112-793-11
5	555	100.0	1634	10	US-09-993-234-9
6	555	100.0	1783	10	US-09-333-966-1
7	541	97.5	1743	9	US-09-954-531-1369
8	486.4	87.6	816	10	US-09-964-824A-292
9	486.4	87.6	1438	9	US-10-081-280-5
10	486.4	87.6	1438	9	US-10-112-793-5
11	486.4	87.6	1438	9	US-10-112-193-5
12	486.4	87.6	1438	10	US-09-884-733-5
13	486.4	87.6	1438	10	US-09-993-234-5
14	350.6	63.2	433	9	US-10-081-280-2
15	350.6	63.2	433	9	US-10-112-793-2
16	350.6	63.2	433	9	US-10-112-193-2
17	350.6	63.2	433	10	US-09-884-733-2
18	350.6	63.2	433	10	US-09-993-234-2
19	171	30.8	10797	9	US-10-092-154-1577

20	171	30.8	10797	10	US-09-764-847-1577	Sequence 1577, Ap
21	55.4	10.0	346	10	US-09-783-590-1252	Sequence 1252, Ap
22	42.2	7.6	543	10	US-09-970-532-3	Sequence 3, Appl1
23	42.2	7.6	2440	10	US-09-970-532-1	Sequence 1, Appl1
24	40.4	7.3	671	9	US-10-184-644-346	Sequence 346, Appl
25	38	6.8	2130	10	US-09-917-800A-1601	Sequence 1601, Ap
26	37.4	6.7	5870	10	US-09-838-718A-8	Sequence 8, Appl1
27	36.4	6.6	301	9	US-10-070-676-7	Sequence 7, Appl1
28	35	6.3	1345	9	US-09-853-450-7	Sequence 7, Appl1
29	34.8	6.3	2173	9	US-09-898-234-14	Sequence 14, Appl1
30	34.8	6.3	2173	9	US-09-899-429A-24	Sequence 24, Appl
31	34.8	6.3	2173	9	US-09-792-356-14	Sequence 14, Appl
32	34.8	6.3	2173	10	US-09-899-422-14	Sequence 14, Appl
33	34.8	6.3	4898	10	US-09-919-497-35	Sequence 35, Appl
34	34.8	6.3	4898	10	US-09-880-107-2323	Sequence 2323, Ap
35	34.8	6.3	5988	12	US-10-044-090-90	Sequence 90, Appl
36	34.6	6.2	20556	10	US-09-880-107-3945	Sequence 3945, Ap
37	34.4	6.2	886	10	US-09-884-441-22	Sequence 22, Appl
38	33.2	6.0	15340	9	US-09-999-121-12	Sequence 12, Appl
39	33.2	6.0	37113	9	US-09-999-121-11	Sequence 11, Appl
40	33.2	6.0	155074	9	US-10-026-188-6	Sequence 6, Appl1
41	32	5.8	1780	10	US-09-917-800A-1521	Sequence 1521, Ap
42	31.6	5.7	299	10	US-09-864-761-25435	Sequence 25435, A
43	31.6	5.7	518	10	US-09-864-761-8725	Sequence 8725, Ap
44	31.6	5.7	746	10	US-09-910-943-165	Sequence 165, App
45	31.6	5.7	1801	10	US-09-822-830A-128	Sequence 128, App

ALIGNMENTS

RESULT 1
US-09-333-966-3
Sequence 3, Application US/09333966
Patent No. US2002000973A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
APPLICATION NUMBER: NO. US2002000973A1 yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688

```

? REFERENCE/DOCKET NUMBER: 1488..0310003/ERS/KR
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-371-2600
? TELEFAX: 202-371-2540
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1254 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: both
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1251
? US-09-333-966-3

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Query Match	100.0%;	Score 555;	DB 10;	Length 1254;
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Matches 555; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

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Db	178	CCTTGACAGGAGACCTTGCGGCAATCCACCTGCTTGTGTGTGCCCAAGACACCTTCTTG	237
QY	181	GCCCTGGGAACACACATTAATTTGTGAATGTGGCCCGTGGCAGGCGCTGTATAGCAGGCC	240
Db	238	GCCCTGGGAACACACATTAATTTGTGAATGTGGCCCGTGGCAGGCGCTGTATAGCAGGCC	297
QY	241	TCCCAAGTGGCGCTGGAGAACTGTTACAGCAGTGGCGGACACCCGCTGTGGCTGTAAAGCA	300
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QY	361	CCATGCTTAGACATGGGGGGCCCTGCACCGGCCACACAGGCTACTGTTCCCGCGAGAGAT	420
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QY	481	CCCACGACACCCCTTGGGAGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGTGGCTGGAAGGAG	540
Db	538	CCCACGACACCCCTTGGGAGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGTGGCTGGAAGGAG	597
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RESULT 2 -
US-10-081-280-9
Sequence 9, Application US/10081280
Patent No. US20020165157A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatla (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: Maerschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-081-280-9

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; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
HS-10-081-380-0

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Best Local Similarity	100.08;	Prod No. 3	2e-161	

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Db	266	CTTTGCACGGAGCCCTCGGCACTCCACACTGCTTGTGTGCCCAAGACACCTTTCTTG	325
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QY	301	GCGTGTGTTTGTGAGTGTCCAGAGTCAGCAATGTGTACAGCATTCACCTTCTACTGTCCAA	360
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QY	361	CCATGCTTAAGACTTGCGGGGCCCTGTACACCGGCACACAGGGTACTCTGTTCCGCGAGAT	420
Db	506	CCATGCTTAAGACTTGCGGGGCCCTGTACACCGGCACACAGGGTACTCTGTTCCGCGAGAT	565
QY	421	ACGAGCTGTGGGACGTCCCGGCTTGTATGAACATGGCGATGGCTCGGTCTCTGC	480
Db	566	ACGAGCTGTGGGACGTCCCGGCTTGTATGAACATGGCGATGGCTCGGTCTCTGC	625
QY	481	CCCAAGAGCAACCTGGGGAGCTGTCCAGAGACGGCTGTCGCGCTGTGTGGCTGGAGGCAAG	540
Db	626	CCCAAGAGCAACCTGGGGAGCTGTCCAGAGACGGCTGTCGCGCTGTGTGGCTGGAGGCAAG	685
QY	541	ATGTTCTTGGGTCCAG	555

Db	146	CTGGGGGGCCCCGGCCAGGGGGGCGACTGCTAGCCCGACAGGTGTGACTGTGCGGGACTTC	205
Qy	61	CACAGGAAGATGTGTCTTTTGTGTGCAGAGGCTGCCAGGGGGCACTACCTAGAGGCC	120
Db	206	CACAGGAAGATGTGTCTTTTGTGTGTGCAGAGGCTGCCAGGGGGCACTACCTAGAGGCC	265
Qy	121	CCCTTCACGAGGACCCCTGGGGCACTCCACCTCCCTTGTGTGTCCCAAGACACCTTTTG	180
Db	266	CCCTTCACGAGGACCCCTGGGGCACTCCACCTCCCTTGTGTGTCCCAAGACACCTTTTG	325
Qy	181	GGCTGGGGAACCCACCAATATTTCGAATGTCCCGGCTGCCAGGCTTGTATGAGCAGGCC	240
Db	326	GGCTGGGGAACCCACCAATATTTCGAATGTCCCGGCTGCCAGGCTTGTATGAGCAGGCC	385
Qy	241	TCCAGAGTGGGCGCTGGAGAACGTTCACAGCAGTGGCGCCACACCCGCTTGGCTGTAAAGCCA	300
Db	386	TCCAGAGTGGGCGCTGGAGAACGTTCACAGCAGTGGCGCCACACCCGCTTGGCTGTAAAGCCA	445
Qy	301	GGCTGTGTTGTGTGAATGCTCCAGAGTACGCCAATGTGTCCAGAGTTACCCCTTCTACTGCCAA	360
Db	446	GGCTGTGTTGTGTGAATGCTCCAGAGTACGCCAATGTGTCCAGAGTTACCCCTTCTACTGCCAA	505
Qy	361	CCATCGCTAGACTGGGGGGCCCTGCACCGGCACACAGGGCTACTGTCTGTCCCGACAGAT	420
Db	506	CCATCGCTAGACTGGGGGGCCCTGCACCGGCACACAGGGCTACTGTCTGTCCCGACAGAT	565
Qy	421	ACTGACTGTGGGACCTGCTGCTCCCTGCGCTTCTATGAACATGGCGATGGCTGCGTGTCTGC	480
Db	566	ACTGACTGTGGGACCTGCTGCTCCCTGCGCTTCTATGAACATGGCGATGGCTGCGTGTCTGC	625
Qy	481	CCACAGGACACCCCTGGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGGCTGTGAGCGCAG	540
Db	626	CCACAGGACACCCCTGGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGGCTGTGAGCGCAG	685
Qy	541	ATGTTCTGGGTCCAG 555	
Db	686	ATGTTCTGGGTCCAG 700	
RESULT 5			
US-09-993-234-9			
Sequence 9, Application US/09993234			
Patent No. US20020146768A1			
GENERAL INFORMATION:			
APPLICANT: Ashkenazi, Avi J.			
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES			
NUMBER OF SEQUENCES: 11			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Genentech, Inc.			
STREET: 460 Point San Bruno Blvd			
CITY: South San Francisco			
STATE: California			
COUNTRY: USA			
ZIP: 94080			
COMPUTER READABLE FORM:			
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Winpaten (Genentech)			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/993,234			
FILING DATE: 19-NO. US20020146768A1-2001			
CLASSIFICATION: <Unknown>			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 08/828,683			
FILING DATE: <Unknown>			
ATTORNEY/AGENT INFORMATION:			
NAME: Marschang, Diane L.			
REGISTRATION NUMBER: 35,600			
REFERENCE/DOCKET NUMBER: P1007P1			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 415/225-5416			

TELEFAX: 415/952-9881
TEL: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9
US-09-993-234-9

Query Match	100.0%	Score 555;	DB 10;	Length 1634;
Best Local Similarity	100.0%	Pred. NO. 3.2e-161;		
Matches 555; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	CTGGGGGCCCCGGCCCGAGGGGGGCACTGTAGGCCCAAGTGTGACTGTGCCGGTACTTC	60
Db	146	CTGGGGGGCCCCGGCCCGAGGGGGGCACTGTAGGCCCAAGTGTGACTGTGCCGGTACTTC	205
QY	61	CACAAGAAATATGTCTGTGTTTGTGGAGAGGCTGCCAGCGGGGGCACTATCTGAAGGCC	120
Db	206	CACAAGAAATATGTGTCTGTGTTTGTGGAGAGGCTGCCAGCGGGGGCACTATCTGAAGGCC	265
QY	121	CCCTTCACAGGAGCCCTGGGGCACTCCACCTGCTGTGTGTCTCCCAAGACACCTTTTG	180
Db	266	CCTTCACAGGAGCCCTGGGGCACTCCACCTGCTGTGTGTCTCCCAAGACACCTTTTG	325
QY	181	GCCTGGAGAAACACCAATTAATTCGATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC	240
Db	326	GCCTGGAGAAACACCAATTAATTCGATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC	385
QY	241	TCCCAAGTGGGGCGTGGAGAACTGTTCAGCAAGTGGCCGCAACCCGCTGTGGCTGTAAGCCA	300
Db	386	TCCCAAGTGGGGCGTGGAGAACTGTTCAGCAAGTGGCCGCAACCCGCTGTGGCTGTAAGCCA	445
QY	301	GGCTTGTTTGTGAGATGGTCCAGCAAGTACAGCAATGTGTACAGCAATCACCTTCCTACTGCA	360
Db	446	GGCTTGTTTGTGAGATGGTCCAGCAAGTACAGCAATGTGTACAGCAATCACCTTCCTACTGCA	505
QY	361	CCATGCTTGAAGTCTGGGGGGCTCTGCACCCGCAACACAGCGTACTCTGTCCCGCAAGAT	420
Db	506	CCATGCTTGAAGTCTGGGGGGCTCTGCACCCGCAACACAGCGTACTCTGTCCCGCAAGAT	565
QY	421	ACTGACTGTGGGACCTGCTGCTCCCTGCGCTTCATTAACATGCGCATGGCTGCGGTCTGAC	480
Db	566	ACTGACTGTGGGACCTGCTGCTCCCTGCGCTTCATTAACATGCGCATGGCTGCGGTCTGAC	625
QY	481	CCCACGAGCACCTTGGGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGGCTTGAGAGCAG	540
Db	626	CCCACGAGCACCTTGGGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGGCTTGAGAGCAG	685
QY	541	ATGTTCTGGGTCGAG 555	
Db	686	ATGTTCTGGGTCGAG 700	
RESULT 6			
US-09-333-966-1			
Sequence 1, Application US/09333966			
Patent No. US2002009773A1			
GENERAL INFORMATION:			
APPLICANT: Yu, Guo-Liang			
APPLICANT: NI, Jian			
APPLICANT: Dixit, Vishva			
APPLICANT: Gentz, Reiner L.			
APPLICANT: Dillon, Patrick J.			
TITLE OF INVENTION: Death Domain Containing Receptors			
NUMBER OF SEQUENCES: 17			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.			
STREET: 1100 New York Ave., Suite 600			
CITY: Washington			
STATE: DC			

COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
APPLICATION NUMBER: No. US20020009773A1 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 198..1481
US-09-333-966-1

Query Match 100.0%; Score 555; DB 10; Length 1783;
Best Local Similarity 100.0%; Pred. No. 3,2e-161;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGGCCCCGGGCCCCAGGCGGCACTCTAGAGCCCGAGGCTGACTGTGCGGCTGACTTC 60
DB 288 CTGGGGGGCCCCGGGCCCCAGGCGGCACTCTAGAGCCCGAGGCTGACTGTGCGGCTGACTTC 347
QY 61 CACAAGAAAGATTGCTGCTGTTTGTTCAGAGAGGCTGCGGCGGCGGCACTAGCTGAAGGCC 120
DB 348 CACAAGAAAGATTGCTGCTGTTTGTTCAGAGAGGCTGCGGCGGCGGCACTAGCTGAAGGCC 407
QY 121 CCTTGACGAGGAGCCCTGCGGCAACTCCACTCGCTTGTGTGTCCCAAGACACTCTTG 180
DB 408 CCTTGACGAGGAGCCCTGCGGCAACTCCACTCGCTTGTGTGTCCCAAGACACTCTTG 467
QY 181 GCGTGGGAGAACCAACCATATTTCTGAATGTGCCGCTGCGAGGCTGTGATGAGAGGCC 240
DB 468 GCGTGGGAGAACCAACCATATTTCTGAATGTGCCGCTGCGAGGCTGTGATGAGAGGCC 527
QY 241 TCCCAAGTGGCGCTGAGAACTGTTTCAGAGTGCGGAGACACCGCTGTGGCTGAAGCCA 300
DB 528 TCCCAAGTGGCGCTGAGAACTGTTTCAGAGTGCGGAGACACCGCTGTGGCTGAAGCCA 587
QY 301 GCGTGGTGTGTGAGAGTCCAGAGTCAAGCAATGTGTACAGCACTTACCCCTTACTGCCAA 360
DB 588 GCGTGGTGTGTGAGAGTCCAGAGTCAAGCAATGTGTACAGCACTTACCCCTTACTGCCAA 647
QY 361 CCATGCTAGACTGCGGGGCGCTGACCGGCAACACAGAGGCTACTGTGTTCCCGCAGAGAT 420
DB 648 CCATGCTAGACTGCGGGGCGCTGACCGGCAACACAGAGGCTACTGTGTTCCCGCAGAGAT 707

QY 421 ACTGACTGTGGAGCACTGCTGCTGCTGCTGTATGAAACATGAGGCACTGCTGCTGCTG 480
DB 708 ACTGACTGTGGAGCACTGCTGCTGCTGCTGTATGAAACATGAGGCACTGCTGCTGCTG 767
QY 481 CCCACAGACACCTGGGAGAGCTGTCCAGAGCGGTGTGCGGCTGTCTGTGCTGAGAGCAG 540
DB 768 CCCACAGACACCTGGGAGAGCTGTCCAGAGCGGTGTGCGGCTGTCTGTGCTGAGAGCAG 827
QY 541 ATGTTCTGGGTCCAG 555
DB 828 ATGTTCTGGGTCCAG 842

RESULT 7
US-09-954-531-1389
Sequence 1389, Application US/09954531
Patent No. US20020165180A1
GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
SOFTWARE: Patentln version 3.0
SEQ ID NO 1389
LENGTH: 1743
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-531-1389

Query Match 97.5%; Score 541; DB 9; Length 1743;
Best Local Similarity 99.1%; Pred. No. 6,5e-157;
Matches 544; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CTGGGGCCCCGGGCCCCAGGCGGCACTCTAGAGCCCGAGGCTGACTGTGCGGCTGACTTC 60
DB 126 CTGGGGGGCCCCGGGCCCCAGGCGGCACTCTAGAGCCCGAGGCTGACTGTGCGGCTGACTTC 185
QY 61 CACAAGAAAGATTGCTGCTGTTTGTTCAGAGAGGCTGCGGCGGCGGCACTAGCTGAAGGCC 120
DB 186 CACAAGAAAGATTGCTGCTGTTTGTTCAGAGAGGCTGCGGCGGCGGCACTAGCTGAAGGCC 245
QY 121 CCTTGACGAGGAGCCCTGCGGCAACTCCACTCGCTTGTGTGTCCCAAGACACTCTTG 180
DB 246 CCTTGACGAGGAGCCCTGCGGCAACTCCACTCGCTTGTGTGTCCCAAGACACTCTTG 305
QY 181 GCGTGGGAGAACCAACCATATTTCTGAATGTGCCGCTGCGAGGCTGTGATGAGAGGCC 240
DB 306 GCGTGGGAGAACCAACCATATTTCTGAATGTGCCGCTGCGAGGCTGTGATGAGAGGCC 365
QY 241 TCCCAAGTGGCGCTGAGAACTGTTTCAGAGTGCGGAGACACCGCTGTGGCTGAAGCCA 300
DB 366 TCCCAAGTGGCGCTGAGAACTGTTTCAGAGTGCGGAGACACCGCTGTGGCTGAAGCCA 425
QY 301 GCGTGGTGTGTGAGAGTCCAGAGTCAAGCAATGTGTACAGCACTTACCCCTTACTGCCAA 360
DB 426 GCGTGGTGTGTGAGAGTCCAGAGTCAAGCAATGTGTACAGCACTTACCCCTTACTGCCAA 485
QY 361 CCATGCTAGACTGCGGGGCGCTGACCGGCAACACAGAGGCTACTGTGTTCCCGCAGAGAT 420
DB 486 CCATGCTAGACTGCGGGGCGCTGACCGGCAACACAGAGGCTACTGTGTTCCCGCAGAGAT 545

QY	1	CTGGGGGCGGGGGCCAGGGGGGCGACCTGTAGCCCAAGGTGTACTGTGCGGGTACTT	60
Db	42	CTGGGGGGCCGGCCGACAGGGGGGACGTGTAGCCCAAGGTGTACTGTGCGGGTACTT	101
QY	61	CACAAGAAGATTGGTCTGTTTGTGTGAGAGGGCTGCCAGGGGGCACTACGTAAAGCC	120
Db	102	CACAAGAAGATTGGTCTGTTTGTGTGAGAGGGCTGCCAGGGGGCACTACCTGAAGGCC	161
QY	121	CTTTGCACGAGGCCCTGCGGCACTCCACCTGCTTGTGTGCCCAAGACACTTTCTTG	180
Db	162	CTTTGCACGAGGCCCTGCGGCACTCCACCTGCTTGTGTGCCCAAGACACTTTTGG	221
QY	181	GCGTGGGAGAAACCACTAATTTCGTGATGTGGCCGCTGCCAGGCTGTATGAGAGGCC	240
Db	222	GCGTGGGAGAAACCACTAATTTCGTGATGTGGCCGCTGCCAGGCTGTATGAGAGGCC	281
QY	241	TCCAGGTGGCGCGTGGAGAACTGTTCAGAGTGGGCCAACAACCGGTGTGGCTGTAAAGCA	300
Db	282	TCCAGGTGGCGCGTGGAGAACTGTTCAGAGTGGGCCAACAACCGGTGTGGCTGTAAAGCA	341
QY	301	GCGTGGTTTGTGAGTGCACAGGTTCAGGCAATGTGTACAGTTCACCTTCTACTGCCAA	360
Db	342	GCGTGGTTTGTGAGTGCACAGGTTCAGGCAATGTGTACAGTTCACCTTCTACTGCCAA	401
QY	361	CCATGCTTAACACTGCGGGGGCCCTGTCACACCGCCACAACAGGCTACTCTGTTCGCGAAGAT	420
Db	402	CCATGCTTAACACTGCGGGGGCCCTGTCACACCGCCACAACAGGCTACTCTGTTCGCGAAGAT	461
QY	421	ACGAGCTGTGGAGCTGCGCTGCGGCTTATGAACATGGGATATGGTCCGTGTCTCG	480

241 TCCGAGGTGGCGCTGAGAACAATCTTTCACCACTGACCACAAACCGCCTGCCTTTAATTA 300

Db 674 TCCAGAGTGGCGCTGGAGAACTGTTACAGCATGGCCGACACCCGCTGTGGCTGAAGCCA 733
QY 301 GGCTGTTTGTGGAGTGGCCAGTCCAAATGTTGACAGATTACCCCTTCTACTAGCCAA 360
Db 734 GGCTGTTTGTGGAGTGGCCAGTCCAAATGTTGACAGATTACCCCTTCTACTAGCCAA 793
QY 361 CCATGCTAGACTGCGGGGCGCTGACCCGACACACAGGCTACTGTCTCCGAGAGAT 420
Db 794 CCATGCTAGACTGCGGGGCGCTGACCCGACACACAGGCTACTGTCTCCGAGAGAT 853
QY 421 ACTGAGTGTGGAGCTGCTGCGGCTTCTATGAACATGGCGATGGCTGCTGTC 480
Db 854 ACTGAGTGTGGAGCTGCTGCGGCTTCTATGAACATGGCGATGGCTGCTGTC 913
QY 481 CCCAGAGACACCTGG 496
Db 914 CCCAGTAATTCCTAG 929

RESULT 10
US-10-112-793-5
Sequence 5, Application US/10112793
Publication No. US20020192729A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 L1 AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-793-5

Query Match 87.6%; Score 486.4; DB 9; Length 1438;
Best Local Similarity 98.8%; Pred. No. 3,9e-140;
Matches 490; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGGGGGCGGGGCGGGGCGGACACGTCGAGCCCGAGTGTGCTGGCGGAGATTC 60
Db 434 CTGGGGGCGGGGCGGGGCGGACACGTCGAGCCCGAGTGTGCTGGCGGAGATTC 493

QY 61 CACAAGAAATTTGGTCTGTTTGTGGAGAGGCTGCCAGCGGGGCACTACTGAAAGCC 120
Db 494 CACAAGAAATTTGGTCTGTTTGTGGAGAGGCTGCCAGCGGGGCACTACTGAAAGCC 553
QY 121 CTTTGACAGAGCCCTGCGGCACTCCACTGCTTGTGTGTCCCAAGACACTTCTTG 180
Db 554 CTTTGACAGAGCCCTGCGGCACTCCACTGCTTGTGTGTCCCAAGACACTTCTTG 613
QY 181 GCGTGGGGAACACCAATTTGAAATGTGCGCGGCGGCGGCTGTGATGAGACAGCC 240
Db 614 GCGTGGGGAACACCAATTTGAAATGTGCGCGGCGGCGGCTGTGATGAGACAGCC 673
QY 241 TCCAGAGTGGCGCTGGAGAACTGTTACAGCACTGGCCGACACCCGCTGTGCTGAAGCA 300
Db 674 TCCAGAGTGGCGCTGGAGAACTGTTACAGCACTGGCCGACACCCGCTGTGCTGAAGCA 733
QY 301 GGCTGTTTGTGGAGTGGCCAGTCCAAATGTTGACAGATTACCCCTTCTACTAGCCAA 360
Db 734 GGCTGTTTGTGGAGTGGCCAGTCCAAATGTTGACAGATTACCCCTTCTACTAGCCAA 793
QY 361 CCATGCTAGACTGCGGGGCGCTGACCCGACACAGGCTACTGTCTCCGAGAGAT 420
Db 794 CCATGCTAGACTGCGGGGCGCTGACCCGACACAGGCTACTGTCTCCGAGAGAT 853
QY 421 ACTGAGTGTGGAGCTGCTGCGGCTTCTATGAACATGGCGATGGCTGCTGCTGC 480
Db 854 ACTGAGTGTGGAGCTGCTGCGGCTTCTATGAACATGGCGATGGCTGCTGCTGC 913
QY 481 CCCAGAGACACCTGG 496
Db 914 CCCAGTAATTCCTAG 929

RESULT 11
US-10-112-193-5
Sequence 5, Application US/10112193
Publication No. US20030004313A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,193
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,069
FILING DATE: 11-Sep-1997
APPLICATION NUMBER: 60/026943
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs


```

1      ZIP: 94080
2
3      COMPUTER READABLE FORM:
4
5      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
6
7      COMPUTER: IBM PC compatible
8
9      OPERATING SYSTEM: PC-DOS/MS-DOS
10
11     SOFTWARE: WinPatIn (Genentech)
12
13     CURRENT APPLICATION DATA:
14
15     APPLICATION NUMBER: US/09/993_234
16
17     FILING DATE: 19-No. US20020146768A1-2001
18
19     CLASSIFICATION: <Unknown>
20
21     PRIOR APPLICATION DATA:
22
23     APPLICATION NUMBER: 08/828,683
24
25     FILING DATE: <Unknown>
26
27     ATTORNEY/AGENT INFORMATION:
28
29     NAME: Marschang, Diane L.
30
31     REGISTRATION NUMBER: 35,600
32
33     REFERENCE/DOCKET NUMBER: P1007P1
34
35     TELECOMMUNICATION INFORMATION:
36
37     TELEPHONE: 415/225-5416
38
39     TELEFAX: 415/952-9881
40
41     TELER: 910/371-7168
42
43     INFORMATION FOR SEQ ID NO: 5:
44
45     SEQUENCE CHARACTERISTICS:
46
47     LENGTH: 1438 base pairs
48
49     TYPE: Nucleic Acid
50
51     STRANDEDNESS: Single
52
53     TOPOLOGY: Linear
54
55     SEQUENCE DESCRIPTION: SEQ ID NO: 5:
56
57     US-09-993-234-5

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	Query Match	87.66	Score 486.4	DB 10	Length 1436
	Best Local Similarity	98.88	Pred. No. 3.9e-140		
	Matches 490	Conservative	0	Mismatches 6	Indels 0
				Gaps	
QY	1	CTGGGGGCCCGGGCCCAAGGGCGGCACTGTATGCCCCAGAGTGTGACTGTGCGGTGACTTC	60		
Db	434	CTGGGGGCCCGGGCCCAAGGGCGGCACTGTATGCCCCAGAGTGTGACTGTGCGGTGACTTC	493		
QY	61	CACAAAGAAGATTGGTCTCTTTTGTTCAGAGAGCTGGCCAGCGGGGCACTACCTGAAGCC	122		
Db	494	CACAAAGAAGATTGGTCTCTTTTGTTCAGAGAGCTGGCCAGCGGGGCACTACCTGAAGCC	553		
QY	121	CGTTGCACAGAGCCCTGGGGCACTCCACCGCTTGTTGTGTCCCAAGACACCTTTTG	180		
Db	554	CGTTGCACAGAGCCCTGGGGCACTCCACCGCTTGTTGTGTCCCAAGACACCTTTTG	613		
QY	181	GCGTGGGGAACCAACATTAATTCTGAATGTCCCGCTGCCAGGCGCTGTGATGACAGGCC	240		
Db	614	GCGTGGGGAACCAACATTAATTCTGAATGTCCCGCTGCCAGGCGCTGTGATGACAGGCC	673		
QY	241	TCCAGGTGGCGCTGGAGAACTGTTCAAGCACTGGCCGACACCCGCTGTGGCTGTAAACCA	300		
Db	674	TCCAGGTGGCGCTGGAGAACTGTTCAAGCACTGGCCGACACCCGCTGTGGCTGTAAACCA	733		
QY	301	GCGTGTGTTGTGGAGATGGCCAGAGTACGCCAATGTGTCAAGCACTTACCCCTTACTGCCAA	360		
Db	734	GCGTGTGTTGTGGAGATGGCCAGAGTACGCCAATGTGTCAAGCACTTACCCCTTACTGCCAA	793		
QY	361	CCATGCTAGACTCGGGGGCCCTGCACCGCCACACAGAGGCTACTCTGTCCCGCAGAGAT	420		
Db	794	CCATGCTAGACTCGGGGGCCCTGCACCGCCACACAGAGGCTACTCTGTGTCCCGCAGAGAT	853		
QY	421	ACTGACTGTGGAGACTGCTGCTGCTCTTATGAAACATGGCGATGGCTGCGTCTCTGC	480		
Db	854	ACTGACTGTGGAGACTGCTGCTGCTCTTATGAAACATGGCGATGGCTGCGTCTCTGC	913		
QY	481	CCCAAGACACCTTGG 496			
Db	914	CCCAAGATTTCTTAG 929			

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1      : Sequence 2 Application US/10081280
2      : Patent No. US20020165157A1
3      :
4      : GENERAL INFORMATION:
5      : APPLICANT: Ashkenazi, Avi J.
6      : TITLE OF INVENTION: Apo-2 Li AND Apo-3 POLYPEPTIDES
7      : NUMBER OF SEQUENCES: 11
8      : CORRESPONDENCE ADDRESS:
9      : ADDRESSEE: Genentech, Inc.
10     : STREET: 460 Point San Bruno Blvd
11     : CITY: South San Francisco
12     : STATE: California
13     : COUNTRY: USA
14     : ZIP: 94080
15     :
16     : COMPUTER READABLE FORM:
17     : MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
18     : COMPUTER: IBM PC compatible
19     : OPERATING SYSTEM: PC-DOS/MS-DOS
20     : SOFTWARE: Winpatin (Genentech)
21     :
22     : CURRENT APPLICATION DATA:
23     : APPLICATION NUMBER: US/10/081,280
24     : FILING DATE: 21-Feb-2002
25     : CLASSIFICATION: <Unknown>
26     :
27     : PRIOR APPLICATION DATA:
28     : APPLICATION NUMBER: US/08/829,270
29     : FILING DATE: 31-Mar-1997
30     :
31     : ATTORNEY/AGENT INFORMATION:
32     : NAME: Marschang, Diane L.
33     : REGISTRATION NUMBER: 35,600
34     : REFERENCE/DOCKET NUMBER: P1007R1
35     : TELECOMMUNICATION INFORMATION:
36     : TELEPHONE: 415/225-5416
37     : TELEFAX: 415/952-9881
38     : TELEX: 910/371-7168
39     :
40     : INFORMATION FOR SEQ ID NO: 2:
41     : SEQUENCE CHARACTERISTICS:
42     : LENGTH: 433 base pairs
43     : TYPE: Nucleic Acid
44     : STRANDEDNESS: Single
45     : TOPOLOGY: Linear
46     :
47     : SEQUENCE DESCRIPTION: SEQ ID NO: 2:
48     : US-10-081-280-2

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Query Match	Similarity	63.28;	Score 350.6;	DB: 9;	Length 433;
Best Local Similarity	96.48;	Pred. No. 1.9e-96;			
Matches 400;	Conservative 0;	Mismatches 11;	Indels 4;	Gaps 4;	
QY	1	CTGGGGGCCCGGGCCACAGGCGGCGCACTGTGTAAGCCACAGGTGTGACTGTGCCGTGACTTC	60		
Db	4	CTGGGGGCCCGGGCCACAGGCGGCGCACTGTGTAAGCCACAGGTGTGACTGTGCCGTGACTTC	63		
QY	61	CACAGAAGATTGGTCTGTCTTTTGTGTCAGAGGCTGCCAGCGGGGC-ACTACTGAAGGC	119		
Db	64	CACAGAAGATTGGTCTGTCTTTTGTGTCAGAGGCTGCCAGCGGGGCACACTGAAGGC	123		
QY	120	CCCTTGCACGGAGGCGCTCTGGGCACTCCACCGCGCTTGTGTGCCCAAGCACTCTTT	179		
Db	124	CCCTTGCACGGAGGCGCTCTGGGCACTCCACCGCGCTTGTGTGCCCAAGCACTCTTT	182		
QY	180	GGCCTGGGAGAACCCACCAATTAATTCGTAATGTGCCGCTGCAGAGGCTGTGATGAGCAGGC	239		
Db	183	GGCCTGGGAGAACCCACCAATTAATTCGTAATGTGCCGCTGCAGAGGCTGTGATGAGCAGGC	242		
QY	240	CTCCGAGGTGGCGCTGGGGAAGTGTTCAGAGTGGCCGACACCGGCTGTGGCTGTAAAGCC	299		
Db	243	CTCCGAGGTGGCGCTGGGGAAGTGTTCAGAGTGGCCGACACCGGCTGTGGCTGTAAAGCA	302		
QY	300	AGGCTGTGTTTGTGAGTACCA-GGTCAACCAATGTGTAGAG-ATTCAACCTTCTACAGC	357		
Db	303	GGGCTGTGTTTGTGAGTGTCCAGGGGTCAACCAATGTGTAGAGTTTCAACCTTCTAATGC	362		
QY	358	CACCATGTGCTTGAATGTGGGGGCTGTGCACGGCCACACAGGCTTACTTGTTCG	412		
Db	363	CACCATGTGCTTGAATGTGGGGGCTGTGCACGGCCACACAGGCTTACTTGTTCG	417		

RESULT 15
US-10-112-793-2

Sequence 2, Application US/10112793
Publication No. US20020192729A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/112,793

FILING DATE: 28-Mar-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/828,683A

FILING DATE: 31-Mar-1997

APPLICATION NUMBER: 08/625328

FILING DATE: 1-Apr-1996

APPLICATION NUMBER: 08/710802

FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1007P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 433 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-112-793-2

Query Match 63.2%; Score 350.6; DB 9; Length 433;
Best Local Similarity 96.4%; Pred. No. 1.9e-98;
Matches 400; Conservative 0; Mismatches 11; Indels 4; Gaps 4;

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DB 4 CTGGGGGCCCCGGGCGGCACTGTAGCCCCAGGTGAGCTGCGCGGTACTTC 63
QY 61 CACAGAGAGATTGCTCTGTTTGTTCAGAGGCTGCCAGCGGGGC-ACCTACTGAAGGC 119
DB 64 CACAGAGAGATTGCTCTGTTTGTTCAGAGGCTGCCAGCGGGGC-ACCTACTGAAGGC 123
QY 120 CCTTGCACGAGCCCTGGGCACTCCACCTGCTGTGTGTCGCCAAGACACTTCTT 179
DB 124 CCTTGCACGAGCCCTGGGCACTCCACCTGCTGTGTGTCGCCAAGACACTTCTT 182
QY 180 GGGCTGGGAGACCAACCAATTTGAATGTGCGCGCTGCCAGGCGCTGTGATGAGCAGGC 239
DB 183 GGGCTGGGAGACCAACCAATTTGAATGTGCGCGCTGCCAGGCGCTGTGATGAGCAGGC 242
QY 240 CTCCAGGTGGGCTGAGAGACTGTTCAACAGTGGCGGACACCCGCTGTGCTTAAGCC 299
DB 243 CTCCAGGTGGGCTGAGAGACTGTTCAACAGTGGCGGACACCCGCTGTGCTTAAGCA 302

QY 300 AGGCTGTTGTGAGTGCCTA-GGTACGCCAATGTGTACAG-TTACCCCTTCTACTGC 357
DB 303 GGGCTGTTGTGAGTGCCTA-GGTACGCCAATGTGTACAG-TTACCCCTTCTACTGC 362
QY 358 CAACCATGCTTACAGTGGGGGCGGCTGCACCGCCACACAGGCTACTGTGTCC 412
DB 363 CAACCATGCTTACAGTGGGGGCGGCTGCACCGCCACACAGGCTACTGTGTCC 417

Search completed: April 6, 2003, 16:30:18
Job time : 128 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 6, 2003, 14:24:03 ; Search time 54 Seconds
(without alignments)
3151.956 Million cell updates/sec

Title: US-09-993-234-9_COPY_146_700

Perfect score: 555
Sequence: 1 CTGGGGGGCCCCGGCCAGGG.....GGCAGATGTCTGCTCCAG 555

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

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5: /cgn2_6/ptodata/1/lna/5A_COMB.seq:*
6: /cgn2_6/ptodata/1/lna/5B_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	555	100.0	1634	4	US-08-928-069-11
3	555	100.0	1634	4	US-08-828-683A-9
4	555	100.0	1783	3	US-08-815-469-1
5	486.4	87.6	1438	4	US-08-928-069-5
6	486.4	87.6	1438	4	US-08-928-683A-5
7	350.6	63.2	433	4	US-08-928-069-2
8	350.6	63.2	433	4	US-08-828-683A-2
9	42.2	7.6	543	4	US-09-513-007-3
10	42.2	7.6	2440	4	US-09-513-007-1
11	37.6	6.8	28804	2	US-08-592-874-1
12	37.6	6.8	28804	2	US-08-592-874-1
13	37.6	6.8	28804	3	US-09-096-942-2
14	37.6	6.8	28804	3	US-09-096-867-2
15	35	6.3	1345	2	US-08-762-308-10
16	35	6.3	1345	1	US-08-592-214A-7
17	35	6.3	1345	3	US-08-659-188-7
18	35	6.3	1345	3	US-08-659-188-7
19	35	6.3	1345	3	US-08-655-227-7
20	35	6.3	1345	3	US-08-655-227-7
21	34.4	6.2	15664	1	US-09-398-326-7
22	34.4	6.2	15664	1	US-09-404-879A-22
23	34.2	6.2	15664	1	US-08-402-282-3
24	34.2	6.2	15664	1	US-08-508-004-3
25	34.2	6.2	15664	1	US-08-402-066-3
26	33.2	6.0	718	1	US-08-402-068-3
27	33.2	6.0	718	4	US-08-918-288-10

28	33.2	6.0	744	4	US-08-918-288-8	Sequence 8, Appl1
29	33.2	6.0	744	4	US-09-282-357-8	Sequence 8, Appl1
30	33	5.9	2240	4	US-09-221-017B-687	Sequence 687, App
31	31	5.6	1691	2	US-08-993-118-8	Sequence 8, Appl1
32	31	5.6	1691	3	US-08-845-528C-8	Sequence 8, Appl1
33	31	5.6	2419	1	US-07-807-043B-7	Sequence 7, Appl1
34	31	5.6	2419	1	US-08-299-849B-7	Sequence 7, Appl1
35	31	5.6	2419	2	US-08-142-368A-7	Sequence 7, Appl1
36	31	5.6	2419	3	US-08-967-727-7	Sequence 7, Appl1
37	31	5.6	2419	4	US-08-037-230C-7	Sequence 7, Appl1
38	31	5.6	2420	1	US-08-465-167A-23	Sequence 23, Appl1
39	31	5.6	2420	4	US-09-056-105-4	Sequence 4, Appl1
40	31	5.6	2420	4	US-08-627-820-23	Sequence 23, Appl1
41	31	5.6	5674	1	US-07-807-043B-8	Sequence 8, Appl1
42	31	5.6	5674	1	US-08-190-411A-1	Sequence 1, Appl1
43	31	5.6	5674	1	US-08-299-849B-8	Sequence 8, Appl1
44	31	5.6	5674	2	US-08-560-024-1	Sequence 1, Appl1
45	31	5.6	5674	2	US-08-142-368A-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-08-815-469-3
Sequence 3, Application US/08815469
Patent No. 6153402

GENERAL INFORMATION:

APPLICANT: Yu, Guo-Liang

APPLICANT: Ni, Jian

APPLICANT: Dixit, Vishva

APPLICANT: Gentz, Reiner L.

APPLICANT: Dillon, Patrick J.

TITLE OF INVENTION: Death Domain Containing Receptors

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., NW, Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/815,469

FILING DATE: HERewith

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: NO. 6153402 yet Assigned

FILING DATE: 06-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/028,711

FILING DATE: 17-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/013,285

FILING DATE: 12-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Steife, Eric K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1254 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: both

Oy	61	CACAGAAATTTGGCTGTTTGGTTTGCAGAGGCTGCCACGCGGGGCACTACGTGAAGCC	120
Db	348	CACAAAGAAATTTGGCTGTTTGGTTTGCAGAGGCTGCCACGCGGGGCACTACGTGAAGCC	407
Oy	121	CCCTGCAGGAGACCCCTGCGGCACTCCACCTGCTGTGTGTCCCAAGACACCTTTG	180
Db	408	CCCTGCAGGAGACCCCTGCGGCACTCCACCTGCTGTGTGTCCCAAGACACCTTTG	467
Oy	181	GGCTGGGGAACCCACCAATTTGAAATGTGCTCCGGCTGCCAGGCTGTGATGACAGGCC	240
Db	468	GGCTGGGGAACCCACCAATTTGAAATGTGCTCCGGCTGCCAGGCTGTGATGACAGGCC	527
Oy	241	TCCCAAGTGGCGCTTGAGAACTGTTTCAGCAGTGGCCCAACACCCGCTTGGCTGAAAGCA	300
Db	528	TCCCAAGTGGCGCTTGAGAACTGTTTCAGCAGTGGCCCAACACCCGCTTGGCTGAAAGCA	587
Oy	301	GGCTGTTGTGTGAGTGGCAGAGGTAGCCATGTGTACAGAGTTACACCTTCTACTGCCAA	360
Db	588	GGCTGTTGTGTGAGTGGCAGAGGTAGCCAAATGTGTACAGAGTTACACCTTCTACTGCCAA	647
Oy	361	CCATGCTAGACTGGGGGGCCCTGCACGCGCACACAGCGCTACTCTGTCCGCAAGAT	420
Db	648	CCATGCTAGACTGGGGGGCCCTGCACGCGCACACAGCGCTACTCTGTCCGCAAGAT	707
Oy	421	ACTGACTGTGGGACCTGCGCTGCTGTATGAAACATGCGCATGGCTGCGCTGTCTGC	480
Db	708	ACTGACTGTGGGACCTGCGCTGCTGTATGAAACATGCGCATGGCTGCGCTGTCTGC	767
Oy	481	CCCAAGAGCACCCCTGGGGAGCTGTCCAGAGAGCGTGTCCGCTGTCTGTGGCTGGAGCAG	540
Db	768	CCCAAGAGCACCCCTGGGGAGCTGTCCAGAGAGCGTGTCCGCTGTCTGTGGCTGGAGCAG	827
Oy	541	ATGTTCTGGGTCCAG	555
Db	828	ATGTTCTGGGTCCAG	842
<p>RESULT 5</p> <p>US-08-928-069-5</p> <p>Sequence 5, Application US/08928069</p> <p>Patent No. 6462176</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Ashkenazi, Avi J.</p> <p>TITLE OF INVENTION: Apo-3 POLYPEPTIDE</p> <p>NUMBER OF SEQUENCES: 15</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Genentech, Inc.</p> <p>STREET: 1 DNA Way</p> <p>CITY: South San Francisco</p> <p>STATE: California</p> <p>COUNTRY: USA</p> <p>ZIP: 94080</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Winpatin (Genentech)</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/928, 069</p> <p>FILING DATE: 11-Sep-1997</p> <p>CLASSIFICATION: 435</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: 60/026943</p> <p>FILING DATE: 09/23/1996</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Marschang, Diane L.</p> <p>REGISTRATION NUMBER: 35,600</p> <p>REFERENCE/DOCKET NUMBER: P1052R1</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 650/225-5416</p> <p>TELEFAX: 650/952-9881</p> <p>INFORMATION FOR SEQ ID NO: 5:</p> <p>SEQUENCE CHARACTERISTICS:</p>			

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; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
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US-08-928-069-5

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Query Match	87.6%;	Score 486.4;	DB 4;	Length 1438;
Best Local Similarity	98.8%;	Pred. No. 2.2e-128;		
Matches 490;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0

QY	1	CTGGGGGGCCCCGGCCAGGGGGGACCTGTGAGCCACAGTGTGACTGTGCCGGGTACTTC	60
Db	434	CTGGGGGGCCCCGGCCAGGGGGGACCTGTGAGCCACAGTGTGACTGTGCCGGGTACTTC	493
QY	61	CACAGAAGATTGGTCTGTGTTTGTGTGACAGAGCTGTCCAGCGGGGACACTACCTTAAGGCC	120
Db	494	CACAGAAGATTGGTCTGTGTTTGTGTGACAGAGCTGTCCAGCGGGGACACTACCTTAAGGCC	555
QY	121	CTTTGCACGAGAGCCCTGCGGCACTCCACCTGCTTGTGTGTGCCCAAGACACCTTCCTG	180
Db	554	CTTTGCACGAGAGCCCTGCGGCACTCCACCTGCTTGTGTGTGCCCAAGACACCTTCCTG	613
QY	181	GCCGTGGGAGAACCAACATAATTCTGAAATGTGATGTCGCCGCTGTCCAGGCGCTGTGATGACAGGCC	240
Db	614	GCCGTGGGAGAACCAACATAATTCTGAAATGTGATGTCGCCGCTGTGATGATGACAGGCC	673
QY	241	TCCCAAGGTGGCGCTGTGAGAACTGTTACAGAGTGGCCGACACCCGCTGTGGCTGTAAAGCA	300
Db	674	TCCCAAGGTGGCGCTGTGAGAACTGTTACAGAGTGGCCGACACCCGCTGTGGCTGTAAAGCA	733
QY	301	GGCTGTGTTTGTGTGAGTGTCCAGAGTACGCCAATGTGTGACAGAGTTACACCTTCTACTGCGAA	360
Db	734	GGCTGTGTTTGTGTGAGTGTCCAGAGTACGCCAATGTGTGACAGAGTTACACCTTCTACTGCGAA	793
QY	361	CCATGCGCTAGACCTGCGGGGGCCCTGCACGGCGACACAGGGCTACTCTGTTCGCCAGAGAT	420
Db	794	CCATGCGCTAGACCTGCGGGGGCCCTGCACGGCGACACAGGGCTACTCTGTTCGCCAGAGAT	853
QY	421	ACTGACTGTGGGACCTGCTGCTGCGCTTGTATGAMCATGAGCGATGGCTGCTGTCCTGC	480
Db	854	ACTGACTGTGGGACCTGCTGCTGCGCTTGTATGAMCATGAGCGATGGCTGCTGTCCTGC	913
QY	481	CCCAACGACACCTGG 496	
Db	914	CCCAACGTAATTCTAG 929	

FILED DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-828-683A-5

Query Match 87.6%; Score 486.4; DB 4; Length 1438;
Best Local Similarity 98.8%; Pred. No. 2.2e-128;
Matches 490; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGGGGGCCCCGGCCGAGGCGGCACTGTAAGCCCAAGTGTGACTGTGCCGGTGACTTC 60
DB 434 CTGGGGGCCCCGGCCGAGGCGGCACTGTAAGCCCAAGTGTGACTGTGCCGGTGACTTC 493
QY 61 CACAAGAGATTGCTGTTGTTTGTTCAGAGGCTGCCAAGCGGGGCACTACCTGAAGGCC 120
DB 494 CACAAGAGATTGCTGTTGTTTGTTCAGAGGCTGCCAAGCGGGGCACTACCTGAAGGCC 553
QY 121 CCTTGACGAGAGCCCTGCGGCACTCCACCTGCTTGTGTGTCGCCAAGACACTTCTTG 180
DB 554 CTTTGACGAGAGCCCTGCGGCACTCCACCTGCTTGTGTGTCGCCAAGACACTTCTTG 613
QY 181 GCCTGGGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATAGCAGGCC 240
DB 614 GCCTGGGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATAGCAGGCC 673
QY 241 TCCCAAGTGGCGCTGAGAGACTGTTTCAGAGTGGCGGACACCGGCTGTGGCTTAAGCCA 300
DB 674 TCCCAAGTGGCGCTGAGAGACTGTTTCAGAGTGGCGGACACCGGCTGTGGCTTAAGCCA 733
QY 301 GCGTGTGTTGTGAGAGTGCAGAGTGCACCAATGTGTGAGCAGTTTACCTTCTACTGCCA 360
DB 734 GCGTGTGTTGTGAGAGTGCAGAGTGCACCAATGTGTGAGCAGTTTACCTTCTACTGCCA 793
QY 361 CCATGCTGTAGACTGGCGGGCCCTGCACCGGCAACAGGCTACTCTGTTCGCCAGAGAT 420
DB 794 CCATGCTGTAGACTGGCGGGCCCTGCACCGGCAACAGGCTACTCTGTTCGCCAGAGAT 853
QY 421 ACTGACTGTGGAGACTGCGCTGCTTCTATGAACATGGGAGGCGTGTGCTCTGC 480
DB 854 ACTGACTGTGGAGACTGCGCTGCTTCTATGAACATGGGAGGCGTGTGCTCTGC 913
QY 481 CCCACGAGCACCCTGG 496
DB 914 CCCACGTAATCTCTAG 929

RESULT 7
US-08-928-069-2
Sequence 2, Application US/08928069
Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-928-069-2

Query Match 63.2%; Score 350.6; DB 4; Length 433;
Best Local Similarity 96.4%; Pred. No. 3.6e-90;
Matches 400; Conservative 0; Mismatches 11; Indels 4; Gaps 4;

QY 1 CTGGGGGCCCCGGCCGAGGCGGCACTGTAAGCCCAAGTGTGACTGTGCCGGTGACTTC 60
DB 4 CTGGGGGCCCCGGCCGAGGCGGCACTGTAAGCCCAAGTGTGACTGTGCCGGTGACTTC 63
QY 61 CACAAGAGATTGCTGTTGTTTGTTCAGAGGCTGCCAAGCGGGGCACTACCTGAAGGCC 119
DB 64 CACAAGAGATTGCTGTTGTTTGTTCAGAGGCTGCCAAGCGGGGCACTACCTGAAGGCC 123
QY 120 CCTTGACGAGAGCCCTGCGGCACTCCACCTGCTTGTGTGTCGCCAAGACACTTCTTG 179
DB 124 CCTTGACGAGAGCCCTGCGGCACTCCACCTGCTTGTGTGTCGCCAAGACACTTCTTG 182
QY 180 GCGTGTGTTGTGAGAGTGCAGAGTGCACCAATGTGTGAGCAGTTTACCTTCTACTGCCA 239
DB 183 GCGTGTGTTGTGAGAGTGCAGAGTGCACCAATGTGTGAGCAGTTTACCTTCTACTGCCA 242
QY 240 CTCCAGGTGGCGCTGAGAGACTGTTTCAGAGTGGCGGACACCGGCTGTGGCTTAAGGCC 299
DB 243 CTCCAGGTGGCGCTGAGAGACTGTTTCAGAGTGGCGGACACCGGCTGTGGCTTAAGGCC 302
QY 300 AGGCTGTGTTGTGAGAGTGCAGAGTGCACCAATGTGTGAGCAGTTTACCTTCTACTGC 357
DB 303 AGGCTGTGTTGTGAGAGTGCAGAGTGCACCAATGTGTGAGCAGTTTACCTTCTACTGC 362
QY 358 CAACCAATGCTAGACTGGCGGGCCCTGCACCGGCAACAGGCTACTCTGTTC 412
DB 363 CAACCAATGCTAGACTGGCGGGCCCTGCACCGGCAACAGGCTACTCTGTTC 417

RESULT 8
US-08-828-683A-2
Sequence 2, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way

```

? APPLICANT: Kehrl, Jr., Marcus
? APPLICANT: Lee, Eun-Kyung
? APPLICANT: Mwang, Simon
? TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
? TITLE OF INVENTION: AND METHODS OF USE
? FILE REFERENCE: 08411-018001
? CURRENT APPLICATION NUMBER: US/09/513,007
? CURRENT FILING DATE: 2000-02-25
? PRIOR APPLICATION NUMBER: 60/112,156
? PRIOR FILING DATE: 1999-02-26
? NUMBER OF SEQ ID NOS: 8
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 3
? LENGTH: 543
? TYPE: DNA
? ORGANISM: Bos taurus
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)...(543)
? US-09-513-007-3

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Query Match	7.68;	Score 42.2;	DB 4;	Length 543;
Best Local Similarity	50.28;	Pred. NO. 0.0058;		
Matches 132; Conservative	0;	Mismatches 128;	Indels 3;	Gaps 1;

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127	CCCTTTCAGGAGGAGGCTTCCGCGACATCCACCTGCTGTGTGTGTGTCGCCCAAGACACCTTTCT	179
Db	124 CCCTTTCAGGAGGAGGCTTCCGCGACATCCACCTGCTGTGTGTGTGTCGCCCAAGACACCTTTCT	182
QY	180 GACCTGGAGAGAACCAACCATATTTCTGAATGTGCCCCGTGTGCAGGCGCTGTGATAGAGAGGC	239
Db	183 GGCCTGGAGAGAACCAACCATATTTCTGAATGTGCCCCGTGTGCAGGCGCTGTGATAGAGAGGC	242
QY	240 CTCCTCAGGTGGCGCTGTGAGAACTGTTTCAGCAGTGTGCGCAGCACCCGCTGTGTGCTGTAAAGCC	299
Db	243 CTCCTCAGGTGGCGCTGTGAGAACTGTTTCAGCAGTGTGCGCAGCACCCGCTGTGTGCTGTAAAGA	302
QY	300 AGGCTGGTTGTGTGAGTGGCA-GGTCAAGCCAAATGTGTGCAGCAG-TTCACCCCTTTACTGC	357
Db	303 GGGCTGGTTGTGTGAGTGGCAAGGCTCAGCCAAATGTGTGCAGCACTTTCACCCCTTTCTAATGC	362
QY	358 CAACCATGCTCAGACTCGGGGGCCCTTCACACCGCACACAGGCTACTCTGTTCCC	412
Db	363 CAACCATGCTCAGACTCGGGGGCCCTTCACACCGCACACAGGCTACTCTGTTCCC	417

RESULT 9
US-09-513-007-3
; Sequence 3, Application US/09513007
; Patent No. 6406907
GENERAL INFORMATION:
APPLICANT: Taylor, J. Michael

RESULT 10
US-09-513-007-1
; Sequence 1, Application US/09513007
; Patent No. 6406907
GENERAL INFORMATION:
APPLICANT: Taylor, J. Michael
APPLICANT: Kehrl, Jr., Marcus
APPLICANT: Lee, Eun-Kyung
APPLICANT: Meangl, Simon
TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 08411-018001
CURRENT APPLICATION NUMBER: US/09/513,007
CURRENT FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 60/122,156
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2440
TYPE: DNA
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: CDS
LOCATION: (294)...(1706)
US-09-513-007-1

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 6, 2003, 13:28:53 ; Search time 236 Seconds

(without alignments)
5296.013 Million cell updates/sec

Title: US-09-993-234-9_COPY_146_700

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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

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16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	100.0	1254	18	AAT89427
2	555	100.0	1254	20	AAK00925
3	555	100.0	1254	21	AAC68777
4	555	100.0	1634	18	AAT91180
5	555	100.0	1634	22	AAH27782
6	555	100.0	1634	22	AAI47186
7	555	100.0	1662	22	AAC91477
8	555	100.0	1662	24	ABK40265
9	555	100.0	1783	18	AAT89426

10	555	100.0	1783	20	AAK00924
11	555	100.0	1783	21	AAC68776
12	555	100.0	1847	19	AAV28700
13	541	97.5	1743	24	ABE64119
14	531	95.7	1250	22	AAH3770
15	486.4	87.6	787	24	AAI47187
16	486.4	87.6	816	24	ABE67258
17	486.4	87.6	1438	18	AAT91179
18	244.2	44.0	1251	19	AAV28701
19	171	30.8	4825	24	AAI47185
20	171	30.8	10797	23	ABK42690
21	60	10.8	60	24	ABN40521
22	49.4	8.9	51	22	AAI26809
23	38	6.8	2130	24	ABK63694
24	37.6	6.8	1036	21	AAV98136
25	37.6	6.8	28804	17	AAH37329
26	37.6	6.8	28804	18	AAH92474
27	37.6	6.8	28804	20	AAV9812
28	37.4	6.8	28804	20	AAV81474
29	36.4	6.7	5870	21	AAV15044
30	36.4	6.6	301	22	AAH79973
31	35.6	6.4	1542	22	AAH85141
32	35	6.3	1342	18	AAH99437
33	35	6.3	1345	19	AAH58307
34	35	6.3	1345	19	AAH58307
35	35	6.3	1345	19	AAH58307
36	35	6.3	1345	19	AAV02763
37	35	6.3	1345	19	AAV06021
38	35	6.3	1345	21	AAH57057
39	35	6.3	1345	21	AAH57057
40	34.8	6.3	1158	21	AAH57057
41	34.8	6.3	2173	11	AAH06289
42	34.8	6.3	2568	11	AAH06289
43	34.8	6.3	4898	22	AAH14891
44	34.8	6.3	4898	24	AAH1824
45	34.8	6.3	4898	24	ABH95825

ALIGNMENTS

RESULT 1	
AAH89427	
ID	AAH89427 standard; cDNA; 1254 BP.
XX	
AC	AAH89427;
XX	
DT	02-MAR-1998 (first entry)
XX	
DE	Death domain containing receptor DR3 cDNA.
XX	
KW	Death domain containing receptor; DR3; human; apoptosis;
KW	Inflammation; NF-kappaB; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	sig_peptide
FT	mat_peptide
FT	
FT	
PN	WO9733904-A1.
XX	
PD	18-SEP-1997.
XX	
PF	17-OCT-1996; 96WO-US16849.
XX	
PR	12-MAR-1996; 96US-0013385.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	(UNMT) UNIV MICHIGAN.
XX	

Death domain conta
Human death domain
Human apoptosis in
Breast cancer rela
Nucleotide sequenc
Human Rheumatoid a
Thyroid cancer rel
Human apoptosis pr
Mouse apoptosis in
Human DR3 gene ass
Genomic sequence #
Human spliced tran
Human SNP oligonuc
Rat sequence diffe
Human differentiat
Sphingomonas genus
Sphingomonas 588 s
Chromosomal fragme
Nucleotide sequenc
Nucleotide sequenc
Human immune/haema
Maize floral meris
Zea mays APL gene.
APETALAI gene from
Maize floral meris
Maize floral meris
cDNA encoding a AP
Zea mays ZAP1 prot
Corn APETALAI (AP)
Human phosphatase
Rat Tumour Necrosi
DNA encoding phosph
Human differential
Gene #2323 used to
Human Tumour Endot

PI. Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
 XX WPI: 1997-470812/43.
 DR P-PSDB; AAW31517.
 XX

Death domain containing receptor polypeptide(s) DR3 and DR3-VI -
 PT for activation of apoptosis and NF-kappaB, antagonists can be used
 PT to treat inflammatory diseases
 XX
 PS
 XX

Claim 6; Page 75-77; 108pp; English.

XX This cDNA clone codes for human death domain containing receptor
 CC DR3 (see AAW31517), a novel member of the tumour necrosis factor
 CC receptor family. It was isolated from a HUVCC cDNA library.
 CC Related death domain containing receptor DR3-VI cDNA (see AAT89426)
 CC has been isolated from a human testis tumour cDNA library. The genes
 CC have also been identified in cDNA libraries of foetal liver,
 CC foetal brain, tonsil and leukocyte. Nucleic acids encoding full-
 CC length or mature DR3, or the extracellular, transmembrane,
 CC intracellular or especially the death domain of DR3, can be used to
 CC produce recombinant polypeptides in transformed host cells. These
 CC polypeptides can be used to treat diseases and disorders associated
 CC with the inhibition of apoptosis. Antagonists can be used to treat
 CC diseases and disorders associated with increased apoptosis and for
 CC treating inflammatory diseases and disorders.
 CC
 XX

Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Query Match 100.0%; Score 555; DB 18; Length 1254;

Best Local Similarity 100.0%; Pred. No. 2.7e-144; Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGGCCCCGGCCAGGCGGCACTGTAAGCCAGGTGTGACTGTCCGGTACTTC 60
 DB 58 CTGGGGGCCCCGGCCAGGCGGCACTGTAAGCCAGGTGTGACTGTCCGGTACTTC 117
 QY 61 CACAAGAGATTGTGTCTTTTGTTCAGAGCTGCCAGCGGGGCACTACTGAAGGCC 120
 DB 118 CACAAGAGATTGTGTCTTTTGTTCAGAGCTGCCAGCGGGGCACTACTGAAGGCC 177
 QY 121 CTTTCACAGGAGCCCTGGCGGCACTCCACTGTTGTGTCCCAAGACACTTCTTG 180
 DB 178 CTTTCACAGGAGCCCTGGCGGCACTCCACTGTTGTGTGTCCCAAGACACTTCTTG 237
 QY 181 GCTTGGGGAACCAACATTAATCTGAATGTGCCCTGCGAGCCCTGTGATGAGAGGCC 240
 DB 238 GCTTGGGGAACCAACATTAATCTGAATGTGCCCTGCGAGCCCTGTGATGAGAGGCC 297
 QY 241 TCCGAGGTGGCGCTGGAGAACTGTTCAGAGTGGCGGACACCCGCTGTGGCTGAAGCCA 300
 DB 298 TCCGAGGTGGCGCTGGAGAACTGTTCAGAGTGGCGGACACCCGCTGTGGCTGAAGCCA 357
 QY 301 GCTTGGTGTGTGAGTGCAGAGTGCAGCAATGTGTGAGAGTTCACCCCTTACTGCCAA 360
 DB 358 GCTTGGTGTGTGAGTGCAGAGTGCAGCAATGTGTGAGAGTTCACCCCTTACTGCCAA 417
 QY 361 CCATGCTAGAGCTGGGGGCGCTGACCGCCACACAGAGCTACTGTGTCCCGCAGAGAT 420
 DB 418 CCATGCTAGAGCTGGGGGCGCTGACCGCCACACAGAGCTACTGTGTCCCGCAGAGAT 477
 QY 421 ACTGACTGTGGAGCTGCTGCTGTGTCTTATGAACATGGCAGTGGCTGTCTTCG 480
 DB 478 ACTGACTGTGGAGCTGCTGCTGTGTCTTATGAACATGGCAGTGGCTGTCTTCG 537
 QY 481 CCCAGAGACACCTGTGGGAGGTGTCCAGAGCGCTGTGCGCGTGTGGGCTGGAGGAG 540
 DB 538 CCCAGAGACACCTGTGGGAGGTGTCCAGAGCGCTGTGCGCGTGTGGGCTGGAGGAG 597
 QY 541 ATGTCTGTGGTCCAG 555
 DB 598 ATGTCTGTGGTCCAG 612

RESULT 2
 AAX00925
 ID AAX00925 standard; cDNA; 1254 BP.
 XX
 AC AAX00925;
 XX
 XX 25-MAR-1999 (first entry)
 DT
 XX
 DE Death domain containing receptor polypeptide (DR3) encoding cDNA.
 XX
 KW Death domain; receptor; DR3-VI; DR3; recombinant; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1254
 FT 1..72 /tag= a
 FT sig_peptide /product= "Death domain containing receptor DR3"
 FT mat_peptide 73..1251 /tag= b
 FT /tag= c
 XX
 PM JP11000170-A.
 XX
 PD 06-JAN-1999.
 XX
 PF 12-MAR-1997; 97JP-0057503.
 XX
 PR 06-FEB-1997; 97US-0037341.
 PR 12-MAR-1996; 96US-0013285.
 PR 17-OCT-1996; 96US-0028711.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (UNMI) UNIT MICHIGAN.
 XX
 DR WPI: 1999-124390/11.
 DR P-PSDB; AAW95538.
 XX
 PT New death domain containing receptor and recombinant vector -
 PT optionally comprising leader sequence
 XX
 PS Claim 6; Fig 3; 50pp; Japanese.
 XX

Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Query Match 100.0%; Score 555; DB 20; Length 1254;

Best Local Similarity 100.0%; Pred. No. 2.7e-144; Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGGCCCCGGCCAGGCGGCACTGTAAGCCAGGTGTGACTGTCCGGTACTTC 60
 DB 58 CTGGGGGCCCCGGCCAGGCGGCACTGTAAGCCAGGTGTGACTGTCCGGTACTTC 117
 QY 61 CACAAGAGATTGTGTCTTTTGTTCAGAGCTGCCAGCGGGGCACTACTGAAGGCC 120
 DB 118 CACAAGAGATTGTGTCTTTTGTTCAGAGCTGCCAGCGGGGCACTACTGAAGGCC 177
 QY 121 CTTTCACAGGAGCCCTGGCGGCACTCCACTGTTGTGTGTCCCAAGACACTTCTTG 180
 DB 178 CTTTCACAGGAGCCCTGGCGGCACTCCACTGTTGTGTGTGTCCCAAGACACTTCTTG 237
 QY 181 GCTTGGGGAACCAACATTAATCTGAATGTGCCCTGCGAGCCCTGTGATGAGAGGCC 240
 DB 598 ATGTCTGTGGTCCAG 612

Db	238	GCCTGGGAGAACCAACCAATTAATTCGATGTGTGCCCGCTGGCCAGGCGTGTATGTAGACAGGCC	297
Qy	241	TCCCAGGTGGCGCTGGAGAACTGTTCAAGCAAGTGGCCGACACCCGCTGTGCTGTAAGCCA	3000
Db	298	TCCCAAGGTGGCGCTGGAGAACTGTTCAAGCAAGTGGCCGACACCCGCTGTGCTGTAAGCCA	3575
Qy	301	GGCTGGTGTGTGGAGTCCAGTCCAGGTCGACCAATGTGTCAAGCAATCAOCCCTCTCACTGCCAA	3600
Db	358	GGCTGGTGTGTGGAGTCCAGGTCGACCAATGTGTCAAGCAATCAOCCCTCTCACTGCCAA	4175
Qy	361	CCATGCTCTAGACTCTGGGGCCCTGCACCGGCACACAGCGCTACTCTGTTCCCGAGAGAT	4200
Db	418	CCATGCTCTAGACTCTGGGGCCCTGCACCGGCACACAGCGCTACTCTGTTCCCGACAGAT	4775
Qy	421	ACTGACTGTGTGGAGCTCTGCTGCTGTGAGTATATGAAATGAGCAATGGCTGCGTGTCTGC	4800
Db	478	ACTGACTGTGTGGAGCTCTGCTGCTGTGAGTATATGAAATGAGCAATGGCTGCGTGTCTGC	5375
Qy	481	CCCAACGACACCCCTGGGGAGCTGTCCAGAGCGCTGTCCGCTGTCTGTGGCTGTGAGGACG	5400
Db	538	CCCAACGACACCCCTGGGGAGCTGTCCAGAGCGCTGTCCGCTGTCTGTGGCTGTGAGGACG	5975
Qy	541	ATGTTCTGGGTCCAG	555
Db	598	ATGTTCTGGGTCCAG	612

CC	XX	PS	Example 2B; Fig 2; 27pp; English.
CC	XX	PT	Treating graft-versus-host disease, cancer, immunodeficiency or an autoimmune disease comprising administering an antibody to Death Domain Containing Receptor proteins and a second therapeutic agent -
CC	XX	DR	P-PSDB; AAB36265.
CC	XX	WI	WIPI: 2000-687263/67.
CC	XX	IY	Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;
CC	XX	PA	(DIXIT/) DIXIT V M.
CC	XX	PA	(GENTZ/) GENTZ R L.
CC	XX	PA	(NIGJ/) NI J.
CC	XX	PA	(YUGG/) YU G.
CC	XX	PA	(UMM-) HUMAN GENOME SCI INC.
CC	XX	PF	21-APR-2000; 2000WO-US10741.
CC	XX	PR	22-APR-1999; 99US-0130488.
CC	XX	PR	28-MAY-1999; 99US-0136741.
CC	XX	PD	02-NOV-2000.
CC	XX	PN	WO200064465-A1.
CC	XX	OS	Homo sapiens.
CC	XX	KW	neurodegenerative disease; angiogenesis; ss.
CC	XX	KW	autoimmune disorder; inflammation; cardiovascular disorder; infection;
CC	XX	RW	Human death domain containing receptor DR3 coding sequence.
CC	XX	D7	20-FEB-2001 (first entry)
CC	XX	ID	AAC68777 standard; CDNA; 1254 BP.
CC	XX	AC	AAC68777;
CC	XX	AC	AAC68777
CC	XX	RESULT 3	
CC	XX	AA	

CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.

XX Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

SQ

[illegible]

FT	/*tag=	b
FT	/*note=	"determined by hydrophathy analysis"
FT	mat_peptide	161..1339
FT	/*tag=	c
XX		
PN	W09737020-A1.	
XX		
PD	09-OCT-1997.	
XX		
PE	31-MAR-1997;	97WO-US05230.
XX		
PR	23-SEP-1996;	96US-0710802.
PR	01-APR-1996;	96US-0625328.
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Ashkenazi AJ;	
XX		
DR	WPI: 1997-503105/46.	
XX		
PT	Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis	
PT	in mammalian cells	
XX		
PS	Example 1; Page 45-46; 70pp; English.	
XX		
CC	CC W26709), designated Apo-3, that stimulates or induces apoptotic	
CC	activity in mammalian cells. It was isolated from a human foetal	
CC	heart cDNA library by screening with probes (see T91183-84) based	
CC	on an EST sequence (GenBank locus W71984) that showed homology to	
CC	the intracellular domain of human TNFR1 and CD95. Amino acid	
CC	residues 1-181 of Apo-3 are identical to another novel apoptosis	
CC	polypeptide, Apo-2LI (see W26708). Nucleic acids encoding Apo-3	
CC	can be used diagnostically for tissue-specific typing and to	
CC	produce recombinant Apo-3 polypeptides, especially the	
CC	extracellular domain (amino acids 1-198) or death domain (amino	
CC	acids 338-417). Apo-3 can be used to induce apoptosis or	
CC	NF-kappa-B or JNK-mediated gene expression for therapeutic	
CC	purposes. Non-human transgenic animals containing cells that	
CC	express Apo-3 nucleic acid, and knockout animals containing	
CC	cells that have an altered Apo-3 gene, can be used in drug	
CC	screening and development.	
XX		
XX	Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;	

QY	361	CCATGCTAGACTCTGGGGCCCTTCCACGGCACACAGGGTACTCTGTCCCGACAGAT	420
Db	506	CCATGCTAGACTCTGGGGCCCTTCCACGGCACACAGGGTACTCTGTCCCGACAGAT	565
QY	421	ACTGACTGTGGGACCTCCTCCCTGGCTTATGAAACATGAGCATGGCTGCTGTCTGC	480
Db	566	ACTGACTGTGGGACCTCCTCCCTGGCTTATGAAACATGAGCATGGCTGCTGTCTGC	625
QY	481	CCCAACAGACACCTCTGGGGAGCTGTCCAGAGCGCTGTCCGCTGTCTGTGGCTGAGGCAG	540
Db	626	CCCAACAGACACCTCTGGGGAGCTGTCCAGAGCGCTGTCCGCTGTCTGTGGCTGAGGCAG	685
QY	541	ATGTCTGGGTCCAG	555
Db	686	ATGTCTGGGTCCAG	700

RESULTS	
AAH27782	
XX	AAH27782 standard; DNA; 1634 BP
XX	
AC	AAH27782;
XX	
DT	15-AUG-2001 (first entry)
XX	

DE human genomic DNA encoding a rheumatoid arthritis associated protein.
XX
KW Rheumatoid arthritis; transmembrane protein; human; ds.
Y

OS Homo sapiens.

Key	Location/Qualifiers
PH	89.1342
PT	/tag= a
PT	/product= "Rheumatoid arthritis associated protein"
PT	

PN	WO200132921-A2.
XX	
PD	10-MAY-2001.
XX	

01-NOV-2000; 2000WO-JP07690.

PR 01-NOV-1999; 99JP-0310805.

PA (SHIO/) SHIOZAWA S.

PI Shiozawa S, Konishi Y;

DR WPI; 2001-308750/32.
DR P-PSDB; AAB97370.

Claim 1, Page 14-18, 21pp; Japanese.

This invention relates to a method of diagnosing chronic rheumatoid arthritis by digesting human genomic DNA with EcoRI and hybridising it with a probe containing a fragment of the present sequence which represents DNA encoding a transmembrane protein. The method is used for the diagnosis of chronic rheumatoid arthritis, and for developing new treatments.

Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Query Match	100.0%;	Score 555;	DB 22;	Length 1634;
Best Local Similarity	100.0%;	Pred. No. 2.9e-144;		
Matches 555;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 CTGGGGCCCCGGCCAGGGCGGCATCTGTAGCCCAAGCTGTGACTGTGCCGTGACTTC 60
 |||||
 Db 146 CTGGGGCCCCGGCCAGGGCGGCATCTGTAGCCCAAGTGTGACTGTGCCGTGACTTC 205


```
QY 61 CACAGAAGATTGGTCTGTTTGTTCAGAGGCTGCCACGGGGGCACTACGTAAGGCC 120
DB 206 CACAGAAGATTGGTCTGTTTGTTCAGAGGCTGCCACGGGGGCACTACGTAAGGCC 265
QY 121 CATTGACGAGGACCGCCGCGGCACTCCACCTGCTGTGTGTCCCAAGACACTCTTGG 180
DB 266 CATTGACGAGGACCGCCGCGGCACTCCACCTGCTGTGTGTCCCAAGACACTCTTGG 325
QY 181 GCCTGGAGAACCAACCATTAATCTGAATGTGCCGCTGCCAGGCTGTGATGAGAGGCC 240
DB 326 GCCTGGAGAACCAACCATTAATCTGAATGTGCCGCTGCCAGGCTGTGATGAGAGGCC 385
QY 241 TCCAGAGTGCGCGCTGGAGAACTGTTCAGAGTGCCGACACCCGCTGTGGCTGTAAAGCA 300
DB 386 TCCAGAGTGCGCGCTGGAGAACTGTTCAGAGTGCCGACACCCGCTGTGGCTGTAAAGCA 445
QY 301 GCGTGGTTTGTGAGAGTCCAGAGTCCAGCAATGTGTACAGCACTTCACCTCTCTACGCA 360
DB 446 GCGTGGTTTGTGAGAGTCCAGAGTCCAGCAATGTGTACAGCACTTCACCTCTCTACGCA 505
QY 361 CCATGCTAGACTGCGGGGCGCTGCACCGCCACACAGGCTACTGTGTCCGAGAGAT 420
DB 506 CCATGCTAGACTGCGGGGCGCTGCACCGCCACACAGGCTACTGTGTCCGAGAGAT 565
QY 421 ACTGACTGTGGAGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 480
DB 566 ACTGACTGTGGAGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 625
QY 481 CCCACAGACACCTGGGGAGAGCTGTCCAGAGCGTGTGCCGCTGTGTGCTGTGAGGAG 540
DB 626 CCCACAGACACCTGGGGAGAGCTGTCCAGAGCGTGTGCCGCTGTGTGCTGTGAGGAG 685
QY 541 ATGTTCTGGGTCCAG 555
DB 686 ATGTTCTGGGTCCAG 700

RESULT 6
ID AAL47186 standard; cDNA; 1634 BP.
AC AAL47186;
DE 22-AUG-2002 (first entry)
XX Human rheumatoid arthritis associated DR3 gene related cDNA #1.
XX Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
KW gene therapy; gene; ss.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 89..1342
FT /tag= a
FT /product= "AA017879"
PN WO200234912-A1.
PD 02-MAY-2002.
XX 24-OCT-2001; 2001WO-JP09313.
XX 24-OCT-2000; 2000JP-0324296.
PR 27-MAR-2001; 2001JP-0090546.
PR 30-MAR-2001; 2001JP-0099990.
XX (NEWI-) NEW IND RES ORG.
PA (SHIO) SHIOZAWA S.
XX Shiozawa S, Konishi Y;
XX
```

```
DR WPI; 2002-417132/44.
DR P-PSDB; AA017879.
PT Genomes, particularly DR3 genomic DNA, participating in rheumatoid
PT arthritis via mutation, useful in evaluating disease onset and its
PT possibility and providing therapy and remedies -
XX Example 1; Page 66-69; 84pp; Japanese.
XX
CC The present invention relates to the human DR3 gene, which is associated
CC with rheumatoid arthritis. Certain mutations in the gene can be linked to
CC the disease. The sequences can be used to evaluate disease onset and its
CC possibility and to provide therapy and remedies. The present sequence is
CC a coding sequence described in the exemplification of the invention.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Query Match 100.0%; Score 555; DB 24; Length 1634;
Best Local Similarity 100.0%; Pred. No. 2,9e-144;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGGCGGGGCGGCGGCGACCTGTAGCCCGAGGTGTGACTGTGCGGTGACTTC 60
DB 146 CTGGGGGCGGGGCGGCGGCGACCTGTAGCCCGAGGTGTGACTGTGCGGTGACTTC 205
QY 61 CACAGAAGATTGGTCTGTTTGTTCAGAGGCTGCCACGGGGGCACTACGTAAGGCC 120
DB 206 CACAGAAGATTGGTCTGTTTGTTCAGAGGCTGCCACGGGGGCACTACGTAAGGCC 265
QY 121 CATTGACGAGGACCGCCGCGGCACTCCACCTGCTGTGTGTCCCAAGACACTCTTGG 180
DB 266 CATTGACGAGGACCGCCGCGGCACTCCACCTGCTGTGTGTCCCAAGACACTCTTGG 325
QY 181 GCCTGGAGAACCAACCATTAATCTGAATGTGCCGCTGCCAGGCTGTGATGAGAGGCC 240
DB 326 GCCTGGAGAACCAACCATTAATCTGAATGTGCCGCTGCCAGGCTGTGATGAGAGGCC 385
QY 241 TCCAGAGTGCGCGCTGGAGAACTGTTCAGAGTGCCGACACCCGCTGTGGCTGTAAAGCA 300
DB 386 TCCAGAGTGCGCGCTGGAGAACTGTTCAGAGTGCCGACACCCGCTGTGGCTGTAAAGCA 445
QY 301 GCGTGGTTTGTGAGAGTCCAGAGTCCAGCAATGTGTACAGCACTTCACCTCTCTACGCA 360
DB 446 GCGTGGTTTGTGAGAGTCCAGAGTCCAGCAATGTGTACAGCACTTCACCTCTCTACGCA 505
QY 361 CCATGCTAGACTGCGGGGCGCTGCACCGCCACACAGGCTACTGTGTCCGAGAGAT 420
DB 506 CCATGCTAGACTGCGGGGCGCTGCACCGCCACACAGGCTACTGTGTCCGAGAGAT 565
QY 421 ACTGACTGTGGAGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 480
DB 566 ACTGACTGTGGAGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 625
QY 481 CCCACAGACACCTGGGGAGAGCTGTCCAGAGCGTGTGCCGCTGTGTGCTGTGAGGAG 540
DB 626 CCCACAGACACCTGGGGAGAGCTGTCCAGAGCGTGTGCCGCTGTGTGCTGTGAGGAG 685
QY 541 ATGTTCTGGGTCCAG 555
DB 686 ATGTTCTGGGTCCAG 700

RESULT 7
ID AAC91477 standard; cDNA; 1662 BP.
AC AAC91477;
DE 21-MAR-2001 (first entry)
XX Human PRO779 cDNA.
XX Human; PRO; antinflammatory; dermatological; antiarthritic;
XX
```

KM antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
 KM antidiabetic; neutrophic; hepatoprotective; hepatotropic; virocidic;
 KM antiallergic; antiaschmatic; immune related disorder;
 KM hepatobiliary disease; autoimmune disease; allergy; ss.
 OS Homo sapiens.
 PN WO200073452-A2.
 PD 07-DEC-2000.
 XX 02-JUN-2000; 2000WO-US15264.
 PF 02-JUN-1999; 99WO-US12252.
 XX 20-JUL-1999; 99US-0144732.
 PR 20-JUL-1999; 99US-0144758.
 PR 28-JUL-1999; 99US-0146222.
 PR 01-SEP-1999; 99WO-US20111.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28634.
 PR 09-DEC-1999; 99US-0170262.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AJ,
 PI Hebert C, Hensel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK,
 PI Wood WT;
 XX WPI: 2001-025253/03.
 DR P-PSDB; AAB50918.
 XX
 PT Thirty three nucleic acids encoding PRO polypeptides which are useful
 PT in the diagnosis and treatment of immune related disorders, e.g.
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 PT thyroiditis and diabetes mellitus -
 XX
 PS Claim 48; Fig 33; 218pp; English.
 XX
 CC The present sequence is one of thirty three nucleic acids encoding PRO
 CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
 CC antagonists are useful for treating and diagnosing immune related
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases
 CC (such as infectious, autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,

CC food hypersensitivity and urticaria), immunological diseases of the
 CC lung (such as eosinophilic pneumonitis, idiopathic pulmonary fibrosis
 CC and hypersensitivity pneumonitis), transplantation associated diseases
 CC including graft rejection and graft-versus-host diseases.
 XX
 SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;
 Query Match 100.0%; Score 555; DB 22; Length 1662;
 Best Local Similarity 100.0%; Pred. No. 2,9e-144;
 Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTGGGGGCCCCGGCCAGGCGGCGACCTGTAGCCCCAGGTGTGACTGTGCCGTGACTTC 60
 DB 160 CTGGGGGCCCCGGCCAGGCGGCGACCTGTAGCCCCAGGTGTGACTGTGCCGTGACTTC 219
 QY 61 CACAAAGATGTGTCTGTGTTTGTGACAGAGCTGCCAGCGGGGCACTACTGAAGCC 120
 DB 220 CACAAGAGATTGTCTGTGTTTGTGACAGAGCTGCCAGCGGGGCACTACTGAAGCC 279
 QY 121 CCTTCACAGGAGCCCTGGCGCACTCCACTCTGTGTGTGCCCAAGACACTTCTTG 180
 DB 280 CTTTCACAGGAGCCCTGGCGCACTCCACTCTGTGTGTGCCCAAGACACTTCTTG 339
 QY 181 GCTTCGGAAGAACCAACATATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGAGGCC 240
 DB 340 GCTTCGGAAGAACCAACATATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGAGGCC 399
 QY 241 TCCCAAGTGGGCTGTGAAGACGTTCACAGATGGCCGACACCCGCTGTGCTGTAAAGCCA 300
 DB 400 TCCCAAGTGGGCTGTGAAGACGTTCACAGATGGCCGACACCCGCTGTGCTGTAAAGCCA 459
 QY 301 GCGTGTGTGTGAGTGCAGAGTGCAGCAATGTGTGCAGAGTTCACCTTGTACTGACCA 360
 DB 460 GCGTGTGTGTGAGTGCAGAGTGCAGCAATGTGTGCAGAGTTCACCTTGTACTGACCA 519
 QY 361 CCATCTAGACACTGGGGGCGCTGCACCGCCACACACAGGCTACTGTGTCCGAGAGAT 420
 DB 520 CCATCTAGACACTGGGGGCGCTGCACCGCCACACACAGGCTACTGTGTCCGAGAGAT 579
 QY 421 ACTGACTGTGGAGACTGCTGCTGCTGCTTATGAAATGAGCGATGGTGGTGTCTTGC 480
 DB 580 ACTGACTGTGGAGACTGCTGCTGCTGCTTATGAAATGAGCGATGGTGGTGTCTTGC 639
 QY 481 CCCACGAGACACTGGGGAGCTGTCCAGAGGCGTGTGCTGTGCTGTGAGAGCAG 540
 DB 640 CCCACGAGACACTGGGGAGCTGTCCAGAGGCGTGTGCTGTGCTGTGAGAGCAG 699
 QY 541 ATGTTCTGGGTCCAG 555
 DB 700 ATGTTCTGGGTCCAG 714
 RESULT 8
 ABR40265
 ID ABR40265 standard; cDNA; 1662 BP.
 XX
 AC ABR40265;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 XX cDNA encoding human PRO779 polypeptide.
 DE Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
 KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;
 KW inflammatory disorder; immune disorder; angiogenic disorder;
 KW gene therapy; cyostatic; neutrophilic; gene; ss.
 OS Homo sapiens.
 XX
 XX WO2000153486-A1.
 PN 26-JUL-2001.
 PD
 XX

CC produce recombinant polypeptides in transformed host cells. These
 CC polypeptides can be used to treat diseases and disorders associated
 CC with the inhibition of apoptosis. Antagonists, such as antibodies
 CC raised against DR3-VI, can be used to treat diseases and disorders
 CC associated with increased apoptosis and for treating inflammatory
 CC diseases and disorders.

XX Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Query Match 100.0%; Score 555; DB 18; Length 1783;

Best Local Similarity 100.0%; Pred. No. 3e-144;

Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CTGGGGGCCCCGGCCAGGCGGCGCACTCGTAGCCCCAGGAGTGTACTGTCCGGTGAATTC 60
DB 288 CTGGGGGCCCCGGCCAGGCGGCGCACTCGTAGCCCCAGGAGTGTACTGTCCGGTGAATTC 347
QY 61 CACAAAGATTTGTCTGTTTGTTCAGAGAGCTGCCAGCGGGGCACTAAGAGGCC 120
DB 348 CACAAAGATTTGTCTGTTTGTTCAGAGAGCTGCCAGCGGGGCACTAAGAGGCC 407
QY 121 CCTTGACGAGAGCCCTGCGGCACTCAGCTGCTGTGTGTGTCGCCAAGACCTTCTTG 180
DB 408 CCTTGACGAGAGCCCTGCGGCACTCAGCTGCTGTGTGTGTCGCCAAGACCTTCTTG 467
QY 181 GCCTGGAGAACCCACCATTAATTCGTATGTGCCCTGCGAGGCCGTGATGAGAGGCC 240
DB 468 GCCTGGAGAACCCACCATTAATTCGTATGTGCCCTGCGAGGCCGTGATGAGAGGCC 527
QY 241 TCCCAAGGTGGCGCTGAGAGACGTTCAGAGTGGCGGACACCGCGCTGTGGCTTAAGCCA 300
DB 528 TCCCAAGGTGGCGCTGAGAGACGTTCAGAGTGGCGGACACCGCGCTGTGGCTTAAGCCA 587
QY 301 GGCTGGTTTGTGAGAGTCCAGAGTCAAGCATGTGTGAGAGTTCACCTTACTAGCCAA 360
DB 588 GGCTGGTTTGTGAGAGTCCAGAGTCAAGCATGTGTGAGAGTTCACCTTACTAGCCAA 647
QY 361 CCATGCTTGAATGTGGGGGCGCTGCACCGCCACACACAGGCTTCTGTTCGCCAGAGAT 420
DB 648 CCATGCTTGAATGTGGGGGCGCTGCACCGCCACACACAGGCTTCTGTTCGCCAGAGAT 707
QY 421 ACTGACTGTGGAGCTGCTGCTGCTTCTATGAACATGGGAGTGGGCTGTGCTCC 480
DB 708 ACTGACTGTGGAGCTGCTGCTGCTTCTATGAACATGGGAGTGGGCTGTGCTCC 767
QY 481 CCCAGAGACACCTTGGGAGAGTGTCCAGAGCGCTGTGCCGTGTGTGGCTGAAGCAG 540
DB 768 CCCAGAGACACCTTGGGAGAGTGTCCAGAGCGCTGTGCCGTGTGTGGCTGAAGCAG 827
QY 541 ATGTTCTGGGTCAG 555
DB 828 ATGTTCTGGGTCAG 842

```

RESULT 10

AAAX00924 standard; cDNA: 1783 BP.

AAAX00924; 25-MAR-1999 (first entry)

XX Death domain containing receptor polypeptide (DR3-VI) encoding cDNA.
 XX Death domain; receptor; DR3-VI; DR3; recombinant; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 198..1484
 FT /tag= a
 FT /product= "Death domain containing receptor DR3-VI"

FT sig_peptide 198..300

FT mat_peptide
 FT 301..1481
 FT /tag= c

JP11000170-A.
 PD 06-JAN-1999.
 PD 12-MAR-1997; 97JP-0057503.
 PR 06-FEB-1997; 97US-0037341.
 PR 12-MAR-1996; 96US-0013285.
 PR 17-OCT-1996; 96US-0028711.

PA (HUMA-) HUMAN GENOME SCI INC.
 (UNMT) UNITE MICHIGAN.

DR WPI, 1999-124390/11.
 DR P-PSDB; AAW95537.

PT New death domain containing receptor and recombinant vector -
 PT optionally comprising leader sequence

PS Claim 2; Fig 1, 2; 50pp; Japanese.

CC The invention provides nucleotide sequences encoding death domain
 CC containing receptor polypeptides DR3-VI and DR3. The DR3-VI cDNA clone
 CC is contained in ATCC depositon No. 97456 and the DR3 cDNA clone is
 CC contained in ATCC depositon No. 97757. Recombinant vectors comprising
 CC the nucleic acid sequences and optionally the leader sequences are
 CC used for the recombinant production of the proteins. The present
 CC sequence represents a cDNA encoding the death domain containing
 CC receptor polypeptide (DR3-VI).

SO Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Query Match 100.0%; Score 555; DB 20; Length 1783;

Best Local Similarity 100.0%; Pred. No. 3e-144;

Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CTGGGGGCCCCGGCCAGGCGGCGCACTCGTAGCCCCAGGAGTGTACTGTCCGGTGAATTC 60
DB 288 CTGGGGGCCCCGGCCAGGCGGCGCACTCGTAGCCCCAGGAGTGTACTGTCCGGTGAATTC 347
QY 61 CACAAAGATTTGTCTGTTTGTTCAGAGAGCTGCCAGCGGGGCACTAAGAGGCC 120
DB 348 CACAAAGATTTGTCTGTTTGTTCAGAGAGCTGCCAGCGGGGCACTAAGAGGCC 407
QY 121 CCTTGACGAGAGCCCTGCGGCACTCAGCTGCTGTGTGTGTCGCCAAGACCTTCTTG 180
DB 408 CCTTGACGAGAGCCCTGCGGCACTCAGCTGCTGTGTGTGTCGCCAAGACCTTCTTG 467
QY 181 GCCTGGAGAACCCACCATTAATTCGTATGTGCCCTGCGAGGCCGTGATGAGAGGCC 240
DB 468 GCCTGGAGAACCCACCATTAATTCGTATGTGCCCTGCGAGGCCGTGATGAGAGGCC 527
QY 241 TCCCAAGGTGGCGCTGAGAGACGTTCAGAGTGGCGGACACCGCGCTGTGGCTTAAGCCA 300
DB 528 TCCCAAGGTGGCGCTGAGAGACGTTCAGAGTGGCGGACACCGCGCTGTGGCTTAAGCCA 587
QY 301 GGCTGGTTTGTGAGAGTGGCAGAGTCAAGCATGTGTGAGAGTTCACCTTACTAGCCAA 360
DB 588 GGCTGGTTTGTGAGAGTGGCAGAGTCAAGCATGTGTGAGAGTTCACCTTACTAGCCAA 647
QY 361 CCATGCTTGAATGTGGGGGCGCTGCACCGCCACACACAGGCTTCTGTTCGCCAGAGAT 420
DB 648 CCATGCTTGAATGTGGGGGCGCTGCACCGCCACACACAGGCTTCTGTTCGCCAGAGAT 707
QY 421 ACTGACTGTGGAGCTGCTGCTGCTTCTATGAACATGGGAGTGGCTGTGCTCC 480
DB 708 ACTGACTGTGGAGCTGCTGCTGCTTCTATGAACATGGGAGTGGCTGTGCTCC 767
QY 481 CCCAGAGACACCTTGGGAGAGTGTCCAGAGCGCTGTGCCGTGTGTGCTGAGAGCAG 540

```

|||||
Db 768 CCCACGACACCCCTGGGAGCTGTCCAGAGCGCTGTGCTGTGGCTGAGGCGAG 827
QY 541 ATGTTCTGGGTCCAG 555
|||||
Db 828 ATGTTCTGGGTCCAG 842
RESULT 11
AAC68776
ID AAC68776 standard; cDNA; 1783 BP.
XX AAC68776:
AC 20-FEB-2001 (first entry)
DT 20-FEB-2001 (first entry)
DE Human death domain containing receptor DR3-VI coding sequence.
XX
XX
KW Human: death domain containing receptor; DR3-VI; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis; ss.
OS Homo sapiens.
XX
XX MO200064465-A1.
PN 02-NOV-2000.
PD 21-APR-2000; 2000MO-US10741.
PF 22-APR-1999; 99US-0130488.
PR 28-MAY-1999; 99US-0136741.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
PA (YUGG/) YU G.
PA (NIJ/) NI J.
PA (GENT/) GENTZ R L.
PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX
XX Yu G, NI J, Gentz RL, Dillon PJ, Dixit VM.
PI WPI: 2000-687263/67.
DR P-PSDB; AAB36264.
XX
PT Treating graft-versus-host disease, cancer, immunodeficiency or an
PT autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent -
XX
XX Example 1; Fig 1; 273pp; English.
PS
XX
CC The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-VI. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune diseases such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.
XX
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;
Query Match 100.0%; Score 555; DB 21; Length 1783;
Best Local Similarity 100.0%; Pred. No. 3e-144;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|||||
Db 348 CACAGAGAGATGTGCTGTGTTTGTGACAGAGGCTGCCAGGGGCGACTTACCTGAAAGCC 407
QY 121 CCTTGACAGAGCCCTGGGCACTCCACCTGCTTGTGTGTCGCCAAGACACCTTTTG 180
Db 408 CCTTGACAGAGCCCTGGGCACTCCACCTGCTTGTGTGTCGCCAAGACACCTTTTG 467
QY 181 GCGTGGGAGAACACCATATATGTAATGTGCCGCTGCCAGGCTGTGATGAGAGGCC 240
Db 468 GCGTGGGAGAACACCATATATGTAATGTGCCGCTGCCAGGCTGTGATGAGAGGCC 527
QY 241 TCCAGAGTGGGCTGGAGAACTGTTACAGCAATGGCCGACACCCGCTGGCTGTAAGCA 300
Db 528 TCCAGAGTGGGCTGGAGAACTGTTACAGCAATGGCCGACACCCGCTGGCTGTAAGCA 587
QY 301 GCGTGGTGGAGTGGCAGGCTGACGCAATGTGTACAGCAATGACCTTGTACGCA 360
Db 588 GCGTGGTGGAGTGGAGAGTGGTTCAGCAATGGCCGACACCCGCTGGCTGTAAGCA 647
QY 361 CCATGCTAGACTCGGGGCCCTGCACCGCCACACAGCGCTACTGTTCCCGAGAGAT 420
Db 648 CCATGCTAGACTCGGGGCCCTGCACCGCCACACAGCGCTACTGTTCCCGAGAGAT 707
QY 421 ACTGACTGTGGGACCTGCTGCTGCTTCTATGAACAATGGCGATGGCTGCTCTGC 480
Db 708 ACTGACTGTGGGACCTGCTGCTGCTTCTATGAACAATGGCGATGGCTGCTCTGC 767
QY 481 CCCAGAGACACCGGGGAGCTGCCAGAGCGCTGCTGCTGCTGCTGAGGCGAG 540
Db 768 CCCAGAGACACCGGGGAGCTGCCAGAGCGCTGCTGCTGCTGCTGAGGCGAG 827
QY 541 ATGTTCTGGGTCCAG 555
|||||
Db 828 ATGTTCTGGGTCCAG 842
RESULT 12
AAV28700
ID AAV28700 standard; cDNA; 1847 BP.
XX
XX AAV28700:
AC 20-AUG-1998 (first entry)
DT 20-AUG-1998 (first entry)
DE Human apoptosis inducing receptor coding sequence.
XX
XX
KW Apoptosis inducing receptor; AIR protein; human; cell death regulator;
KW Type I transmembrane protein; tumour cell death; autoimmune disease;
KW therapy; ss.
XX
XX Homo sapiens.
OS
XX
FH Key location/Qualifiers
FT CDS 236..1489
FT /*tag= a
FT /product= AIR
XX
PN MO9814565-A1.
XX
XX 09-APR-1998.
PD 03-OCT-1997; 97MO-US17876.
PF 04-OCT-1996; 96US-0044456.
PR (TMV) IMMUNEX CORP.
PA Perkins PA;
PI
XX WPI: 1998-240077/21.
DR P-PSDB; AAW57045.
XX
PT DNA encoding apoptosis inducing receptor - which is Type I

transmembrane protein, useful for regulating cell death

Claim 2; Page 28-30; 45pp; English.

This sequence encodes the human apoptosis inducing receptor (AIR) of the CC invention. AIR is a Type I transmembrane protein, soluble forms of which CC can be used to regulate cell death in a therapeutic setting. Soluble AIR CC can also be used in vitro to block apoptosis or AIR-expressing cells, or CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain CC of AIR can be used to develop assays for inhibitors of AIR-induced cell CC death, which is useful to regulate cell death in a therapeutic setting as CC well as in vitro. Agonists of AIR activity can be used to kill tumor CC cells that express AIR, or T cells expressing AIR in autoimmune diseases.

Sequence 1847 BP; 316 A; 605 C; 579 G; 347 T; 0 other;

Query Match 100.0%; Score 555; DB 19; Length 1847;
Best local Similarity 100.0%; Pred. No. 3e-144;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGGCCCCGGGCCCCGAGGCGGCGACTGTAGCCCGAGGTGACTGTGCGGTGACTTC 60
DB 293 CTGGGGGCCCCGGGCCCCGAGGCGGCGACTGTAGCCCGAGGTGACTGTGCGGTGACTTC 352
QY 61 CACAGAAGATTGCTGTTTGTTCAGAGAGCTGCCAGCGGCGGCGACTGACCTGGAAGGCC 120
DB 353 CACAGAAGATTGCTGTTTGTTCAGAGAGCTGCCAGCGGCGGCGACTGACCTGGAAGGCC 412
QY 121 CCTTGACGAGAGCTGCGGCACTCCACTGCTGTGTGTCCGAGACCTTCTTG 180
DB 413 CCTTGACGAGAGCTGCGGCACTCCACTGCTGTGTGTCCGAGACCTTCTTG 472
QY 181 GCCTGGAGAACCATTAATTTGTAATGTCCCGCTGCCAGGCTGTGATGAGCAGGCC 240
DB 473 GCCTGGAGAACCATTAATTTGTAATGTCCCGCTGCCAGGCTGTGATGAGCAGGCC 532
QY 241 TCCGAGTGGCGGTGAGAACTGTTGAGAGTGGCGGAGACCCGCTGCTGTAGCCCA 300
DB 533 TCCGAGTGGCGGTGAGAACTGTTGAGAGTGGCGGAGACCCGCTGCTGTAGCCCA 592
QY 301 GCGTGTGTTGTGGAGTCCAGAGTCAACCATGTGTGAGCAGTTCACTTACTGCCAA 360
DB 593 GCGTGTGTTGTGGAGTCCAGAGTCAACCATGTGTGAGCAGTTCACTTACTGCCAA 652
QY 361 CCATGCTTGAATGCGGGGCGCTGCACCGCCACACAGGCTACTGTTCCGACAGAT 420
DB 653 CCATGCTTGAATGCGGGGCGCTGCACCGCCACACAGGCTACTGTTCCGACAGAT 712
QY 421 ACTGACTGAGGACCTGCTGCTGTATGAAATGAGGAGGAGGCTGCTCTTC 480
DB 713 ACTGACTGAGGACCTGCTGCTGTATGAAATGAGGAGGAGGCTGCTCTTC 772
QY 481 CCCAGAGACCCCTGGGAGAGTGTCCAGAGCGCTGTGCGGTGTGGTGGAGAGCAG 540
DB 773 CCCAGAGACCCCTGGGAGAGTGTCCAGAGCGCTGTGCGGTGTGGTGGAGAGCAG 832
QY 541 ATGTTCTGGGTCCAG 555
DB 833 ATGTTCTGGGTCCAG 847

RESULT 13

ABL64119
ID ABL64119 standard; DNA; 1743 BP.

ABL64119;

15-MAY-2002 (first entry)

Breast cancer related gene sequence SEQ ID NO.2456.

Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumor; cancerous;

cytostatic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;
gene; ds.

Homo sapiens.

WO200194629-A2.

13-DEC-2001.

30-MAY-2001; 2001WO-US10838.

05-JUN-2000; 2000US-209473P.
05-JUN-2000; 2000US-209531P.
18-SEP-2000; 2000US-233133P.
18-SEP-2000; 2000US-233617P.
20-SEP-2000; 2000US-234009P.
20-SEP-2000; 2000US-234034P.
20-SEP-2000; 2000US-234052P.
22-SEP-2000; 2000US-234509P.
22-SEP-2000; 2000US-234567P.
25-SEP-2000; 2000US-234923P.
25-SEP-2000; 2000US-234924P.
25-SEP-2000; 2000US-235077P.
25-SEP-2000; 2000US-235082P.
25-SEP-2000; 2000US-235134P.
25-SEP-2000; 2000US-235280P.
26-SEP-2000; 2000US-235637P.
26-SEP-2000; 2000US-235638P.
27-SEP-2000; 2000US-235711P.
27-SEP-2000; 2000US-235720P.
27-SEP-2000; 2000US-235840P.
27-SEP-2000; 2000US-235863P.
28-SEP-2000; 2000US-236028P.
28-SEP-2000; 2000US-236032P.
28-SEP-2000; 2000US-236033P.
28-SEP-2000; 2000US-236034P.
28-SEP-2000; 2000US-236109P.
28-SEP-2000; 2000US-236111P.
29-SEP-2000; 2000US-236842P.
29-SEP-2000; 2000US-236891P.
02-OCT-2000; 2000US-237172P.
02-OCT-2000; 2000US-237173P.
02-OCT-2000; 2000US-237278P.
02-OCT-2000; 2000US-237294P.
02-OCT-2000; 2000US-237295P.
02-OCT-2000; 2000US-237315P.
03-OCT-2000; 2000US-237425P.
03-OCT-2000; 2000US-237598P.
03-OCT-2000; 2000US-237604P.
03-OCT-2000; 2000US-237606P.
03-OCT-2000; 2000US-237608P.
01-NOV-2000; 2000US-244867P.
01-NOV-2000; 2000US-245084P.

(AVAL-) AVALON PHARM.

Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
Soppet DR, Weaver Z;

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a
chemical agent to be tested for anti-neoplastic activity, and
determining a change in expression of a gene of a signature gene set -

Claim 1; SEQ ID 2456; 44pp; English.

The present invention describes a method (M1) for screening for an
anti-neoplastic agent. The method involves exposing cells to a chemical
agent to be tested for anti-neoplastic activity, determining a change in
expression of at least one gene (I) of a signature gene set, where (1)
comprises a sequence (S) selected from 8447 sequences (given in ABL61664
to ABL70110), or is at least 95% identical to (S), where a change in

CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms' tumour.

XX Sequence 1743 BP; 347 A; 543 C; 549 G; 304 T; 0 other;

Query Match 97.5%; Score 541; DB 24; Length 1743;

Best Local Similarity 99.1%; Pred. No. 2, 3e-140;

Matches 544; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGGGGGCCCCGGCCGACGCTGAGCCGAGGTGTGACGTGTGCGGTGACTTC 60
 DB 126 CTGGGGGCCCCGGCCGACGCTGAGCCGAGGTGTGACGTGTGCGGTGACTTC 185
 QY 61 CACAGAGATGTGCTGTTGTGTGAGAGGCTGCCAGGGGACATCTGGAAGGCC 120
 DB 186 CACAGAGATGTGCTGTTGTGTGAGAGGCTGCCAGGGGACATCTGGAAGGCC 245
 QY 121 CCTTGACAGGAGGCTGCGGCACTCCACTGCTGTGTGTGCCAAGACACTTCTTG 180
 DB 246 CATTGACAGGAGGCTGCGGCACTCCACTGCTGTGTGTGCCAAGACACTTCTTG 305
 QY 181 GCCTGGAGAACACCATTAATTTGTAATGTCCCGCTGCGAGGCTGTGTGAGACAGCC 240
 DB 306 GCCTGGAGAACACCATTAATTTGTAATGTCCCGCTGCGAGGCTGTGTGAGACAGCC 365
 QY 241 TCCAGGTGGCGCTGAGAGACTGTTCAGAGGCGGACACCGGCTGTGCTTAAGCCA 300
 DB 366 TCCAGGTGGCGCTGAGAGACTGTTCAGAGGCGGACACCGGCTGTGCTTAAGCCA 425
 QY 301 GGTGGTTGTGTGAGAGTGCAGTCAATGTGTGAGAGTTCACCTTCTACTGCCAA 360
 DB 426 GGTGGTTGTGTGAGAGTGCAGTCAATGTGTGAGAGTTCACCTTCTACTGCCAA 485
 QY 361 CCATGCTTGTGAGTGGGGGCTGACACCGCCACACAGGCTACTGTGTCCCGAGAGAT 420
 DB 486 CCATGCTTGTGAGTGGGGGCTGACACCGCCACACAGGCTACTGTGTCCCGAGAGAT 545
 QY 421 ACTGACTGTGGAGCTGCTGCTGCTTATGAACATGGCGATGGCTGCTGCTGCTGC 480
 DB 546 ACTGACTGTGGAGCTGCTGCTGCTTATGAACATGGCGATGGCTGCTGCTGCTGC 605
 QY 481 CCCACAGACACCTTGGGAGAGCTGTCCAGAGCGCTGTGCTGTGTGCTGGAGCAG 540
 DB 606 CCCACAGACACCTTGGGAGAGCTGTCCAGAGCGCTGTGCTGTGTGCTGGAGCAG 665
 QY 541 ATGTTCTGG 549
 DB 666 AGTAGGTGG 674

RESULT 14

ID AAF83770 standard; DNA; 1250 BP.

AC AAF83770;

DT 06-AUG-2001 (first entry)

DE Nucleotide sequence of human TR3 gene.

XX TR3: cell proliferation; leukemia; immunosuppressive; cytostatic;
 XX dermatological; antidiabetic; antidiabetic; neuroprotective; candidant;
 KW antithyroid; antinflammatory; antiallergic; T-cell-inhibitor; ds.

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..1250
 FT /tag- a
 FT /transl_except- "(pos:481..482, aa:Asp)"
 FT /note- "this codon has an apparent 1 nucleotide
 FT deletion which alters the reading frame"
 FT /transl_except- "(pos:558..559, aa:Cys)"
 FT /note- "this codon has an apparent 1 nucleotide
 FT deletion which alters the reading frame"
 FT /transl_except- "(pos:638..639, aa:Leu)"
 FT /note- "this codon has an apparent 1 nucleotide
 FT deletion which alters the reading frame"
 FT /transl_except- "(pos:718..719, aa:Met)"
 FT /note- "this codon has an apparent 1 nucleotide
 FT deletion which alters the reading frame"
 FT sig_peptide 1..72
 FT /tag- b
 FT mat_peptide 73..1247
 FT /tag- c
 FT
 PN WO200135995-A2.
 XX
 PD 25-MAY-2001.
 XX
 PE 17-NOV-2000; 2000MO-US31692.
 XX
 PR 19-NOV-1999; 99US-0166583.
 XX
 PA (TITV/) TITTLE T V.
 PA (WEGM/) WEGMANN K W.
 XX
 PI Tittle TV, Wegmann KW;
 XX
 DR WPI; 2001-343711/36.
 DR P-PSDB; AAB84941.
 XX
 PT Composition for treatment of T-cell mediated disease e.g. arthritis,
 PT cancer comprises a biologically active TR3-specific binding agent
 PT especially a monoclonal antibody -
 XX
 PS Disclosure; Page 72; 77pp; English.
 XX
 CC The invention relates to a composition comprising a biologically active
 CC TR3-specific binding agent (I) that binds to TR3 and inhibits the
 CC proliferation of cells expressing TR3. (I) identified by the methods are
 CC useful for treating a subject suspected of having a disease associated
 CC with a proliferation of cells expressing TR3 especially leukemias or
 CC lymphomas or a T-cell mediated disease especially autoimmune diseases
 CC such as myasthenia gravis, systemic lupus erythematosus, rheumatoid
 CC arthritis, diabetes, multiple sclerosis, sarcoidosis, myocarditis,
 CC thyroiditis and tumours. (I) is also useful for treating a subject
 CC suspected of having graft-versus-host disease, rejection of a
 CC transplanted organ such as heart, liver, lung, kidney, pancreas, bowel,
 CC skin or an appendage, or inflammatory diseases, allergies and contact
 CC dermatitis. The present sequence represents the nucleotide sequence of
 CC human TR3 gene.
 CC
 XX
 SQ Sequence 1250 BP; 201 A; 419 C; 406 G; 224 T; 0 other;

Query Match 95.7%; Score 531; DB 22; Length 1250;
 Best Local Similarity 99.6%; Pred. No. 1, 2e-137;
 Matches 553; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 CTGGGGGCCCCGGCCGACGCTGAGCCGAGGTGTGACGTGTGCGGTGACTTC 60
 DB 58 CTGGGGGCCCCGGCCGACGCTGAGCCGAGGTGTGACGTGTGCGGTGACTTC 117
 QY 61 CACAGAGATGTGCTGTTGTGTGAGAGGCTGCCAGGGGACATCTGGAAGGCC 120
 DB 118 CACAGAGATGTGCTGTTGTGTGAGAGGCTGCCAGGGGACATCTGGAAGGCC 177

GenCore version 5.1.4_p5-4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:19:54 ; Search time 444.113 Seconds
(without alignments)
2589.161 Million cell updates/sec

Title: US-09-993-234-6_COPY_339_409
Perfect score: 368
Sequence: 1 MDAYPARMKKEFVRLGLRE.....LGAVYALERMGLDCCVEDL 71

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+pn.model -DEV=xlh
-O/cgcn2.1/USPTO.spool/US0999323/runat.27032003.115456.15362/app.query.fasta_1.2346
-DB=EST -QFMT=fastap -SUFFIX=1st -MINMATCH=0.1 -DOOPCL=0 -LOOPEXT=0
-UNITS=b1cs -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.coi -LIST=45
-DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=plco -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0999323.cgcn.1.1.4749 @runat.27032003.115456.15362 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MAP -LARGEOUTERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estc2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_liv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	368	100.0	510	14	BM695193
2	368	100.0	550	13	BM666370
3	368	100.0	687	10	BE670189
4	361	98.1	618	10	AM074008
5	354	96.2	587	9	A1380959
6	354	96.2	587	9	A1380959
7	351	95.4	289	12	BF655336
8	345	93.8	582	10	AM182875
9	328	89.1	647	14	BM794760
10	325	88.3	544	9	A1380900
11	323	87.8	439	14	BM824360
12	323	87.8	633	10	BB212432
13	316	85.9	274	12	BF552058
14	305	82.9	499	10	BQ027499
15	304	82.6	507	10	AM964958
16	291	79.1	539	12	BF726557
17	289	78.5	537	14	A1266746
18	278	75.5	523	14	W171984
19	272	73.9	681	10	BE563566
20	246.5	67.0	739	9	AA524052
21	225	61.1	292	9	AA088350
22	213	57.9	433	10	AM134494
23	204.5	55.6	605	9	A1913906
24	191	51.9	437	10	AA492480
25	187	50.8	651	13	BM009354
26	169	45.9	348	9	A1703436
27	162	44.8	536	9	AA887388
28	161	43.8	530	10	BE014705
29	161	43.8	619	12	BE334962
30	161	43.8	789	10	BF138948
31	161	43.8	853	13	B1525375
32	154	41.8	506	12	BF118096
33	152	41.3	582	10	AW355430
34	151	41.0	504	13	B1468367
35	151	41.0	556	14	W99099
36	151	41.0	591	14	BM694442
37	151	41.0	620	14	BM767536
38	151	41.0	636	12	BG035257
39	151	41.0	669	14	BM742388
40	151	41.0	739	13	B1520191
41	151	41.0	889	9	AU117362
42	151	41.0	894	14	BO880824
43	151	41.0	923	14	BQ228387
44	151	41.0	1055	13	BM555065
45	151	41.0	1076	14	BM923204

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
BM695193	BM695193	UI-E-COI-aev-1-03-0-UI.r1 UI-E-COI Homo sapiens	BM695193	BM695193.1	GT.19008451	EST.	Homo sapiens human.	1 (bases 1 to 510)	Bonaldo,M.F., Lennon,G. and Soares,M.B.	Normalization and subtraction: two approaches to facilitate gene
BM695193	BM695193	UI-E-COI-aev-1-03-0-UI.r1 UI-E-COI Homo sapiens	BM695193	BM695193.1	GT.19008451	EST.	Homo sapiens human.	1 (bases 1 to 510)	Bonaldo,M.F., Lennon,G. and Soares,M.B.	Normalization and subtraction: two approaches to facilitate gene
BM695193	BM695193	UI-E-COI-aev-1-03-0-UI.r1 UI-E-COI Homo sapiens	BM695193	BM695193.1	GT.19008451	EST.	Homo sapiens human.	1 (bases 1 to 510)	Bonaldo,M.F., Lennon,G. and Soares,M.B.	Normalization and subtraction: two approaches to facilitate gene

JOURNAL
MEDLINE
COMMENT

discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@iue.wiuee.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 Reverse.

FEATURES

Source
1.510
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-CQ1-aev-1-03-0-UI"
/clone_1ib="UI-E-CQ1"
/tissue_type="optic nerve"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-CQ1 is a normalized cDNA library containing the following tissue(s): optic nerve. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCATTAGTG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
BASE COUNT 100 a 152 c 170 g 88 t
ORIGIN
Alignment Scores:
Pred. No.: 1.62e-38 Length: 510
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x BM695193 (1-510)

QY 1 Metaspalavalproalargargtrpyrsgluhphevalargthleuglyleuarglu 20
DB 4 ATGGAGGGGGTCCAGCGGGCGGTGGAAGAGTTCTGCGCACCTGGCGTGGCGAG 63
QY 21 Aaagiullleualavaigluvalleuglyargpheargspglnlntfryglmet 40
DB 64 GCAGAGATCGAAGCGGTGAGATGAGATCGCCCTTCCGAGACAGACAGTACGAGATG 123
QY 41 Leuylsargtpparglncglnlncproalacgylleuglyalavaltyralalaleuglu 60
DB 124 CTCAAGCCCTGCGCGCACAGACGCCGCGGCGCTCGGAGCGCTTACGCGCGCTGAG 183
QY 61 Argmetglyleuaspclgycystalgluaspieu 71
DB 184 CGCATGGGGCTGGACGCGCTGGAGACACTTG 216

RESULT 2
BM66370/c

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BM66370 550 bp mRNA linear EST 27-FEB-2002
UI-E-CQ1-aev-1-03-0-UI.s1 UI-E-CQ1 Homo sapiens cDNA clone
BM66370
BM66370.1 GI:18974007
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 550)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
MEDLINE
COMMENT

97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@iue.wiuee.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-37, >POLY_A\$imple_repeat (matched complement)
Seq primer: M13 Forward
POLYA=Yes.
FEATURES
Source
1.550
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-CQ1-aev-1-03-0-UI"
/clone_1ib="UI-E-CQ1"
/tissue_type="optic nerve"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-CQ1 is a normalized cDNA library containing the following tissue(s): optic nerve. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCATTAGTG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
BASE COUNT 90 a 175 c 156 g 129 t
ORIGIN

Alignment Scores:
Pred. No.: 1.81e-38 Length: 550
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x BM66370 (1-550)

QY 1 Metaspalavalproalaaargatgtrpplysgluphevalargthrleuglyleuargglu 20
|||||
DB 536 ATGAGCGCGGTCCACGCGCGCTTGGAAGAGTCTGTCGCGACGCTGGGGCTGCCGAG 477
QY 21 Alagluillegluualavalgluvalgluileglylarypphaeargaspnglntyrglumet 40
|||||
DB 476 GCAGAGATCGAAGCCGTGGAGGTGGAGATCGCCGCTCCGAGACCAAGATCGAGATG 417
QY 41 Leulysargtrpargnglnglncpialaglyleuglylavaltyralaaleuglu 60
|||||
DB 416 CTCAGACGCTGGCGCAGCAGACGCCGCGGCTCGGAGCCCTTACGCGCCCTGGAG 357
QY 61 Argmetglyleuaspplcysvalgluaspleu 71
|||||
DB 356 CGCATGGGCTGGAGCGCTGCTGGAAGACTTG 324

RESULT 3
BE670189/c 687 bp mRNA linear EST 08-SEP-2000
LOCUS 7e3ic12.x1 NCI-CGAP_Lu24 Homo sapiens CDNA clone IMAGE:3284086 3'
DEFINITION similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN PRECURSOR ; mRNA
sequence.
ACCESSION BE670189 GI:10030730
VERSION BE670189
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 687)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
infelimage.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 466.
FEATURES
source
1..687
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3284086"
/clone_1lb="NCI-CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: lung; Vector: pF73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI-CGAP_Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonoids
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 111 a 215 c 225 g 134 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 2,51e-38 Length: 687
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x BB670189 (1-687)

QY 1 Metaspalavalproalaaargatgtrpplysgluphevalargthrleuglyleuargglu 20
|||||
DB 516 ATGAGCGCGGTCCACGCGCGCTTGGAAGAGTCTGTCGCGACGCTGGGGCTGCCGAG 457
QY 21 Alagluillegluualavalgluvalgluileglylarypphaeargaspnglntyrglumet 40
|||||
DB 456 GCAGAGATCGAAGCCGTGGAGGTGGAGATCGCCGCTCCGAGACCAAGATCGAGATG 397
QY 41 Leulysargtrpargnglnglncpialaglyleuglylavaltyralaaleuglu 60
|||||
DB 396 CTCAGACGCTGGCGCAGCAGACGCCGCGGCTCGGAGCCGTTTACGCGCCCTGGAG 337
QY 61 Argmetglyleuaspplcysvalgluaspleu 71
|||||
DB 336 CGCATGGGCTGGAGCGCTGCTGGAAGACTTG 304

RESULT 4
AM074008/c 618 bp mRNA linear EST 13-OCT-1999
LOCUS xD06c09.x1 NCI-CGAP_GU1 Homo sapiens CDNA clone IMAGE:2575504 3'
DEFINITION similar to TR:000278 000278 LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH
7. [2] TR:000279 ; mRNA sequence.
ACCESSION AM074008
VERSION AM074008
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 618)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 383.
FEATURES
source
1..618
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2575504"
/clone_1lb="NCI-CGAP_GU1"
/tissue_type="2 pooled high-grade transitional cell
tumors"
/lab_host="DH10B"
/note="Organ: genitourinary tract; Vector: pCMV-SPORT6;
Site_1: SalI; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dt. Library constructed by Life
Technologies."
BASE COUNT 110 a 204 c 182 g 120 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 1.8e-37 Length: 618
Score: 361.00 Matches: 70
Percent Similarity: 98.59% Conservative: 0
Best Local Similarity: 98.59% Mismatches: 1
Query Match: 98.10% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x AW074008 (1-618)

QY	1	MetaspAlaValProAlaArgArgTrpLysGluIheValArgTrpLeuGluLeuArgGlu	20
Db	513	ATGNAACGGGCTCCACGGCGCGCTGGAGAGAGTTCGTCCGCACACGCTGGGGCTCGCGAG	455
QY	21	AlaGluIleGluAlaValGluValGluIleGluYArgPheArgAspGlnGlnTrpGluMet	40
Db	453	GCAAGAGATCGAAGCCGTGGAGGTGGAGATGGCCGCTTCCGACACAGCATACGAGATG	394
QY	41	LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGluLysAlaValTyrAlaAlaLeuGlu	60
Db	393	CTCAAGCGCTGGCCCGACACACACCCGCGGGGCTCTCGAGACCGTTACGCGGCCCTGGAG	334
QY	61	ArgMetGlyLeuAspGlyCysValGluAspLeu	71
Db	333	CGCATGGGGCTGGACGGCTGCGTGGAGAACTTG	301

RESULT	5
A138095/c	
LOCUS	A138095
DEFINITION	b18bcl1.x1 NCI-CGAP CL11 Homo sapiens cDNA clone IMAGE:2109120 3'
ACCESSION	Similar to TR:000278 C00278 LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH 7. [2] TR:000279 ; mRNA sequence. A138095

FEATURES
source

BASE COUNT	99 a	192 c	176 g	120 t
ORIGIN				

Alignment Scores:		
Pred. No.:	1.4e-36	Length:
Score:	354.00	Matches:
		587
		69

Percent Similarity:	97.18%	Conservative:	0
Best Local Similarity:	97.18%	Mismatches:	2
Query Match:	96.20%	Indels:	0
DB:	9	Gaps:	0

QY	1	MetspAlaValProAlaArgArTrpLeuIshValArqTrrLeuGlyLeuArgLu	20
Db	515	ATGGACGGCTGCCAACGCCGGCGCTGGAGAAGATTCTGCGCACGCTGGGGCTGGCGGAG	456
QY	21	AlaGluIleGluAlaValGluValIleGlyArpPheArgAspGlnGlnTrpGluMet	40
Db	455	GCAGAGATCGAAGCCGTGGAGGTGGAGATCGCGCGCTTCGAGACACAGCATACGAGATG	356
QY	41	LeuLysArqTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTrpAlaAlaLeuGlu	60
Db	395	CTCAAGCGCTGGCCGACAGACACCGCGGGCGCTTCGGAGCCGTTTACGGCGCCCTGGAG	356

UY	b1	ArgmetGlyLeuaspGlycysValcGluspleu	71
Db	335	CGCATGGGGCTGAACGCCTGCCTGGAAACACTTG	303
RESULT 6			
A1811528/c			
LOCUS	A1811528	623 bp	mRNA linear EST 15-DEC-1999
DEFINITION	tva43h06.x1 NCI CGAP vrl Homo sapiens cDNA clone IMAGE:2262491 3'		
	similar to TR:000278 000278 LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH		
	7 [2] PR:000279 ; mRNA sequence.		
ACCESSION	U014320		

FEATURES
source

BASE COUNT	105 a	188 c	199 g	128 t	3 others
ORIGIN					

Alignment Scores:		
Pred. No.:	1.53e-36	Length: 623
Score:	354.00	Matches: 69

Percent Similarity:	95.77%	Conservative:	1
Best local Similarity:	94.37%	Mismatches:	0
Query Match:	93.75%	Indels:	3
DB:	10	Gaps:	0

BASE COUNT 92 a 174 c 168 g 108 t 2 others
ORIGIN

Alignment Scores:

Pred. No.: 8,32e-33 Length: 544
Score: 325.00 Matches: 65
Percent Similarity: 91.558 Conservative: 0
Best Local Similarity: 91.558 Mismatches: 6
Query Match: 88.328 Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x A1809000 (1-544)

QY 1 Metaspalava[Pro]laa[Arg]trp[lys]glu[ph]e[Val]arg[thr]leu[glu]leu[Arg]lu 20
Db 515 ATGACGCGTCCCGCCAGCGCGCTGNAAGAGTGTGCGGACGCGTGGCGGCGGAG 456
QY 21 Alaglu[ile]glu[Val]glu[Val]glu[ile]glu[Arg]phe[Arg]asp[glu]int[Arg]lu[Met] 40
Db 455 GCAGACATGAGCCCGCTGGAGTGCAGCCGCTTCCGAGACGACGAGTACGAGATG 396
QY 41 Leu[Arg]trp[Arg]ing[ing]in[Pro]la[glu]leu[glu]Val[tyr]ala[ala]leu[glu] 60
Db 395 CTCACGCGTGGCGCCAGCAGCAGCCCGCGGCGCTGCGAGCCGTTTACGCGCGCTGGAG 336
QY 61 Arg[Met]glu[Leu]asp[glu]Cys[Val]glu[Asp]leu 71
Db 335 CGCATGGGCGCTGAGCGGCTGCGTGAAGACTTG 303

RESULT 11
LOCUS BM824360 439 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0095844 S22SNUI6n1 Homo sapiens CDNA clone S22SNUI6n1-85-D08
5', mRNA sequence.
ACCESSION BM824360
VERSION BM824360.1 GI:19180773
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 439)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 85 row: D column: 08
High quality sequence stop: 439.
Location/Qualifiers
1. 439

FEATURES

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S22SNUI6n1-85-D08"
/clone_1ib="S22SNUI6n1"
/sex="F"
/tissue_type="Asclites"
/cell_type="Lymphoblast-like"
/cell_line="SNO-16"
/lab_host="DH10B"
/note="Organ: Stomach; Vector: pT73-Pac; Site_1: EcoRI;
Site_2: NotI; The S22SNUI6 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldi, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested

cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."

BASE COUNT 76 a 148 c 150 g 65 t

Alignment Scores:

Pred. No.: 1.11e-32 Length: 439
Score: 323.00 Matches: 62
Percent Similarity: 90.148 Conservative: 2
Best Local Similarity: 87.328 Mismatches: 7
Query Match: 87.778 Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x BM824360 (1-439)

QY 1 Metaspalava[Pro]laa[Arg]trp[lys]glu[ph]e[Val]arg[thr]leu[glu]leu[Arg]lu 20
Db 194 ATGACGCGTCCCGCCAGCGCGCTGNAAGAGTGTGCGGACGCGTGGCGGCGGAG 253
QY 21 Alaglu[ile]glu[Val]glu[Val]glu[ile]glu[Arg]phe[Arg]asp[glu]int[Arg]lu[Met] 40
Db 254 GCATTAATCGAAGCCCGGAGGTGATGCGCCGCTTACGAGACGACGAGTACGAGATG 313
QY 41 Leu[Arg]trp[Arg]ing[ing]in[Pro]la[glu]leu[glu]Val[tyr]ala[ala]leu[glu] 60
Db 314 CTCACGCGTGGCGCCAGCAGCAGCCCGCGGCGCTGCGAGCCGTTTACGCGCGCTGGAG 373
QY 61 Arg[Met]glu[Leu]asp[glu]Cys[Val]glu[Asp]leu 71
Db 374 CGCATGGGCGCTGAGCGGCTGCGTGAAGACTTG 406

RESULT 12
LOCUS BB212432 633 bp mRNA linear EST 31-AUG-2001
DEFINITION BB212432 RIKEN full-length enriched, 0 day neonate thymus Mus
musculus CDNA clone A430110L2.3', mRNA sequence.
ACCESSION BB212432
VERSION BB212432.2 GI:15410061
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 633)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
, M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
, D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jun 30, 2000 this sequence version replaced gi:887385.
CONTACT: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
, M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagci,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
, S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and

Percent Similarity: 98.468
Best Local Similarity: 93.858
Query Match: 85.87%

Conservative: 3
Matches: 1
Indels: 0
Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x BF552058 (1-274)

QY 1 MetaspalvaIprAlaIarGArGTpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
DB 80 ATGATGCGGTCCAGCAGAGAGTGTGTGCGACGCTGGGGCTGGCGAG 139
QY 21 AlAGluIlleGluAlaValAGluValIlleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
DB 140 GCAAAATTTGAGGCTGTGAGGTGAGATCTGCCCTCCGACACAGCAGTATGAGATG 199
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
DB 200 CTCACACGCTGGCGGACGACGACCTGCGAGCTTGCGGTCCATCTATGCGGCCCTGGAG 259
QY 61 ArgMetClyLeuAsp 65
|||||
DB 260 CGCATGGGCTGGAA 274

RESULT 14

BQ027499/c 499 bp mRNA linear EST 27-MAR-2002
LOCUS UI-H-C00-aqg-a-09-0-UI.s1 NCI-CGAP_Sub9 Homo sapiens cDNA clone
IMAGE:3104895 3', mRNA sequence.

ACCESSION BQ027499
VERSION BQ027499.1 GI:19762778
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 499)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgap@remail.nih.gov

Tissue Procurement: Dr. Jose Mercuende
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/BLM at: <http://image.llnl.gov>
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES Location/Qualifiers

source

1..499
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/db_xref="taxon:9606"
/clone="IMAGE:3104895"
/clone_1lb="NCI-CGAP_Sub9"
/tissue_type="mixed"
/dev_stage="mixed"
/lab_host="DH10B (Life Technologies)"
/note="Vector: p7773-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoR I; Site_2: Not I; tissues:
Cholonic mucosa with Crohns disease, Cholonic mucosa with
ulcerative colitis, Fetal thymus, Cervix, Cervical
adenosquamous carcinoma, Ligament cells, Prostate
carcinoma, Bladder carcinoma, Brain oligodendrocyte;
NCI-CGAP_Sub9 is a substracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p7773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is

located between the Not I site and the (drr)18 tail. The
sequence tags for this library are GGTG, AACG, GGGCC,
GGAG, TAGC, ATGC, AGCA, ATGAC. For additional
information, contact: Bento Soares, bento-soares@uiowa.edu
TAG_LTB-UI-H-C00
TAG_TISSUE-Bladder Carcinoma
TAG_SEQ-AGACA"

BASE COUNT 85 a 155 c 145 g 113 t 1 others

ORIGIN

Alignment Scores:
Pred. No.: 3.18e-30 Length: 499
Score: 305.00 Matches: 60
Percent Similarity: 96.77% Conservative: 0
Best Local Similarity: 96.77% Mismatches: 2
Query Match: 82.88% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x BQ027499 (1-499)

QY 10 LysGluPheValArgThrLeuGlyLeuArgGluAlaGluValGlu 29
|||||

DB 499 AAGGAGTTCGTGCGACGCTGGGGCTGCGGAGCAGATCGAACCCGTGAGGTGAG 440

QY 30 IlleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGlnGlnPro 49
|||||

DB 439 ATGCNCGCTTCGAGACGACAGTACGATGTCATGAGCGCTGGGCCGACGACGCC 380

QY 50 AlAGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetClyLeuAspGlyCysValGlu 69
|||||

DB 379 GCGGGCTCGAGACCGCTTACGGCGCCCTGAGGCGCATGCGGCTGAGCGGCTGTGAA 320

QY 70 Aspleu 71
|||||

DB 319 GACTTG 314

RESULT 15

AW964958 507 bp mRNA linear EST 01-JUN-2000
LOCUS EST376926 MAGE resequences, MAGH Homo sapiens cDNA, mRNA sequence.

ACCESSION AW964958
VERSION AW964958.1 GI:8154689
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 507)

AUTHORS Hegde,P., Qi,R., Abernathy,R., Dharap,S., Gaspard,R., Gay,C., Holt
I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.

Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)

COMMENT Contact: John Quackenbush
The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528

Fax: 301 838 0208
Email: johnq@tigr.org

Plate: 207

Seq primer: Forward.

FEATURES Location/Qualifiers

source

1..507
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="MAGE resequences, MAGH"
/note="Vector: pBluescriptSKm"

BASE COUNT 85 a 155 c 156 g 111 t

ORIGIN

Alignment Scores:

4.4e-30 Length: 507

Score: 304.00
 Percent Similarity: 94.038
 Best Local Similarity: 89.554
 Query Match: 82.614
 DB: 10
 Matches: 60
 Conservative: 3
 Mismatches: 4
 Indels: 0
 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x MW964958 (1-507)

QY 5 ProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluLeu 24
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 Db 505 CCAGCCCGGCGATGAAGAAGTTCGTGCGACGCTGGGCTGGCGAGCAAGATCAAA 446
 |||||
 QY 25 AlaValGluValGluLeuLeuArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrp 44
 |||||
 Db 445 CCCGTGAAGGTGAGATCGCGCTCCCGACAGCAGTACGATGCTCAAGCGCTGG 386
 |||||
 QY 45 ArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeu 64
 |||||
 Db 385 CGCCACAGCAGCAGCCCGGCGCTCGAGCCGTTTACCGCGCTGGAGCGCATGGGCTG 326
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 QY 65 AspGlyCysValGluAspLeu 71
 |||||
 Db 325 GACGCTCGCTGGAGAGACTTG 305
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Search completed: April 6, 2003, 23:25:32
 Job time : 447.113 secs

GenCore version 5.1.4_p5-4578
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OM nucleic - nucleic search, using sw model

Run on: April 6, 2003, 13:30:03 ; Search time 2014 Seconds

(without alignments)
8019.889 Million cell updates/sec

Title: US-09-993-234-9_COPY_146_700

Perfect score: 555
Sequence: 1 CTGGGGGCCCGGCCCGAGG.....GGCAGATGTTCTGGTCCAG 555Scoring table: IDENTITY_MUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pln:*
35: em_hg_rod:*
36: em_hg_mam:*
37: em_hg_vtl:*
38: em_sy:*
39: em_hggo_hum:*
40: em_hggo_mus:*
41: em_hggo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	100.0	1254	6 ARI19657	ARI19657 Sequence
2	555	100.0	1254	9 HSU72763	HSU72763 Human death
3	555	100.0	1254	9 HSU78029	HSU78029 Human apopto
4	555	100.0	1254	9 HSU94501	HSU94501 Human lymph
5	555	100.0	1257	9 HSU94502	HSU94502 Human lymph
6	555	100.0	1634	9 HSU74611	HSU74611 Human Apo-3
7	555	100.0	1662	6 AX055442	AX055442 Sequence
8	555	100.0	1662	6 AX201344	AX201344 Sequence
9	555	100.0	1783	6 ARI19656	ARI19656 Sequence
10	553.4	99.7	1528	9 HSU83587	HSU83587 Human death
11	553.4	99.7	1557	9 HSU95380	HSU95380 Human apopt
12	541	97.5	1143	9 HSU94510	HSU94510 Human lymph
13	541	97.5	1355	9 HSU94503	HSU94503 Human lymph
14	541	97.5	1743	6 AX331947	AX331947 Sequence
15	541	97.5	1743	9 HSN5L1	Y09302 H. sapiens m
16	531	95.7	1250	6 AX150176	AX150176 Sequence
17	512.2	92.3	1669	9 AF026070	AF026070 Homo sapi
18	511	92.1	1763	9 AF026071	AF026071 Homo sapi
19	488	87.9	1087	9 HSU94505	HSU94505 Human lymph
20	486.4	87.6	808	9 HSU75381	HSU75381 Human apopt
21	486.4	87.6	809	9 HSU94512	HSU94512 Human lymph
22	486.4	87.6	816	6 AX335086	AX335086 Sequence
23	486.4	87.6	816	9 HSU83598	HSU83598 Human death
24	485	87.4	1198	9 HSU94504	HSU94504 Human lymph
25	322	58.0	651	9 HSU83599	HSU83599 Human alter
26	319	57.5	1119	9 HSU94509	HSU94509 Human lymph
27	252	45.4	952	9 HSU94506	HSU94506 Human lymph
28	242.6	43.7	1665	10 AF329969	AF329969 Mus muscu
29	206	37.1	1619	10 BC017526	BC017526 Mus muscu
30	171.2	30.8	838	9 HSU94507	HSU94507 Human lymph
31	171	30.8	4811	9 AB051851	AB051851 Homo sapi
32	171	30.8	4825	9 AB051850	AB051850 Homo sapi
33	171	30.8	53982	9 AL158217	AL158217 Human DNA
34	134.8	24.3	665	9 HSU83600	HSU83600 Human death
35	103	18.6	705	9 HSU94508	HSU94508 Human lymph
36	95.4	17.2	196368	2 AL772240	AL772240 Mus muscu
37	90.8	16.4	97483	2 AC118359	AC118359 Rattus no
38	85.4	15.4	281	9 HSU94511	HSU94511 Human lymph
39	57.4	10.3	1581	9 AK094463	AK094463 Homo sapi
40	51.6	9.3	2053	9 AK094468	AK094468 Homo sapi
41	50.2	9.0	125020	9 AF429315	AF429315 Homo sapi
42	44.4	8.0	667	9 HSA329641	AJ329641 Homo sapi
43	44.4	8.0	125020	9 AF429315	AF429315 Homo sapi
44	42.2	7.6	2440	4 BT090937	BT090937 Bos taurus
45	39	7.0	280473	2 AC068823	AC068823 Homo sapi

ALIGNMENTS

RESULT 1
LOCUS ARI19657
DEFINITION Sequence 3 from patent US 6153402.
ACCESSION ARI19657
VERSION ARI19657.1 GI:14102356
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1254)
AUTHORS Yu, G.-L., Ni, J., Gentz, R.L. and Dillon, P.J.
TITLE Death domain-containing receptors
JOURNAL Patent: US 6153402-A 3 28-NOV-2000;
FEATURES Location/Qualifiers

BASE COUNT	201 a	420 c	407 g	226 t	
ORIGIN	1. .1254 /organism="unknown"				
Query Match	100.0%; Score 555; DB 6; Length 1254;				
Best Local Similarity	100.0%; Pred. No. 9,6e-133;				
Matches 555; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
Y	1 CTTGGGGGGCCGGGGCCGAGCGGCGACCTGCTAGCGCCGAGGTGAGCTGTGCGCGTACCTTC 60				
Db	58 CTGGGGGGCCGGGGCCGAGCGGCGACCTGCTAGCGCCGAGGTGAGCTGTGCGCGTACCTTC 117				
Y	61 CACAAAGAAATTGTCCTGTTTGTTCAGAGGCTGCGACGAGGAGCAGTACCTGAAAGGCC 120				
Db	118 CACAAAGAAATTGTCCTGTTTGTTCAGAGGCTGCGACGAGGAGCAGTACCTGAAAGGCC 177				
Y	121 CTTTGACGGAGCCCTGCGGGCAATCCACCTGCTTGTGTGTGCCAGACACCTTCTTG 180				
Db	178 CTTTGACGGAGCCCTGCGGGCAATCCACCTGCTTGTGTGTGCCAGACACCTTCTTG 237				
Y	181 GCCTGGAGAACACCATATTCGATGTGCGCCGCTGCGAGGCCGTGTAGAGAGGCC 240				
Db	238 GCCTGGAGAACACCATATTCGATGTGCGCCGCTGCGAGGCCGTGTATGAGAGGCC 297				
Y	241 TCCCAAGTGGCGCTGGAGAACTGTCAGAGTGGCCGACACCCGCTGTGGCTGAAGCCA 300				
Db	298 TCCCAAGTGGCGCTGGAGAACTGTCAGAGTGGCCGACACCCGCTGTGGCTGAAGCCA 357				
Y	301 GCGTGGTTTGTGAGAGTCCAGGTCAGGCCAATGTGCAGAGTTCAACCTTTACTGCCAA 360				
Db	358 GCGTGGTTTGTGAGAGTCCAGGTCAGGCCAATGTGCAGAGTTCAACCTTTACTGCCAA 417				
Y	361 CCATGCGTAGACTGCGGGGCCCTGACACGCCACACAGCGGTACTGTGTTCCGCGAGAGT 420				
Db	418 CCATGCGTAGACTGCGGGGCCCTGACACGCCACACAGCGGTACTGTGTTCCGCGAGAGT 477				
Y	421 ACTGACTGGGAGACCTGCTGCTGCTGCTTCTATGAACATGGGATGGCTGCTGCTGCG 480				
Db	478 ACTGACTGGGAGACCTGCTGCTGCTGCTTCTATGAACATGGGATGGCTGCTGCTGCG 537				
Y	481 CCCACGAGACACCTGGGAGAGTGTCCAGAGCGCTGTGCGGCTGTGTGGCTGGAGGCGAG 540				
Db	538 CCCACGAGACACCTGGGAGAGTGTCCAGAGCGCTGTGCGGCTGTGTGGCTGGAGGCGAG 597				
Y	541 ATGTCTGGGCTCCAG 555				
Db	598 ATGTCTGGGCTCCAG 612				
RESULT 2					
HSU72763	LOCUS				
DEFINITION	Human death receptor 3 (DR3) mRNA, complete cds.				
ACCESSION	U72763				
VERSION	U72763.1 GI:1669511				
KEYWORDS					
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1254)				
TITLE	Chinnaiyan,A.M., O'Rourke,K., Yu,G.-L., Lyons,R.H., Garg,M., Duan,D.R., Xing,L., Gentz,R., Ni,J. and Dixit,V.M., Signal transduction by DR3, a death domain-containing receptor related to TNFR-1 and CD95 Science 274 (5289), 990-992 (1996)				
JOURNAL	MEDLINE				
PUBMED	97081063				
REFERENCE	2 (bases 1 to 1254)				
AUTHORS	Chinnaiyan,A.M., O'Rourke,K., Yu,G.-L., Lyons,R.H., Garg,M., Duan,R., Xing,L., Gentz,R., Ni,J. and Dixit,V.M.				
TITLE	Direct Submission				

JOURNAL
Submitted (20-Sep-1996) Pathology, University of Michigan Medical
School, 1301 Catherine St., Box 0602, Ann Arbor, MI 48109, USA

FEATURES

SOURCE

1. 1254
/organism="Homo sapiens"
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1. 1254
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1. 1254
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/db_xref="gi:1669512"
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LEFCRGPAGHYILKAPCTREBCGNSTCLVCPDPTFLAENHNNSCARQACDBEASQV
ALEBNSAVADIRCCCKPFGMEVBCOVSSPFCPCILDCGALHRRTRILCSRDPD
DLGCLGFGFYEHGSDGVCSPSTLGSCEPERCAANCGMRMTWVLLAGLAVPILLASA
TLTYTTRHCPWHKPLVTADEAGMEALTPPATHTLSPLDASHLLAPDSEKICTVOI
VGNSSMTPGYETQCALCPQVYWSWDQPSRALGPAAALPTLSESPACSPAMMLDQGO
LYEDMAADVAPARWKEFEVFTGLREALEVEAVEELIGRRDQGYEMLKRWRRQQPAGLGA
VYALAEMLGDCGVEDLRSLRQRP"

BASE COUNT

201 a 420 c 407 g 226 t

ORIGIN

Query Match	100.0%;	Score 555;	DB 9;	Length 1254;
Best Local Similarity	100.0%;	Prod. No. 9.6e-133;		
Matches	555;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0
QY	1	CTGGGGGCCCCGGGGCCAGGGGGGCGACTGGTACCCCGAGGTGTGACTGTGCGCGGTGACTTC	60	
Db	58	CTGGGGGCCCCGGGGCCAGGGGGGCGACTGGTACCCCGAGGTGTGACTGTGCGCGGTGACTTC	117	
QY	61	CACAAGAGATTGGCTCTTTTGTGTGCAGAGGCTGCCAGCGGGGCACTACTGAAAGGCC	120	
Db	118	CACAAGAGATTGGCTCTTTTGTGTGCAGAGGCTGCCAGCGGGGCACTACTGAAAGGCC	177	
QY	121	CGTTGCACGGAGCCCTGGGGCAACTCCACTCTGTGTGTGTGCCCAAGACACTTCTTG	180	
Db	178	CGTTGCACGGAGCCCTGGGGCAACTCCACTCTGTGTGTGTGCCCAAGACACTTCTTG	237	
QY	181	GCCGTGGGGAACACCATTAATTCTGATGTGCGCGCTGCCAGGCTGTGTATGAGCAGGCC	240	
Db	238	GCCGTGGGGAACACCATTAATTCTGAAATGTGCGCGCTGCCAGGCTGTGTATGAGCAGGCC	297	
QY	241	TCCCGAGGGGGGCGAGGAGACTGTTCAACAGGGGCGGACACCGCGTGGCGCTGTAAAGCA	300	
Db	298	TCCCGAGGGGGGCGAGGAGACTGTTCAACAGGGGCGGACACCGCGTGGCGCTGTAAAGCA	357	
QY	301	GCGTGGTTTGTGAGTGCAGGTCAAGCCAAATGTGTACAGCAAGTTTCAACCCCTTACTAGCCAA	360	
Db	358	GCGTGGTTTGTGAGTGCAGGTCAAGCCAAATGTGTACAGCAAGTTTCAACCCCTTACTAGCCAA	417	
QY	361	CCATGGCCCTAGACTCGGGGGCCCTGTGACCGCCACACAGGCGTACTGTGTTCCCGCAGAGAT	420	
Db	418	CCATGGCCCTAGACTCGGGGGCCCTGTGACCGCCACACAGGCGTACTGTGTTCCCGCAGAGAT	477	
QY	421	ACTGACTGTGGAGACTCGTCTGCTGCGCTTCTATGAACAATGGGATGGGTGGGTGTCCGCGC	480	
Db	478	ACTGACTGTGGAGACTCGTCTGCTGCTGCTTCTATGAACAATGGGATGGGTGGGTGTCCGCGC	537	
QY	481	CCCAAGAGACACCTTGGGGAGCTGTCCAGAGGCGCTGTGCCGCTGTCTGTGGCTGAGAGCAG	540	
Db	538	CCCAAGAGACACCTTGGGGAGCTGTCCAGAGGCGCTGTGCCGCTGTCTGTGGCTGAGAGCAG	597	
QY	541	ATGTTCCTGGGCTCCAG	555	
Db	598	ATGTTCCTGGGCTCCAG	612	
LOCUS	HSUT8029	1254 bp	mrna	linear PRI 15-JAN-1997
RESULT 3				
LOCUS	HSUT8029	1254 bp	mrna	linear PRI 15-JAN-1997

DEFINITION	Human apoptosis inducing receptor AIR mRNA, complete cds.
ACCESSION	U78029
VERSION	U78029.1 GI:1778763
KEYWORDS	
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE	
AUTHORS	Degli-Esposti, M.A., Din, W.S., Cosman, D., Smith, C.A. and Goodwin, R.G.
TITLE	AIR, A Novel Member of the TNF Receptor Family, Is a Strong Inducer of Apoptosis
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1254)
AUTHORS	Degli-Esposti, M.A. and Goodwin, R.G.
TITLE	Direct Submission
JOURNAL	Submitted (12-NOV-1996) Biochemistry, Immunex Corporation, 51 University St., Seattle, WA 98101, USA
FEATURES	
source	Location/Qualifiers 1..1254
CDS	/organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="1" /map="1pter" /cell_type="peripheral blood T-cells" 1..1254 /codon_start=1 /product="apoptosis inducing receptor AIR" /protein_id="AAB0918.1" /db_xref="GI:1778764" /translation="MEORPRGCAVAALALLVLGARAAGSTRSPDCAGADFHKIGLEFCRGPAGHYLAKPCTEPGNGSTLCVCFODPLAENHNHNSPCACQADBOASOVALENCSAVADPRGCRGKRFWEQVSOCSVSSPEPYRCDLDCGALHNHTYLLCSRPTDCGCLRCPEFHEDGCSCTSPSTIGSPREKCAVCSKRNQFWOYLVLADGLVPLLLCATLTYTTHCPHPRKPLVTADENGMALPPRYTHLSPDSNHTLLAPDSSEKICTVOLVGNSTWGPYEPETDIALCPYVWTSMDQLPSRALGPAAPTLSPSPASPMMLQDPQOLYDMVAIVPARMRKEFVFTLGLREALEAVEVEIGRRDDOYEMLKRWRODPAGLGA VYALENMGIDGCVEDLRSLRQRP"
BASE COUNT	201 a 420 c 407 g 226 t
ORIGIN	
Query Match	100.0%; Score 555; DB 9; Length 1254;
Best Local Similarity	100.0%; Pred. No. 9, 6e-133;
Matches 555; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
1	CTGGGGGGCCGGCCGACGGCGGCACTGTGAGCCGAGGTGAGCTGCGGAGACTTC 60
58	CTGGGGGGCCGGCCGACGGCGGCACTGTGAGCCGAGGTGAGCTGCGGAGACTTC 117
61	CACAAGAAGATTGCTGTTGTTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGC 120
118	CACAAGAAGATTGCTGTTGTTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGC 177
121	CCTTCGACGGAGACCTCTGGGGCACTCCACCTGCTGTGTGTGCCCAAGACACTTCTTG 180
178	CCCTTCGACGGAGACCTCTGGGGCACTCCACCTGCTGTGTGTGCCCAAGACACTTCTTG 237
181	GCTTCGGGGAACCAACCAATAATTCTGAATGTCGCCGCTCCAGAGCCTGTGATGAGCAGGCC 240
238	GCTTCGGGGAACCAACCAATAATTCTGAATGTCGCCGCTCCAGAGCCTGTGATGAGCAGGCC 297
241	TCCACAGTGGCGCTTGAGACACTGTTCAGACAGTGGCCGACACCCGCTGTGGCTGTAGGCCA 300
298	TCCACAGTGGCGCTTGAGACACTGTTCAGACAGTGGCCGACACCCGCTGTGGCTGTAGGCCA 357
301	GAGCTGTTGTGGAGTGCAGAGTCAAGCAATGTGCACACTTCAACCTTCTACTGCGCAA 360
358	GAGCTGTTGTGGAGTGCAGAGTCAAGCAATGTGCACACTTCTACTGCGCAA 417
361	CCATGCTTAGACTGGGGGCGCTGCACCGGCACACACAGGCTACTCTGTGTTCCCGAGAGAT 420
418	CCATGCTTAGACTGGGGGCGCTGCACCGGCACACACAGGCTACTCTGTGTTCCCGAGAGAT 477

QY	421	ACTGACTGTGGAGCTGGCTGGCTGGCTTCTATATGAACATGGGAGTGGCTGTCCTGC	480
Db	478	ACTGACTGTGGAGCTGGCTGGCTGGCTTCTATATGAACATGGGAGTGGCTGTCCTGC	537
QY	481	CCACAGACACCTCTGGGAGCTGTCCAGAGCGCTTGCCTGTCTGTGGCTGAGGACG	540
Db	538	CCACAGACACACCTCTGGGAGCTGTCCAGAGCGCTTGCCTGTCTGTGGCTGAGGACG	597
QY	541	ATGTCTGTGGTCCAG	555
Db	598	ATGTCTGTGGTCCAG	612
RESULT 4			
HSU94501		1254 bp	mRNA
DEFINITION			Human lymphocyte associated receptor of death 1a mRNA, complete cds.
ACCESSION			U94501
VERSION			U94501.1
KEYWORDS			GI:2071948
ORGANISM			Homo sapiens.
SOURCE			Homo sapiens
REFERENCE			Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS			1 (bases 1 to 1254)
TITLE			Screation, G.R., Xu, X.N., Olsen, A.L., Cowper, A.E., Tan, R., McMichael, A.J., and Bell, J.I.
JOURNAL			LARD: a new lymphoid-specific death domain containing receptor
MEDLINE			regulated by alternative pre-mRNA splicing
PUBMED			Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
REFERENCE			9114039
AUTHORS			2 (bases 1 to 1254)
TITLE			Screation, G.R.
JOURNAL			Direct Submission
MEDLINE			Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
PUBMED			Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
REFERENCE			9D0, UK
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			/cell_line="Hela"
			/cell_type="lymphocyte"
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			/function="mediates apoptosis"
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			DLGTCLPGFTFEGHGDCVSCPTSTGSCPERCAACGMRMTWVYVLLAGIAPLLGA
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			VGNSFTPGPETOALCPQYTWMDOLPSRLGPAALPTLSPSPAGSPAMMLOPGPO
			LYDMADVAPARMKKEFVRTGIRAEATLEAVEVEIGRRDDOYIEHLKKMRDQAPAGL
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BASE COUNT			201 a 420 c 407 g 226 t
ORIGIN			
Query Match			100.0%; Score 555; DB 9; Length 1254;
Best Local Similarity			100.0%; Pred. No. 9.6e-133;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	CTGGGGGCCCCGGCCAGGCGGCGCACTGTAGCCCAAGTGTGACTGTGCCGTGACTTTC	60
Db	58	CTGGGGGCCCCGGCCAGGCGGCGCACTGTAGCCCAAGTGTGACTGTGCCGTGACTTTC	117

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OY 61 CACAAAGATTGCTGCTTTTGTTCAGAGGCTGCCAGCGGGGCACTACTGAAAGCC 120
DB 118 CACAAAGATTGCTGCTTTTGTTCAGAGGCTGCCAGCGGGGCACTACTGAAAGCC 177
OY 121 CCTTGACGAGAGCCCTGCGGCACTCCACCTGCTGTGTGTCGCAAGACACTTCTTG 180
DB 178 CCTTGACGAGAGCCCTGCGGCACTCCACCTGCTGTGTGTCGCAAGACACTTCTTG 237
OY 181 GCGTGGAGAACCCACCATTAATTCGATGTGCCGCTGCCAGGCTGTGATGAGCAGGCC 240
DB 238 GCGTGGAGAACCCACCATTAATTCGATGTGCCGCTGCCAGGCTGTGATGAGCAGGCC 297
OY 241 TCCCGAGTGGCGCTGGAGAACTTTAGAGAGTGGCCGACACCGCTGTGCTTAAGCCA 300
DB 298 TCCCGAGTGGCGCTGGAGAACTTTAGAGAGTGGCCGACACCGCTGTGCTTAAGCCA 357
OY 301 GCGTGGTGTGAGAGTGCAGAGTGCAGCCATGTGTGAGAGTTCACCTTTACTGACCA 360
DB 358 GCGTGGTGTGAGAGTGCAGAGTGCAGCCATGTGTGAGAGTTCACCTTTACTGACCA 417
OY 361 CCATGCTTGAAGTGGGGGCGCTGCACCGCCACACAGGCTACTGTTCGCGCAGAGAT 420
DB 418 CCATGCTTGAAGTGGGGGCGCTGCACCGCCACACAGGCTACTGTTCGCGCAGAGAT 477
OY 421 ACTGACTGGAGACCTGCTGCTGCTTCTATGAAACATGGGAGTGGCTGCTGCTTCG 480
DB 478 ACTGACTGGAGACCTGCTGCTGCTTCTATGAAACATGGGAGTGGCTGCTGCTTCG 537
OY 481 CCCAGAGACACCTGCGGAGCTGTCCAGAGCGCTGTGCCCTGTGCTGTGAGAGCAG 540
DB 538 CCCAGAGACACCTGCGGAGCTGTCCAGAGCGCTGTGCCCTGTGCTGTGAGAGCAG 597
OY 541 ATGTTCTGGGTCCAG 555
DB 598 ATGTTCTGGGTCCAG 612

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RESULT 5
HSU94502
LOCUS HSU94502 1257 bp mRNA linear PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 1b mRNA,
alternatively spliced, complete cds.
ACCESSION U94502
VERSION U94502.1 GI:2071950
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1257)
Screaton, G.R., Xu, X.N., Olsen, A.L., Cowper, A.E., Tan, R.,
McMichael, A.J., and Bell, J.I.
AUTHORS LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL 97272273
MEDLINE 9114039
PUBMED 2 (bases 1 to 1257)
Screaton, G.R.
REFERENCE Direct Submission
Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
Source Location/Qualifiers
1..1257
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..1257
/function="mediates apoptosis"
/note="LARD-1b; membrane protein; similar to Fas and
TNF-R1; contains a death domain"

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DCGICLPFEYHGDGCVSCPTSTLSSCEPCAAVCGMFMVVOYLALGVLVLLIGA
TLTVYRHCWPHKPLVPTAADFAGMGLPPPATNHLSPIDSAHTLLAPPDSSEKCTVO
LVGNSMPGYPETGALCROYTWSMDQPSRALGTPAAAPTISPSPACSPAMLOPSP
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/misc_feature
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Accession Number U94501, probably represents alternative
3' splice site"
BASE COUNT 202 a 421 c 408 g 226 t
ORIGIN
Query Match 100.0%; Score 555; DB 9; Length 1257;
Best Local Similarity 100.0%; Pred. No. 9.6e-133;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTGGGGGCCCGGGCCCGAGGCGGCACTGTAAGCCAGGTGTGACTGTGCCGTGACTTC 60
DB 58 CTGGGGGCCCGGGCCCGAGGCGGCACTGTAAGCCAGGTGTGACTGTGCCGTGACTTC 117
OY 61 CACAAAGATTGCTGCTTTTGTTCAGAGGCTGCCAGCGGGGCACTACTGAAAGCC 120
DB 118 CACAAAGATTGCTGCTTTTGTTCAGAGGCTGCCAGCGGGGCACTACTGAAAGCC 177
OY 121 CCTTGACGAGAGCCCTGCGGCACTCCACCTGCTGTGTGTCGCAAGACACTTCTTG 180
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DB 478 ACTGACTGGAGACCTGCTGCTGCTTCTATGAAACATGGGAGTGGCTGCTGCTTCG 537
OY 481 CCCAGAGACACCTGCGGAGCTGTCCAGAGCGCTGTGCCCTGTGCTGTGAGAGCAG 540
DB 538 CCCAGAGACACCTGCGGAGCTGTCCAGAGCGCTGTGCCCTGTGCTGTGAGAGCAG 597
OY 541 ATGTTCTGGGTCCAG 555
DB 598 ATGTTCTGGGTCCAG 612

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RESULT 6
HSU74611
LOCUS HSU74611 1634 bp mRNA linear PRI 02-JAN-1997
DEFINITION Human Apo-3 mRNA, complete cds.
ACCESSION U74611
VERSION U74611.1 GI:1763292
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 1634)
Masters, S.A., Sheridan, J.P., Donahue, C.J., Pittl, R.M., Gray, C.L., Goddard, A.D., Bauer, K.D., and Ashkenazi, A.,
Apo-3, a new member of the tumor necrosis factor receptor family, contains a death domain and activates apoptosis and NF-kB
Curr. Biol. (1996) In press
2 (bases 1 to 1634)
Masters, S.A., Sheridan, J.P., Donahue, C.J., Pittl, R.M., Gray, C.L., Goddard, A.D., Bauer, K.D., and Ashkenazi, A.
Direct Submission
Submitted (15-Oct-1996) Molecular Oncology, Genentech, 460 Pt. San Bruno Blvd., South San Francisco, CA 94080, USA
Location/Qualifiers
1. 1634
/organism="Homo sapiens"
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/chromosome="1"
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/tissue_type="heart"
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89. 1342
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BASE COUNT 300 a 528 c 519 g 287 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9.4e-133;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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121 CCTTGACGAGAGCGCTGCGGCACTCCACTGCTGTGTGTGTCGCCAAGACACTTCTTG 180
266 CCTTGACGAGAGCGCTGCGGCACTCCACTGCTGTGTGTGTCGCCAAGACACTTCTTG 325
181 GCGTGGAGAACCAACCATTAATCTGAATGTGCCGCTGCAGGCTGTGTGAAGAGCC 240
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421 ACTGACTGTGGAGACTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTCTCTGC 480

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OY 541 ATGTTCTGGGTCCAG 555
Db 686 ATGTTCTGGGTCCAG 700
RESULT 7
AX055442 1662 bp DNA linear PAT 13-JAN-2001
LOCUS Sequence 72 from Patent W00073452.
DEFINITION AX055442
ACCESSION AX055442
VERSION AX055442.1 GI:12228713
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 1662)
Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J., Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L., Tumas, D., Watanabe, C.K., and Wood, W.I.
Compositions and methods for the treatment of immune related diseases
Patent: WO 0073452-A 72 07-DEC-2000;
Genentech, Inc. (US)
Location/Qualifiers
1. 1662
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 302 a 540 c 531 g 289 t
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Best Local Similarity 100.0%; Pred. No. 9.4e-133;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTGGGGCCCGGGCCGAGGCGGCACTCGTAGCCGCCAGGTGACGTGCGGAGACTTC 60
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QY 481 CCCACGAGACCCCTGGGAGCTGTCCAGAGCGCTGTCCGCTGTCTGTGCTGGAGCAG 540
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QY 541 ATGTTCTGGGTCCAG 555
DB 700 ATGTTCTGGGTCCAG 714

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LOCUS Sequence 23 from Patent WO0153486.
DEFINITION AX201344
ACCESSION AX201344.1 GI:15391165
VERSION
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1662)
AUTHORS Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L.,
Hillan, K.J., Masters, S.A., Pan, J., Pitti, R.M., Roy, M.A., Smith, V.,
Stone, D.M., Watanabe, C.K., and Wood, W.I.
TITLE Compositions and methods for the treatment of tumour
JOURNAL Patent: WO 0153486-A 23 26-JUL-2001;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
1..1662
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 302 a 540 c 531 g 289 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.4e-133;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGGCCCCGGGCCCCGAGGCGGCACTGTACCCAGGCTGTGACTGTCCGGTACTTC 60
DB 160 CTGGGGGCCCCGGGCCCCGAGGCGGCACTGTACCCAGGCTGTGACTGTCCGGTACTTC 219
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DB 220 CACAGAAGATTGCTCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGTAAGGCC 279
QY 121 CCTTCACAGGAGCCCTGGGCGCACTCCACCTGCTGTGTGTCGCCAAGACACTTCTTG 180
DB 280 CCTTCACAGGAGCCCTGGGCGCACTCCACCTGCTGTGTGTCGCCAAGACACTTCTTG 339
QY 181 GCTTGGGGAACCAACATTAATTCGATGTGCCGCTGCCAGGCTGTGATGAGCAGGCC 240
DB 340 GCTTGGGGAACCAACATTAATTCGATGTGCCGCTGCCAGGCTGTGATGAGCAGGCC 399
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DB 400 TCCCAAGTGGGCGCTGGAGAACTGTTCACAGTGGCCGACACCCGCTGTGGCTGTAAGCCA 459
QY 301 GGCTGTTTGTGGAGTGTCCAGGTTCAGCAATGTGTACAGATTCACCTTCTACTGCCAA 360
DB 460 GGCTGTTTGTGGAGTGTCCAGGTTCAGCAATGTGTACAGATTCACCTTCTACTGCCAA 519
QY 361 CCATGCTAGAGCTGGGGGCGCTGCACCGCCACACAGGCTACTCTGTTCGCGAGAGAT 420
DB 520 CCATGCTAGAGCTGGGGGCGCTGCACCGCCACACAGGCTACTCTGTTCGCGAGAGAT 579
QY 421 ACTGACTGTGGAGCTGCTGCTGCTGCTTATGAACTGCGATGGCTGCTGCTGC 480
DB 580 ACTGACTGTGGAGCTGCTGCTGCTGCTTATGAACTGCGATGGCTGCTGCTGC 639
QY 481 CCCACGAGACCCCTGGGAGCTGTCCAGAGCGCTGTCCGCTGTCTGTGCTGGAGCAG 540

DB 640 CCCACGAGACCCCTGGGAGCTGTCCAGAGCGCTGTCCGCTGTCTGTGCTGGAGCAG 699
QY 541 ATGTTCTGGGTCCAG 555
DB 700 ATGTTCTGGGTCCAG 714

RESULT 9
AR119656 1783 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 1 from patent US 6153402.
DEFINITION AR119656
ACCESSION AR119656
VERSION AR119656.1 GI:14102355
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1783)
AUTHORS Yu, G.-L., Ni, J., Gentz, R.L., and Dillon, P.J.
TITLE Death domain containing receptors
JOURNAL Patent: US 6153402-A 1 28-NOV-2000;
FEATURES
source Location/Qualifiers
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/organism="unknown"
BASE COUNT 330 a 562 c 564 g 327 t
ORIGIN

Query Match 100.0%; Score 555; DB 6; Length 1783;
Best Local Similarity 100.0%; Pred. No. 9.3e-133;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGGCCCCGGGCCCCGAGGCGGCACTGTACCCAGGCTGTGACTGTCCGGTACTTC 60
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QY 61 CACAGAAGATTGCTCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGTAAGGCC 120
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DB 828 ATGTTCTGGGTCCAG 842

RESULT 10

HSU83597	LOCUS	HSU83597	1528 bp	mRNA	linear	PRI 27-JAN-1997
	DEFINITION	Human death domain receptor 3 (DDR3) mRNA, partial cds.				
	ACCESSION	U83597				
	VERSION	U83597.1	GI:1800292			
	KEYWORDS					
	SOURCE	Homo sapiens.				
	ORGANISM	Homo sapiens.				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 1528)					
AUTHORS	Chaudhary, P.M. and Hood, L.E.					
TITLE	Direct Submission					
JOURNAL	Submitted (03-JAN-1997) Molecular Biotechnology, University of Washington, 1705 NE Pacific Street, HSB-K360, Seattle, WA 98195, USA					

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		human EST clone 298913, GenBank Accession Number N71143"
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		PGYETDEALCPQVLTWSMDQLPSRALGPAAAPVLTSPSPASGPAAMLQGPOLVDVND
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QY	61	CACAAAGAATGGTCTGTTTGTTCAGAGGCTGCCAGCGGGCACTACTGTAAAGCC	120	
Db	102	CACAAAGAATGGTCTGTTTGTTCAGAGGCTGCCAGCGGGCACTACTGTAAAGCC	161	
QY	121	CTTTCAGGGAGCCCTGGGGGCACTCCACCTGCTGTGTGTGCCCAAGACACCTTCCTG	180	
Db	162	CTTTCAGGGAGCCCTGGGGGCACTCCACCTGCTGTGTGTGCCCAAGACACCTTCCTG	221	
QY	181	GCGTGGGAAACACCATTAATCTGAATGTGCCCGCTGCCAGGCGCTGTATGAGCAGCC	240	
Db	222	GCGTGGGAAACACCATTAATCTGAATGTGCCCGCTGCCAGGCGCTGTATGAGCAGCC	281	
QY	241	TCCCAAGTGGCGCTGGAAACTGTTCAAGCAGTGCGGACACCCGCTGTGGCTGTAAAGCA	300	
Db	282	TCCCAAGTGGCGCTGGAAACTGTTCAAGCAGTGCGGACACCCGCTGTGGCTGTAAAGCA	341	
QY	301	GCGTGTGTGTGGAATGCCAGGTCAAGCCAAATGTGTACAGCAAGTTCACCTTCTACTAGCCAA	360	
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OY	361	CCATGCCCAAGACTGGGGGGCCCTCACCGCAGCAGACAGGGTACTCTTCCGACAGAT	420
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Db	462	ACTGACTGTGGAGCTGCTGCTCCCTTATGATGACATGGCGATGGCTGCATGCTCTGC	521
OY	481	CCCACGAGCACCCTGGGGAGCTGTCTCCAGAGCGCTGTCTCCCTGTCTTGCTTGAGGACAG	540
Db	522	CCCACGAGCACCCTGGGGAGCTGTCTCCAGAGCGCGTCCCTGTCTTGCTTGAGGACAG	581
OY	541	ATGTTCTGGTCCAG	555
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LOCUS	HSU75380	1557 bp	mRNA	linear	PRI 05-APR-1997
DEFINITION	Human apoptosis-mediating receptor TRAMP mRNA, partial cds.				
ACCESSION	U75380				
VERSION	U75380.1	GI:1695924			
KEYWORDS					
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
AUTHORS	1 (bases 1 to 1557) Bodmer, J.L., Burns, K., Schneider, P., Hofmann, K., Steiner, V., Thome, M., Bornand, T., Hahne, M., Schroter, M., Becker, K., Wilson, A., French, L.E., Browning, J.L., Macdonald, R. and Tschopp, J.				
TITLE	TRAMP, a novel apoptosis-mediating receptor with sequence homology to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95)				
JOURNAL	Immunity 6 (1), 79-88 (1997)				
MEDLINE	97205335				
PUBMED	9052839				
REFERENCE	2 (bases 1 to 1557) Bodmer, J.L., Burns, K., Schneider, P., Hofmann, K., Steiner, V., Thome, M., Bornand, T., Hahne, M., Schroter, M., Wilson, A., French, L.E., Browning, J.L., Macdonald, R. and Tschopp, J.				
AUTHORS	Direct Submission				
TITLE	Submitted (18-OCT-1996) Institute of Biochemistry, University of Lausanne, 155 Chemin des Boveresses, Epalinges, CH 1066, Switzerland				

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Query Match	99.7%	Score 553.4; DB 9; Length 1557;
Best Local Similarity	99.8%;	Pred. No. 2.4e-132;

Matches 554: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 589 ATGTCTGTGGTCCAG 603
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RESULT 12

LOCUS

HSU94510

DEFINITION

Human lymphocyte associated receptor of death 9 mRNA, alternatively

spliced, complete cds.

ACCESSION

U94510

VERSION

U94510.1

KEYWORDS

GT:2071966

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

TITLE

JOURNAL

MEDLINE

FBI

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

FBI

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

FBI

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

FBI

1143 bp mRNA linear PRI 15-MAY-1997

Human lymphocyte associated receptor of death 9 mRNA, alternatively

spliced, complete cds.

U94510

U94510.1

GT:2071966

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

TITLE

JOURNAL

MEDLINE

FBI

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

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AUTHORS

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JOURNAL

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AUTHORS

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JOURNAL

MEDLINE

FBI

REFERENCE

AUTHORS

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Best Local Similarity 100.0%; Pred. No. 4e-129;

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DB 598 A 598
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RESULT 13

LOCUS

HSU94503

DEFINITION

Human lymphocyte associated receptor of death 2 mRNA, alternatively

spliced, complete cds.
ACCESSION U94503.1 GI:2071952
VERSION U94503.1
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 1355)
Screation,G.R., Xu,X.N., Olsen,A.L., Comper,A.E., Tan,R., McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
PUBMED 97272273
REFERENCE 2 (bases 1 to 1355)
AUTHORS Screation,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK
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DB 598 ACTAGGTGG 606

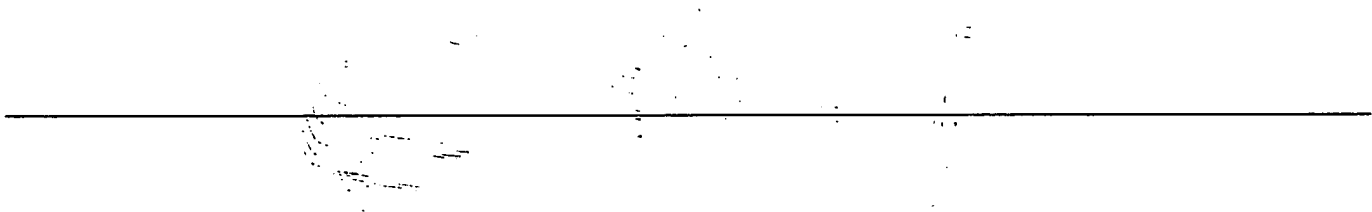
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DEFINITION Sequence 2456 from Patent WO0194629.
ACCESSION AX331947
VERSION AX331947.1 GI:18122581
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ehner,R., Endress,G., Horrigan,S., Soppet,D.R. and Weaver,Z.
TITLE Cancer gene determination and therapeutic screening using signature gene sets
JOURNAL Patent: WO 0194629-A 2456 13-DEC-2001; Avalon Pharmaceuticals (US)
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Best Local Similarity 99.1%; Pred. No. 3.8e-129;
Matches 544; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Page 11

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